



Protein Kinase C beta in the tumor microenvironment promotes mammary tumorigenesis

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Protein kinase C beta (PKC β) expression in breast cancer is associated with a more aggressive tumor phenotype, yet the mechanism for how PKC β is pro-tumorigenic in this disease is still unclear. Interestingly, while it is known that PKC β mediates angiogenesis, immunity, fibroblast function and adipogenesis, all components of the mammary tumor microenvironment (TME), no study to date has investigated whether stromal PKC β is functionally relevant in breast cancer. Herein, we evaluate mouse mammary tumor virus–polyoma middle T-antigen (*MMTV–PyMT*) induced mammary tumorigenesis in the presence and absence of PKC β . We utilize two model systems: one where PKC β is deleted in both the epithelial and stromal compartments to test the global requirement for PKC β on tumor formation, and second, where PKC β is deleted only in the stromal compartment to test its role in the TME. *MMTV–PyMT* mice globally lacking PKC β live longer and develop smaller tumors with decreased proliferation and decreased macrophage infiltration. Similarly, when PKC β is null exclusively in the stroma, *PyMT*-driven B6 cells form smaller tumors with diminished collagen deposition. These experiments reveal for the first time a tumor promoting role for stromal PKC β in *MMTV–PyMT* tumorigenesis. In corroboration with these results, PKC β mRNA (*Prkcb*) is increased in fibroblasts isolated from *MMTV–PyMT* tumors. These data were confirmed in a breast cancer patient cohort. Combined these data suggest the continued investigation of PKC β in the mammary TME is necessary to elucidate how to effectively target this signaling pathway in breast cancer.

Keywords: protein kinase C beta, breast cancer, mammary neoplasms (experimental), tumor microenvironment, stroma, fibroblasts

INTRODUCTION

A role for protein kinase C (PKC) in cancer has been known for over 20 years when it was first recognized that phorbol esters promoted tumor formation through activation of the PKC family [reviewed in Ref. (1)]. There are 10 isozymes that make up this family of serine–threonine kinases, which is classified into three major groups by their mode of activation: the classical PKCs (PKC α , PKC β I, PKC β II, and PKC γ) are calcium and diacylglycerol (DAG) dependent; the novel PKCs (PKC δ , PKC ϵ , PKC η , and PKC θ) are activated by DAG; and the atypical PKCs (PKC ξ and PKC ι) are independent of calcium and DAG. PKC β is comprised of two splice variants, PKC β I and PKC β II, which are from the same gene (*PRKCB*) and differ only in their last 50 amino acids (2, 3). Differential PKC expression has been documented in essentially every histological cancer type including carcinomas (e.g., breast, colorectal), sarcomas (e.g., glioma), lymphomas (e.g., diffuse large B-cell lymphoma), and leukemias (e.g., B-cell chronic

lymphocytic leukemia) [reviewed in Ref. (1, 4)]. Functionally, PKCs mediate various physiological processes such as proliferation, differentiation, apoptosis, cellular motility, and angiogenesis (1, 4).

Relevance for PKC in breast cancer was first reported in 1986 when Borner and colleagues observed that PKC is increased in more aggressive estrogen receptor- α (ER α) negative mammary tumor cells compared to their less aggressive ER α positive counterparts (5). This putative tumor promoting role was supported shortly thereafter by evidence of increased PKC enzymatic activity in breast tumor versus normal patient samples (6, 7). Evaluation of the specific PKC isozymes soon followed and PKC α (8–14), PKC β (as discussed below), PKC δ (15, 16), PKC ϵ (17), and PKC η (18, 19) were all found to have roles in breast cancer progression. Investigation of PKC β , specifically, has revealed that both splice variants (PKC β I and PKC β II) are upregulated in breast tumor versus matched normal patient tissue (20), with cytoplasmic PKC β II

associating with Ki-67 expression and HER2 positivity (21). Functionally, ectopic overexpression of either wild type (WT) or constitutively active PKC β I or PKC β II increases breast cancer cell line growth *in vitro* through upregulation of cyclin D1, while inhibition of kinase activity decreases growth as seen via introduction of dominant negative PKC β I or PKC β II, and through treatment with LY379196, a PKC β selective inhibitor (22). Interestingly, even though PKC β II is associated with increased proliferation and highly aggressive HER2 positive disease, its expression does not correlate with patient survival in this cohort (21). An independent study also observed that PKC β mRNA (*PRKCB*) correlates with increased grade and triple negative (ER α -/PR-/HER2-) disease, but not relapse-free survival (23).

This discrepancy between the *in vitro* breast cancer cell line and patient survival data may be due to PKC β -mediating physiological processes within the breast tumor microenvironment (TME), which could cause the evaluation of PKC β expression in whole tumor tissue, which contains both tumor and stroma, to be misleading. All epithelial-derived tumors (i.e., carcinomas) are surrounded by a complex TME that contains extracellular matrix proteins, endothelial cells, immune cells, and fibroblasts [reviewed in Ref. (24)]. Importantly, PKC β function in non-epithelial cell types has been described in several model systems. Within the endothelial compartment of the TME, PKC β is a well-known downstream effector of vascular endothelial growth factor (VEGF) signaling, which mediates angiogenesis (25–27). PKC β is also involved in immunity through activation of NF- κ B (28–30). Less is known about PKC β specifically in tumor-associated fibroblasts, but it was recently shown that PKC is required for pancreatic cancer-associated fibroblast (CAF) invasiveness (31) as well as resistance to irradiation-induced apoptosis in primary human fibroblasts (32). PKC β is, however, required for extracellular matrix and collagen deposition in rodent models of diabetes (33, 34). The breast TME also includes adipocytes and PKC β null mice have decreased adipose tissue with altered lipid metabolism (35, 36). Combined, these studies suggest important roles for PKC β in the breast TME and the need for further elucidation of PKC β 's roles in this context.

Herein, we utilized PKC β genomic knockout mice (37) to evaluate mammary tumorigenesis through the use of two model systems: one where PKC β is deleted in both the mammary epithelium and the TME, and one where PKC β is deleted only in the TME. We reveal for the first time a requirement for PKC β in *MMTV-PyMT* (mouse mammary tumor virus–polyoma middle T-antigen) induced mammary tumor growth. *MMTV-PyMT* mice lacking PKC β (*Prkcb*^{-/-}) in both epithelial and stromal compartments have increased tumor latency with a decrease in tumor load and tumor volume. Decreased tumorigenesis in the *MMTV-PyMT*; *Prkcb*^{-/-} mice is accompanied by diminished tumor proliferation and macrophage infiltration with angiogenesis seemingly unaffected. To test directly whether PKC β in the TME is functionally relevant, we orthotopically injected B6 *PyMT* tumor cells, a *MMTV-PyMT* derived mammary tumor cell line (38), into WT or *Prkcb*^{-/-} mice. Tumor volume was similarly decreased in the absence of stromal PKC β confirming a requirement for PKC β in the mammary cancer TME. Most interestingly, collagen deposition was decreased in this model. Moreover, fibroblasts

isolated from the *MMTV-PyMT* tumors have dramatically higher levels of PKC β II mRNA (*Prkcb*) than WT mammary fibroblasts, whereas *Prkcb* in the *MMTV-PyMT* epithelium is decreased. This increase in stromal *PRKCB* is similarly observed in a human breast cancer patient cohort confirming the translational relevance of PKC β function in the TME.

MATERIALS AND METHODS

ANIMAL BREEDING

All animal procedures were approved by The Ohio State University Institutional Animal Care and Use Committee (protocol #2007A0120-R2). *Prkcb*^{-/-} (35, 37) and *MMTV-PyMT* mice (39) have been described. The *MMTV-PyMT* mice were bred into C57Bl/6 at least 10 generations. *MMTV-PyMT* males were bred with *Prkcb*^{+/-} females to generate *MMTV-PyMT*; *Prkcb*^{+/-} male progeny. The *MMTV-PyMT*; *Prkcb*^{+/-} males were then bred with *Prkcb*^{+/-} females to generate *MMTV-PyMT*; *Prkcb*^{+/+} and *MMTV-PyMT*; *Prkcb*^{-/-} female progeny for tumor analysis. Genotyping primers and conditions for the *Prkcb*^{-/-} mice have been previously reported (35). Genotyping primers and conditions for the *MMTV-PyMT* mice are described on The Jackson Laboratory website.

TUMOR STUDIES AND FIBROBLAST/EPITHELIAL ISOLATION

MMTV-PyMT; *Prkcb*^{+/+} and *MMTV-PyMT*; *Prkcb*^{-/-} mice were palpated starting at 3 months of age. Upon detection of palpable tumors, tumorigenesis was allowed to progress three additional weeks, upon which the tumors were harvested. At the time of harvest, tumor burden was measured as a percentage of the tumor weight relative to total body weight, and total tumor volume was calculated by caliper measurements (length \times width \times height). Each tumor was then either frozen or fixed in formalin for later histological analysis. For the orthotopic injection study, we injected 3×10^6 B6 *PyMT* tumor cells into the inguinal mammary fat pads of either *Prkcb*^{+/+} or *Prkcb*^{-/-} mice. Tumors were monitored by weekly palpation. When the largest tumor reached 1 cm in diameter, a final measurement was determined by caliper and all tumors were harvested. B6 *PyMT* cells were a generous gift from Tsonwin Hai and have been described previously (38). B6 *PyMT* cells were maintained *in vitro* using DMEM/F-12 plus 10% fetal bovine serum plus penicillin/streptomycin. Isolation of mammary fibroblasts and epithelium was performed by gravity separation as has been described (40, 41).

IMMUNOFLUORESCENCE AND HISTOLOGICAL STAINING

Tumor tissue was fixed in formalin for 24 h, transferred to 70% ethanol, paraffin embedded, and sectioned (5 μ m). Sections were rehydrated through xylenes and an ethanol series. Antigen retrieval was performed using DAKO antigen retrieval in a steamer for 30 min and sections were blocked with DAKO protein block. Primary detection of F4/80 (Molecular Probes), Ki-67 (DAKO), and MECA-32 (BD Pharmingen), was performed overnight at 4°C. Alexafluor-488 and Alexafluor-596 (Invitrogen) were used for secondary detection and DAPI as a nuclear counterstain. To quantify, five images (20 \times fields) were taken per mouse. Quantification of F4/80 and Ki-67 staining was done using the count tool in Adobe Photoshop CS5. Percent positivity of each stain was determined

relative to the total number of cells as visualized by the DAPI counterstain. Quantification of MECA-32 staining was measured as percent positive area using Image J (42). Hematoxylin and eosin (H&E) and Masson's Trichrome staining was performed by the Solid Tumor Pathology Core at OSU.

RNA ISOLATION AND QUANTITATIVE REAL-TIME PCR

Total RNA was isolated using Trizol reagent (Invitrogen), treated with Turbo DNase I (Ambion) and cDNA generated using Super-script III Reverse Transcriptase (Invitrogen), all per manufacturer's recommendations. *Prkcb* (F = gaaactcgaacgcaaggaga; R = accggtcgaagttttcagc; Probe #83) and *Rpl4* (F = gatgagctgtatggcacttg; R = cttgtcatggcagggtta; Probe #38) were detected using the Roche Universal Probe Library system.

DATASET AND STATISTICAL ANALYSES

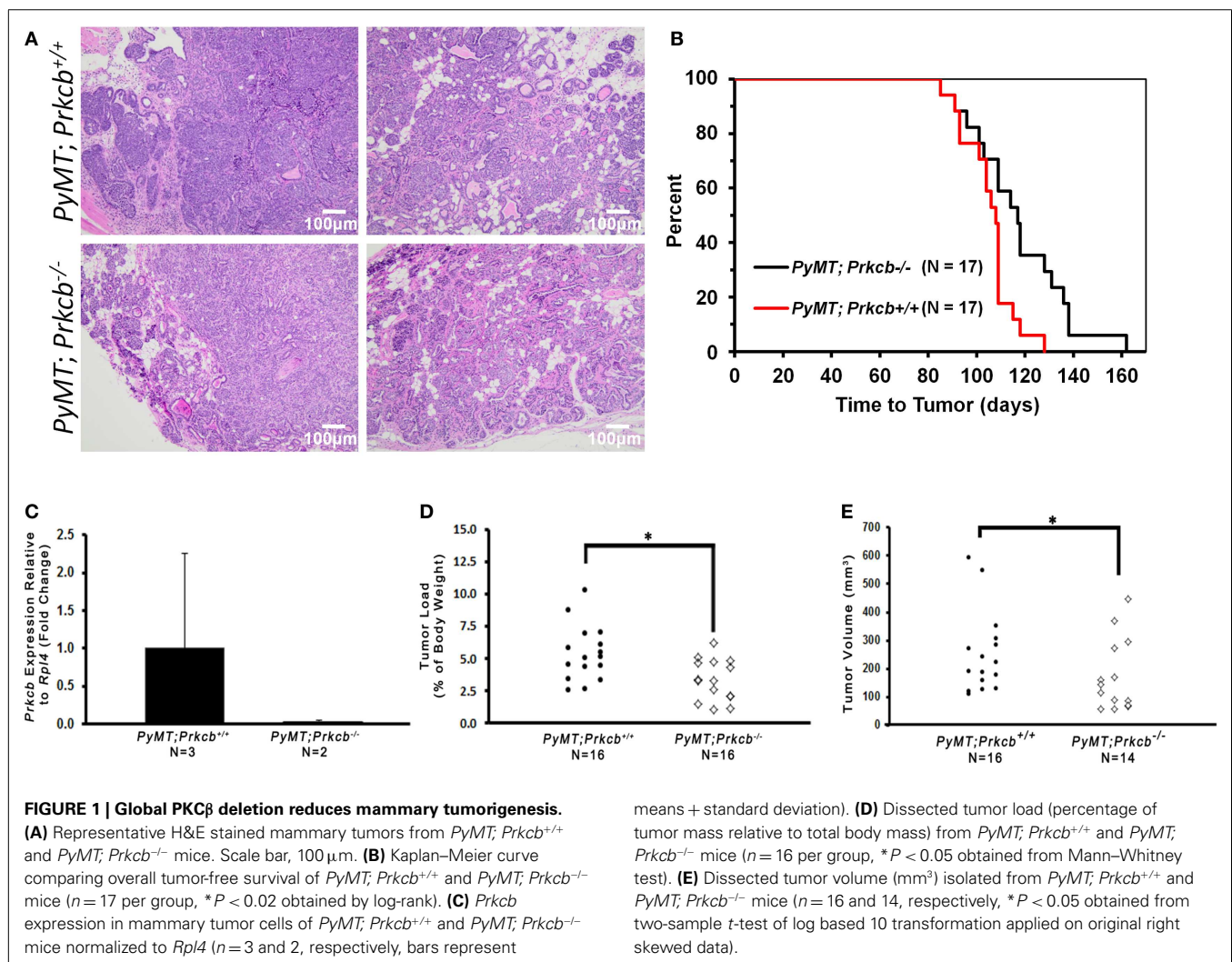
The Karnoub breast cDNA microarray dataset of human breast tumors was retrieved from Oncomine (oncomine.org) for *in silico* analyses (43). *PRKCB* expression was compared between invasive ductal breast carcinoma samples versus normal breast tissue. Statistical significance was determined by Student's *t*-test assuming a two-tailed distribution and equal variance. Kaplan–Meier

survival curves were generated and statistical significance determined using log-rank. Tumor volume measurements and genetic marker staining was compared between two genetic groups. Log transformation of the data was performed if needed. Two-sample *t*-test or non-parametric Mann–Whitney test was applied after normality check. Type I error level was controlled at 0.05 level, and adjusted by Bonferroni's method when multiple comparisons were made.

RESULTS

GLOBAL PKC β DELETION REDUCES MAMMARY TUMORIGENESIS

Members of the PKC family are known to influence proliferation, differentiation, apoptosis, cellular motility, and angiogenesis (1, 4), leading us to hypothesize that loss of PKC β would cause decreased mammary tumorigenesis in the *MMTV–PyMT* mammary tumor model. To evaluate the role for PKC β in tumorigenesis, we bred the *Prkcb*^{-/-} knockout mice with those harboring the *MMTV–PyMT* transgene, a well-characterized murine model of mammary tumor formation (44). We monitored tumor development and harvested tumors 3 weeks after initial palpation. Although the tumors between the two groups looked histologically similar by hematoxylin and eosin (H&E) staining (Figure 1A), *MMTV–PyMT*



mice lacking PKC β (*MMTV-PyMT; Prkcb*^{-/-}) developed tumors at a longer latency when compared to control *MMTV-PyMT; Prkcb*^{+/+} mice (**Figure 1B**). The absence of *Prkcb* in the tumors was confirmed (**Figure 1C**). Not only did the absence of PKC β delay tumor onset, but the tumors that developed in the *MMTV-PyMT; Prkcb*^{-/-} mice were smaller as measured by both tumor load (**Figure 1D**) as well as total volume (**Figure 1E**). These data indicate that the global absence of PKC β in this mouse model has a measurable impact on mammary tumorigenesis.

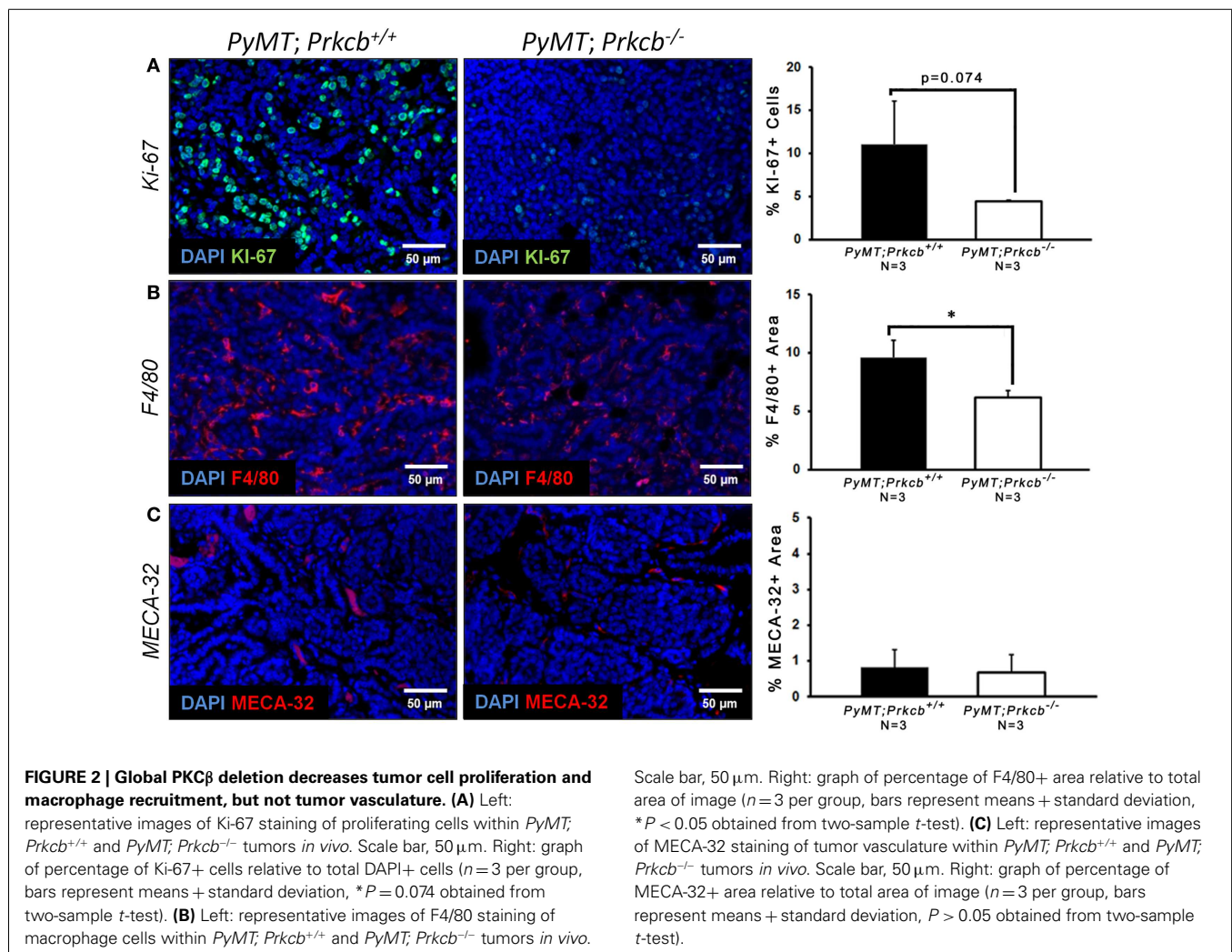
GLOBAL PKC β DELETION DECREASES TUMOR CELL PROLIFERATION AND MACROPHAGE RECRUITMENT, BUT NOT TUMOR VASCULATURE

To explain the delayed onset and decreased tumor size in mice lacking PKC β , we stained for a proliferation marker (Ki-67) within the *PyMT* tumors of both genetic groups. We saw an observable decrease in the percentage of Ki-67 positive cells in *MMTV-PyMT; Prkcb*^{-/-} mice (**Figure 2A**), indicating that PKC β influences *PyMT* tumor progression by modulating tumor cell proliferation capacity. Given the recent knowledge that the TME can influence tumor cell proliferation (41), as well as the known function for PKC β in endothelium and immune cells, we also

investigated macrophage infiltration and tumor vasculature in the *MMTV-PyMT* tumors with and without PKC β . We saw a significant decrease in percentage of F4/80 positive area, a macrophage marker, in *MMTV-PyMT; Prkcb*^{-/-} tumors (**Figure 2B**), indicating that loss of PKC β within macrophages influences their recruitment to the tumor site. We saw no measurable difference in tumor vascularization, as measured by MECA-32 staining, between the *Prkcb*^{-/-} and WT groups (**Figure 2C**), demonstrating that the delayed tumor onset and growth observed in *Prkcb*^{-/-} mice was independent of vasculature formation.

LOSS OF PKC β IN STROMAL COMPARTMENTS DECREASES TUMOR VOLUME AND COLLAGEN DEPOSITION, BUT HAS NO EFFECT ON TUMOR CELL PROLIFERATION, VASCULARIZATION, OR MACROPHAGE INFILTRATION

To determine the importance of PKC β signaling within the stroma, we orthotopically injected *Prkcb*^{-/-} and WT mice with B6 *PyMT*-derived tumor cells. As seen with the genetic model, tumors developing in *Prkcb*^{-/-} mice exhibited no obvious histological differences (**Figure 3A**), but did result in significantly smaller tumor volumes compared to WT controls (**Figure 3B**). This result, in



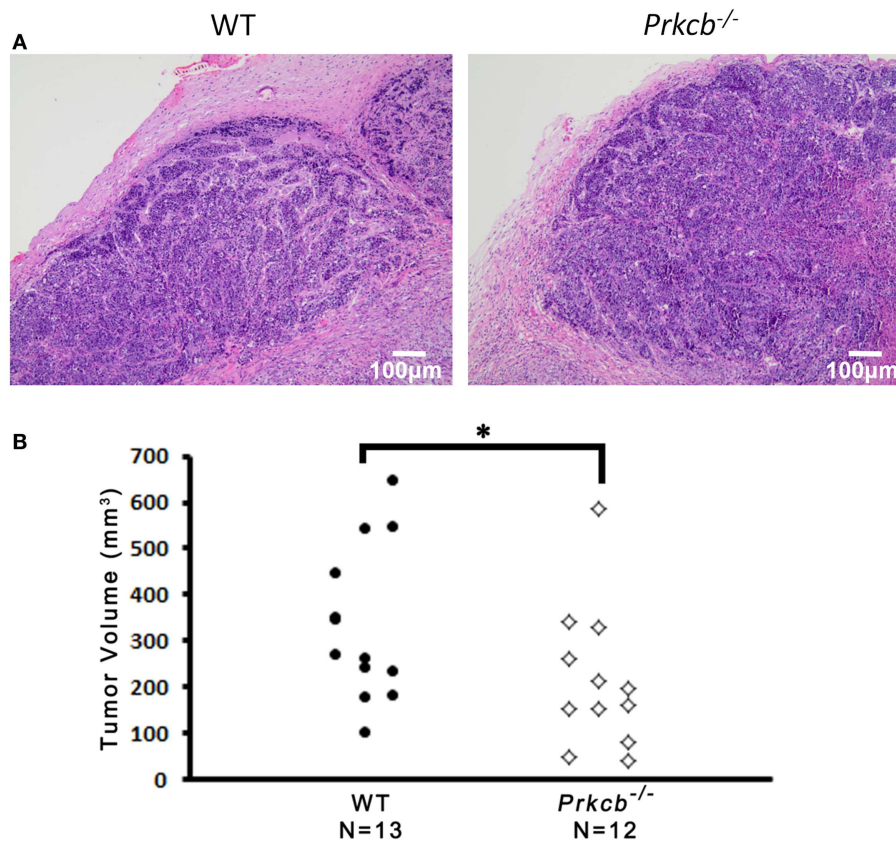


FIGURE 3 | Loss of PKC β in stromal compartments decreases tumor volume. (A) Representative H&E stained B6 *PyMT* tumors developed in wild type (WT) and *Prkcb*^{-/-} mice. Scale bar, 100 μ m. (B) Dissected B6

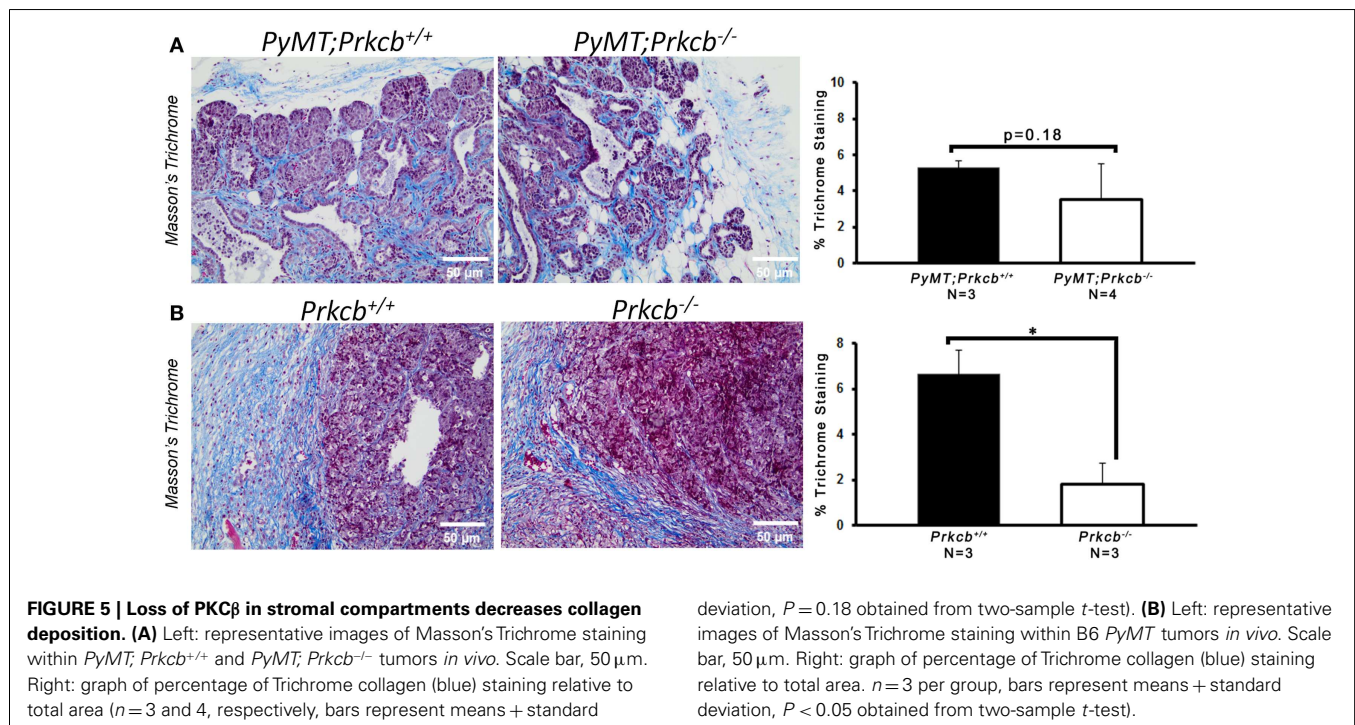
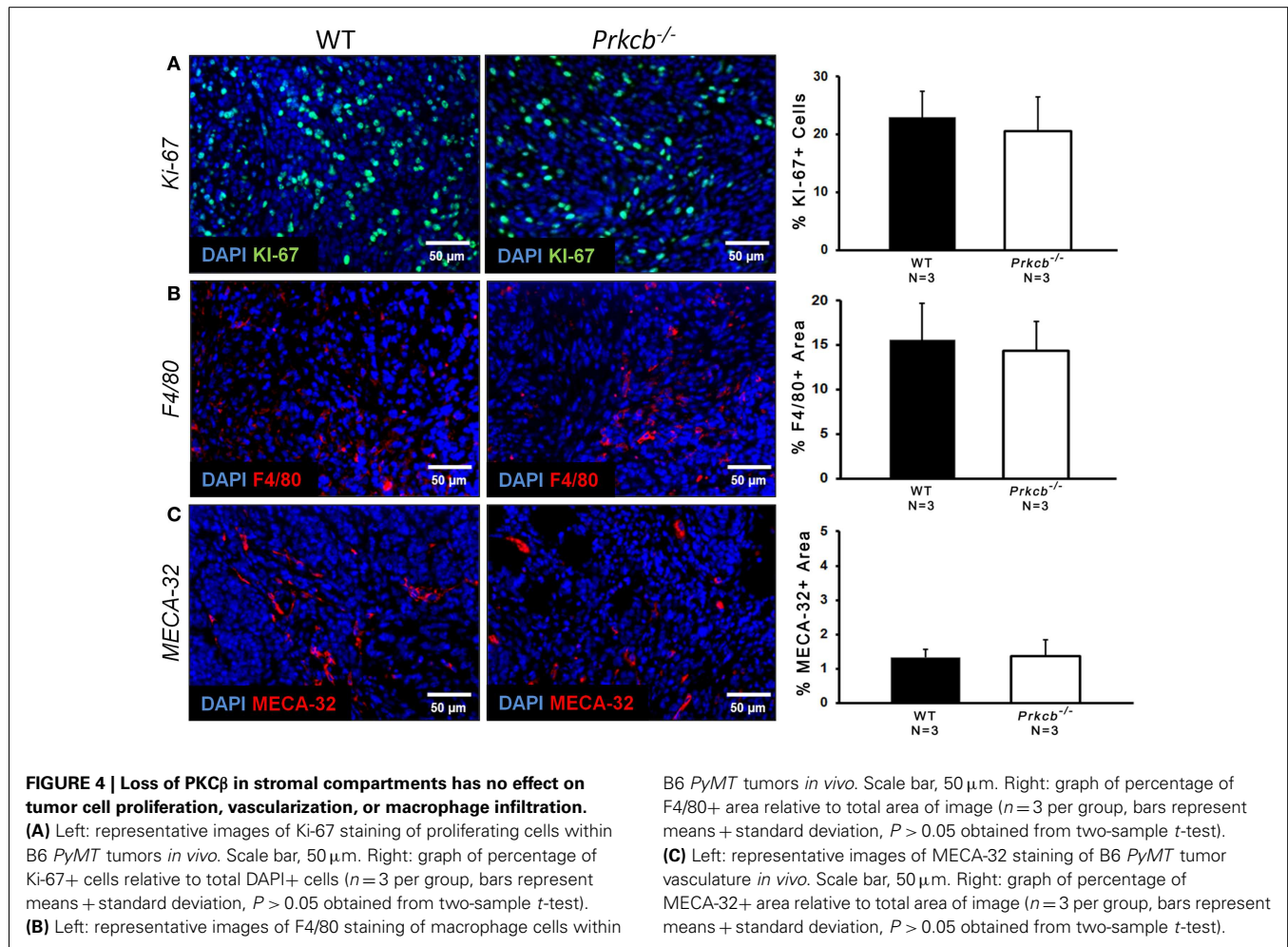
PyMT tumor volume isolated from wild type (WT) and *Prkcb*^{-/-} mice ($n = 13$ and 12 , respectively, $*P < 0.05$ obtained from Mann-Whitney test).

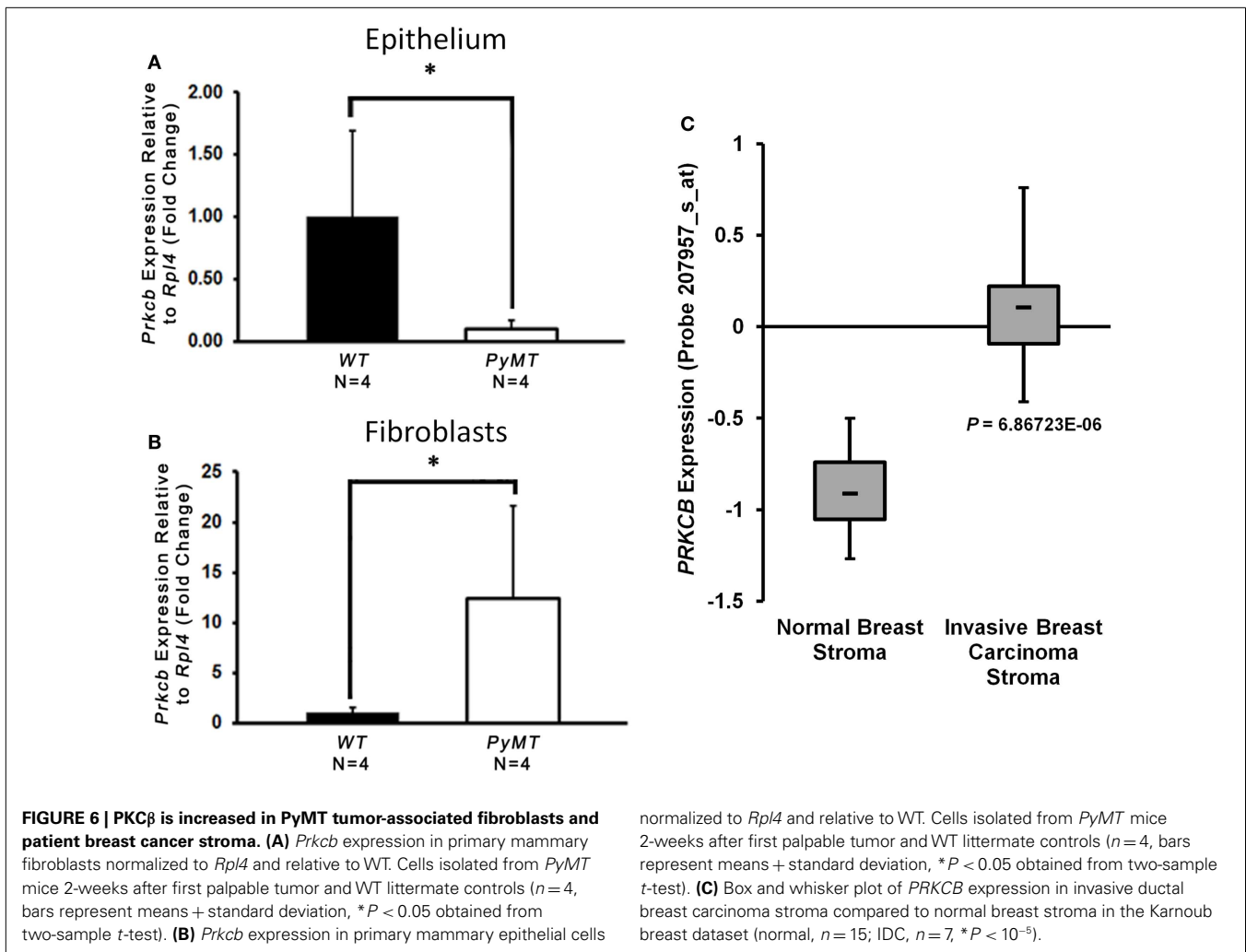
conjunction with the results presented in **Figure 1**, confirms that stromal PKC β is important in *PyMT* mammary tumor formation. In order to further assay the effect of stromal PKC β deletion within the tumor and its microenvironment, tumors were also evaluated for histological alterations within the distinct cellular compartments. Interestingly, there was no difference in Ki-67, F4/80, or MECA-32 positivity between *Prkcb*^{-/-} and WT mice (**Figure 4**). Thus, losing PKC β signaling in the stroma decreased tumor size, but had no effect on tumor cell proliferation, vascularization, or macrophage recruitment. To evaluate whether stromal fibroblasts could be responsible for the observed decrease in tumor size in *Prkcb*^{-/-} mice, we evaluated collagen deposition through Masson's Trichrome staining. The absence of PKC β specifically in the stroma resulted in significantly diminished collagen deposition while this decrease was not as pronounced in the global knockout model (**Figure 5**). These results imply that PKC β signaling in fibroblasts is pro-tumorigenic in the mammary gland.

PKC β IS INCREASED IN *PyMT* TUMOR-ASSOCIATED FIBROBLASTS AND PATIENT BREAST CANCER STROMA

Given the decreased collagen deposition in the absence of stromal PKC β as just discussed, in addition to previously described roles for PKC β in fibroblast function (31–34), we further hypothesized

that *MMTV-PyMT* tumorigenesis may be, at least in part, due to aberrant PKC β expression in the mammary fibroblasts. To this end, we isolated primary mammary tumor epithelial cells and tumor-associated fibroblasts from *PyMT* mice 2 weeks after palpable tumor formation. We also isolated mammary epithelial cells and fibroblasts from age-matched WT littermate controls. We assayed the expression level of *Prkcb* mRNA in both cellular compartments by quantitative real-time PCR (qRT-PCR), and observed a significant decrease in *Prkcb* expression in mammary epithelial cells derived from *PyMT* tumors (**Figure 6A**), possibly indicating that epithelial PKC β is tumor suppressive during *PyMT*-driven tumor formation. In contrast, a dramatic increase in *Prkcb* mRNA in *PyMT* tumor-associated fibroblasts was observed compared to WT mammary fibroblasts (**Figure 6B**). These data, in combination with the decreased tumor formation we observed in *Prkcb*^{-/-} mice, suggest a pro-tumorigenic role for PKC β in mammary tumor fibroblasts. To confirm these findings in human disease, we evaluated *PRKCB* in a publicly available breast cancer dataset [Karnoub et al. (43)] comparing stroma isolated from invasive ductal breast carcinoma compared to normal breast tissue. In this dataset, *PRKCB* is significantly increased in breast cancer stroma versus normal confirming the translational relevance of PKC β in the breast TME (**Figure 6C**).





DISCUSSION

The PKC family is well-documented to have a variety of roles in cancer [reviewed in Ref. (1, 4)] with PKC β functioning specifically in a number of cancer types including in breast (20–23, 45). Prior evaluation of PKC β in breast cancer has utilized over-expression studies *in vitro* (20, 45) and expression analyses in patient tumor tissue: both by immunohistochemistry of tumor sections (21) and through whole tumor extraction (20, 23). While the *in vitro* breast cancer cell line data are highly suggestive of a tumor promoting role for PKC β in breast cancer, tumor expression at both RNA (23) and protein (21) levels does not correlate with breast cancer patient survival. Given that PKC β is required for VEGF-induced angiogenesis (25–27), immunity via NF- κ B signaling (28–30), pro-tumorigenic fibroblast properties (31, 32), and adipocyte lipid metabolism (35, 36), it is likely that our understanding of how PKC β functions in breast tumorigenesis requires further evaluation of its role in the breast TME.

In this study, we took advantage of the genomic *Prkcb*^{-/-} mouse (37). These mice are viable allowing for investigation of mammary tumorigenesis in the absence of PKC β either throughout the whole animal as we investigated in *MMTV-PyMT* mice

with and without PKC β , or through transplantation approaches where we injected a *MMTV-PyMT* derived tumor cell line (B6 *PyMT* cells) into either WT or PKC β null mammary fat pads. The *Prkcb*^{-/-} mice were crossed with the *MMTV-PyMT* mouse model of breast cancer, which is a valuable translational tool given that tumor formation in these mice recapitulates disease progression as seen in humans (44). Furthermore, the importance of the mammary TME in *MMTV-PyMT*-induced tumorigenesis has been well-described. Alterations in signaling from the endothelium (46), fibroblasts (41, 47, 48), immune cells (49–52), and adipocytes (53–55) have all been shown to alter tumor growth and/or metastatic progression in these mice. Moreover, increased stromal collagen deposition hastens *MMTV-PyMT* tumor development and metastatic spread (56).

As described herein, *MMTV-PyMT*; *Prkcb*^{-/-} mice develop smaller tumors at a longer latency than their *MMTV-PyMT*; *Prkcb*^{+/+} counterparts. This decrease in tumorigenesis is associated with a reduction in proliferation and macrophage recruitment. Tumor-associated macrophages in breast cancer act in a pro-tumor manner by upregulation of M2 functions such as promoting angiogenesis, remodeling of the tumor matrix, and

suppressing the adaptive immune response (57, 58). Furthermore, M2 macrophages are thought to have an immunomodulatory function that activates tumor cell proliferation (59) suggesting a possible mechanistic connection between the observed differences in proliferation and macrophage number upon loss of PKC β . Surprisingly, even with the well-described role for PKC β in VEGF signaling (25–27), there was no alteration in the tumor vasculature in PKC β null *PyMT* mice. Similar findings were observed in the injection model. However, in this case we saw no difference in proliferation, macrophage recruitment, or angiogenesis, but did see a decrease in collagen deposition. These results imply a mechanistic role for PKC β signaling in fibroblast activity, specifically in the synthesis of collagen. It is important to note that this model only evaluates tumor progression, not initiation, since the B6 *PyMT* cells are already transformed. Future studies are required using *Prkcb* floxed mice to conditionally delete PKC β in the endothelial (*Tie2-cre*), macrophage (*Lys-cre*), and fibroblast (*Fsp-cre*) specific cellular compartments. These mice can then be crossed with the *MMTV-PyMT* as well as other murine models of breast cancer to investigate how PKC β alters mammary tumor initiation. While this investigation is well beyond the scope of the current study, it will be necessary to truly define the specific breast TME component where PKC β has the most tumor altering effect.

Support for a pro-tumorigenic role for PKC β in the breast TME is evidenced by the significantly upregulated expression of *Prkcb* in fibroblasts isolated from *MMTV-PyMT* mammary tumors when compared to WT mammary glands. Increased *PRKCB* in breast tumor stroma versus normal stroma was confirmed in a breast cancer patient cohort. Interestingly, we observed a significant decrease in *Prkcb* expression in the epithelial fraction of the *MMTV-PyMT* tumors. The concomitant decrease of *Prkcb* in epithelium and increase in the stroma suggests that whole tumor analysis of PKC β either at the mRNA or protein level could be misinterpreted as showing no observable difference in expression. Likewise, observable differences may be reflective of expression changes in specific cellular populations confounding any predictive power of PKC β . This is supported by the fact that similar to published studies (21, 23), we observed no significant correlation of *PRKCB* with patient outcome in several publicly available breast cancer datasets (data not shown). Given its role in the TME as described herein, PKC β expression can only be truly defined through immunohistological evaluation of whole tumor sections in order to delineate tumor versus stromal expression. Pursuing whether PKC β expression is predictive in breast cancer is critical because a number of PKC β selective inhibitors have shown efficacy in pre-clinical and clinical trials for a multitude of cancer types (4, 60). To date, no studies have proven efficacious in breast cancer patients, but this could be due to the absence of a proper biomarker as tumor expression of PKC β has not been evaluated in trial participants [(61, 62); clinicaltrials.gov]. Continued investigation into the mechanism of PKC β function in breast tumor stroma through the use of the conditional knockout models as described above will undoubtedly translate to a greater understanding of how to clinically evaluate PKC β tumor expression and ultimately use this aberrant signaling pathway as a therapeutic target.

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