

Role of COX-2 in epithelial–stromal cell interactions and progression of ductal carcinoma in situ of the breast

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Epithelial–stromal cell interactions have an important role in breast tumor progression, but the molecular mechanisms underlying these effects are just beginning to be understood. We previously described that fibroblasts promote, whereas normal myoepithelial cells inhibit, the progression of ductal carcinoma in situ (DCIS) to invasive breast carcinomas by using a xenograft model of human DCIS. Here, we report that the tumor growth and progression-promoting effects of fibroblasts are at least in part due to increased COX-2 expression in tumor epithelial cells provoked by their interaction with fibroblasts. Up-regulation of COX-2 in DCIS xenografts resulted in increased VEGF and MMP14 expression, which may contribute to the larger weight and invasive histology of COX-2-expressing tumors. Administration of celecoxib, a selective COX-2 inhibitor, to tumor-bearing mice decreased xenograft tumor weight and inhibited progression to invasion. Coculture of fibroblasts with DCIS epithelial cells enhanced their motility and invasion, and this change was associated with increased MMP14 expression and MMP9 protease activity. We identified the NF- κ B pathway as one of the mediators of stromal fibroblast-derived signals regulating COX-2 expression in tumor epithelial cells. Inhibition of NF- κ B and COX-2 activity and down-regulation of MMP9 expression attenuated the invasion-promoting effects of fibroblasts. These findings support a role for COX-2 in promoting the progression of DCIS to invasive breast carcinomas, and suggest that therapeutic targeting of the NF- κ B and prostaglandin signaling pathways might be used for the treatment and prevention of breast cancer.

breast cancer | stroma | tumor progression | DCIS | celecoxib

Increasing evidence supports the importance of epithelial–stromal cell interactions in tumor growth, progression, angiogenesis, and therapeutic resistance (1–4). Despite the importance of these interactions in tumorigenesis, the underlying molecular mechanisms are poorly characterized, in part because of their complexity and redundancy. Multiple factors secreted by multiple cell types can exert the same effects, creating a challenge for approaches aiming at their therapeutic targeting. Most studies analyzing epithelial–stromal cell interactions have focused on cytokines and chemokines as potential mediators of this cross-talk (5, 6), whereas the involvement of lipid signaling including various prostaglandins (PGs) has not been extensively investigated.

The prostaglandin synthetase complex of enzymes has a key role in converting membrane arachidonic acid to PGs that subsequently mediate their effects by means of G protein-coupled receptors (GPCRs) (7). One of the components of this complex is the COX-2 cyclooxygenase enzyme that is expressed in a cell type-specific manner and is inducible by various mitogenic and inflammatory stimuli (8). COX-2 has been implicated to have a role in breast tumorigenesis based on its increased expression in a significant fraction of breast carcinomas and the protective effects of nonsteroidal antiinflammatory drugs (NSAIDs) against breast cancer (9). Immunohistochemical analysis of COX-2 expression in human

breast carcinomas have revealed variable and sometimes contradictory results both with regards of the fraction of tumors expressing COX-2 and the associations between its expression and clinicopathologic characteristics of the tumors (9). Variability of antibodies, heterogeneous expression of COX-2 within tumors, small sample size, and differences in data interpretation are potential explanations of the conflicting results. However, the general agreement is that a significant subset of breast tumors express COX-2, and that its expression is associated with unfavorable clinical behavior, including poorly differentiated histology, higher risk of distant metastasis, and shorter survival (10).

The potential role of COX-2 in the preinvasive stages of breast tumorigenesis has especially been intensely investigated due to human epidemiological studies linking the use of NSAIDs to decreased risk of breast cancer (11), and to our relative inability to predict the clinical course of these early stage lesions. Analysis of COX-2 expression in combination with that of other markers (p16 and Ki67) in DCIS was found to be associated with subsequent tumor events, although it did not predict the risk of invasive recurrence potentially due to small sample size (12). In line with this observation, a recent study reported that COX-2 expression in atypical epithelial hyperplasia correlated with the development of subsequent breast cancer, identifying COX-2 as a potential biomarker for risk prediction and selection of patients for chemopreventive studies (13).

We have previously analyzed the progression of in situ to invasive breast carcinomas by molecular profiling of human tumors and experiments in DCIS models (14–16). Using these approaches, we identified dramatic changes in the gene expression and epigenetic profiles of each cell type composing the microenvironment, and demonstrated a role for these alterations in the progression of DCIS tumors. In the present study, we investigated whether COX-2 is a potential mediator of tumor epithelial–stromal cell interactions that promote the growth and progression of in situ tumors using a xenograft model of human DCIS.

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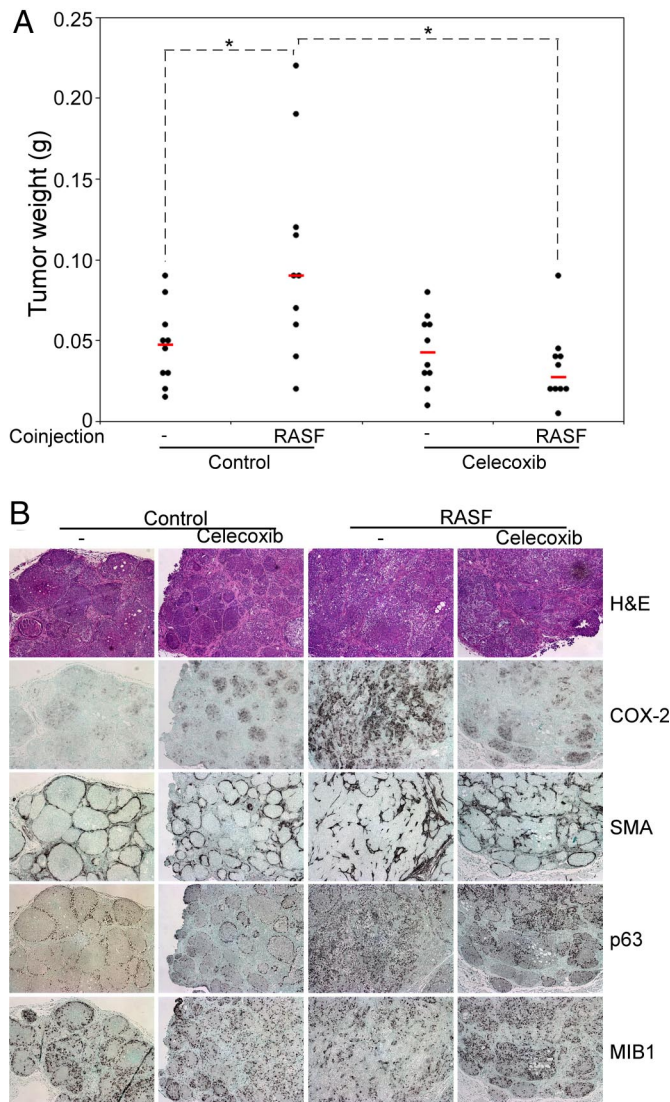


Fig. 2. The effect of celecoxib on MCFDCIS xenografts. The effect of a selective COX-2 inhibitor (celecoxib) on the weight (A) and histology (B) of MCFDCIS xenografts derived from cells injected alone (–) or coinjected with RASFs on control or celecoxib-containing diet. Xenografts from MCFDCIS cells alone (–) had DCIS histology and low COX-2 expression, regardless of diet. Tumors from MCFDCIS cells coinjected with RASF showed invasive phenotype and high COX-2 levels in the control diet group. Celecoxib abolished the tumor growth-stimulating effects of RASF ($P = 0.0001$), partially inhibited the progression to invasive tumors, and decreased COX-2 protein levels. No significant difference in the number of cycling (MIB1+) cells was detected after celecoxib treatment, but this observation does not exclude the possibility of decreased proliferation due to increased cell cycle length or increased apoptosis after celecoxib treatment. Statistically significant ($P < 0.05$) differences in tumor weight are marked with dashed lines and asterisks.

of RASFs by celecoxib, because these cells do not survive long term in mice (15), and coinjection of lethally irradiated cells had even more pronounced tumor-promoting effects. The absence of neutrophils and macrophages that were supposed to be functional even in NCRNU mice in the xenografts is interesting and may reflect lack of inflammatory reaction in this model, which could potentially influence the histology of the resulting tumors. However, the potential inhibition of macrophages and leukocytes by celecoxib cannot be completely excluded.

Epithelial–Stromal Cell Interactions in Cell Culture Models. To begin delineating molecular mechanisms underlying interactions between

MCFDCIS tumor epithelial cells and fibroblasts, and the role of these interactions in invasive progression, we developed 2D and 3D coculture models including both cell types. We previously described that coculture of MCFDCIS cells with breast stromal fibroblasts in Matrigel resulted in invasive branching growth, compared with spheroids formed by MCFDCIS cells cultured alone (20). We extended these studies further and determined that coculture of MCFDCIS cells with fibroblasts in Matrigel led to the invasive branching growth of MCFDCIS cells, and this behavior was suppressed by the inclusion of HME cells (Fig. 3A). These results were consistent with our findings in MCFDCIS xenografts, where all fibroblasts promoted progression to invasion and HME cells were able to suppress this effect (15). Based on these observations, we concluded that at least some aspects of invasive progression and cell–cell interactions that occur in MCFDCIS xenografts can be reproduced in our cell culture models; thus, these cultures can be used for the dissection of signaling pathways involved in these processes.

To quantitate the proinvasive effects of cocultured RASFs on MCFDCIS cells, we performed Boyden chamber assays using fluorescently labeled MCFDCIS cells to differentiate between the 2 cell types. These experiments showed that RASFs dramatically increased the motility of MCFDCIS cells and their invasion through Matrigel (Fig. 3B). The invasion-promoting effects of RASFs did not require direct cell–cell contact, because conditioned media of RASF cells produced essentially the same effects. Correlating with this finding, when conditioned media from these cocultures was analyzed by zymography, we detected increased MMP9 gelatinase activity, compared with conditioned media from epithelial cell only cultures (Fig. 3C).

To investigate gene expression alterations in MCFDCIS cells that accompanied changes in their phenotype provoked by RASFs, we performed quantitative RT-PCR (qPCR) analysis of selected genes. Using this approach, we determined that COX-2 and MMP14 mRNA levels were significantly higher in MCFDCIS cells recovered from 2D cocultures with RASFs correlating with results in xenografts (Fig. 3D). Despite increased MMP9 gelatinase activity in these cocultures, we were not able to detect changes in MMP9 mRNA and protein levels in MCFDCIS cells in any of the conditions analyzed. MMP14 (MT1-MMP) is an upstream activator of multiple MMPs (21); thus, increased MMP14 levels in cocultures might lead to increased MMP9 activity without altering MMP9 mRNA and protein levels. However, due to the complex regulation of MMPs and other ECM degrading proteases, alternative hypotheses cannot be excluded. Quantitative PCR analyses of MCFDCIS cells recovered from 3D colonies grown embedded in Matrigel essentially reproduced the findings obtained in 2D cultures with respect of COX-2, MMP14, and MMP9 expression. Thus, based on these results, the up-regulation of COX-2 and subsequent induction of MMP14 and MMP9 in MCFDCIS cells due to RASF coculture might be responsible for the invasion promoting effects of RASFs.

NF- κ B Pathway As a Mediator of Epithelial–Stromal Cell Interactions in DCIS. COX-2 activity and expression are regulated at multiple levels, including transcriptional and posttranscriptional mechanisms (22). One of the main transcriptional regulators of COX-2 expression is NF- κ B (22), a pathway activated by many cytokines and chemokines secreted by inflammatory and mesenchymal cells (23). Gene expression profiling of invasion promoting RASFs and tumor-suppressing HMEs identified dramatic differences in the expression of numerous genes encoding for secreted proteins that might explain the opposing effects of these 2 cell types on in situ invasive breast carcinoma progression (15). To extend these studies further, we assessed the levels of 120 cytokines in conditioned media of RASFs and HMEs, and found high levels of CCL2, IGFBP3, TIMP1, and TIMP2, specifically in RASFs (Fig. S4). Correlating with this data, conditioned media or coculture with

