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Increased Th17 Cells in the Tumor Microenvironment Is Mediated by IL-23 via Tumor-Secreted Prostaglandin E₂

Xuesong Qian,*† Ling Gu,*† Huan Ning,*† Yanping Zhang, † Eddy C. Hsueh, † Mingui Fu, † Xiaoyu Hu, ‡ Lin Wei,*† Daniel F. Hoft, * and Jianguo Liu*

Tumor cell–derived molecules such as cytokines and lipid mediators play a critical role in inducing chronic inflammation in the tumor microenvironment. We found that Th17 cells were increased in the peripheral blood, spleen, and tumor tissues of mammary gland tumor-bearing mice. The Th17 cell survival factor, IL-23, was also overexpressed in tumor tissues isolated from mice and human breast cancer patients. Soluble molecules secreted from breast tumor cells, but not normal breast epithelial cells, induced IL-23 protein secretion in dendritic cells via induction of p19 mRNA expression. Our data further indicate that tumor-secreted PGE₂ through EP2 and EP4 receptors enhanced IL-23 p19 gene transcription through binding to the cAMP-response element in the p19 promoter. Blocking PGE₂ synthesis by NS398, a COX2 inhibitor, abrogated the enhancement of p19 expression both in vitro and in vivo. Furthermore, blocking protein kinase A (PKA) by H89 completely abrogated the inductive effects of tumor-conditioned medium and PGE₂ on p19 transcription, whereas the cAMP active analog, Forskolin, mimics the PGE₂ effect. Taken together, our results indicate that tumor-secreted PGE₂ induces IL-23, but not IL-12, production in the tumor microenvironment. We found that Th17 cells were increased in the tumor microenvironment during tumor progression, including breast, prostate, and gastric cancers (7–9). As a signature cytokine secreted by Th17 cells, IL-17 promotes tumor growth and metastasis through angiogenic effects and induction of chronic inflammation (6). In contrast, it has also been reported that Th17 cells and IL-17 have antitumor effects by attracting CTL and NK cells migrating into the tumor, suppressing tumor growth and metastasis (5). Nevertheless, increased Th17 cells were documented in many types of solid tumors (5), but the mechanisms by which the tumor microenvironment promotes Th17 cell development in breast cancer are still largely unknown.

Initial differentiation of Th17 cells depends on IL-6 and TGF-β stimulation, whereas IL-23 is known to be essential for Th17 cell survival and expansion, and for making pathogenic Th17 cells (10–16). Therefore, overexpression of IL-23 in the tumor microenvironment could be critical for Th17 cell development during tumor progression. Indeed, it has been reported that IL-23 was overexpressed in different types of tumors, including colon, ovarian, lung, and breast cancers. Mice deficient in IL-23 were resistant to chemically induced papillomas (17). More recently, reports have been published demonstrating that IL-23 can promote tumor growth and metastasis through inhibition of perforin and IFN-γ production by NK cells independent of Th17 cells/IL-17 during carcinogenesis (18). In contrast with the protumor effects of IL-23, several reports have described antitumor functions of IL-23. Overexpression of IL-23 in tumor cells reduced tumor growth and metastasis through induction of CD8⁺ T cell responses (19, 20). It is likely that the functions of IL-23 in tumor progression are determined by the types of tumors, the immune competence of the host, and the source of IL-23 being produced. Nevertheless, IL-23 is consistently overexpressed in both human breast cancer and mouse mammary gland tumor. However, the mechanisms that trigger IL-23 overexpression in breast tumors are still largely unknown.

IL-23 is an IL-12 family cytokine composed of two different subunits, one shared subunit with IL-12, p40, and another unique subunit, p19 (21). IL-23 gene expression is tightly controlled at both transcriptional and posttranscriptional levels. It has been
reported that NF-κB c-Rel physically binds to the p19 promoter and induces IL-23 p19 gene expression. Conversely, deletion of c-Rel abolished IL-23 p19 expression in both dendritic cells (DCs) and macrophages (22, 23). In addition, Sma- and Mad-related protein-3, activating transcription factor-2, and AP-1 also play important roles in control of IL-23 p19 gene expression (24). Silencing of Sma- and Mad-related protein-3 and activating transcription factor-2 expression by short hairpin RNA reduced p19 promoter activity and protein expression in RAW264.7 cells infected with Theiler’s murine encephalomyelitis virus or treated with polyinosinic-polycytidylic acid (25). MAPKs including p38, JNK, and ERK have been shown to be involved in LPS-induced IL-23 p19 gene transcription (24). So far, most studies have focused on the transcriptional regulation of p19 expression and little is known about how IL-23 is posttranscriptionally regulated despite the fact that IL-23 p19 mRNA has a long 3’-untranslated region containing multiple putative adenosine/uridine-rich elements (26). Our recent work showed that IFN-γ suppresses IL-23 expression by selectively targeting p19 mRNA stability through its 3’-untranslated region (27), indicating that the expression of IL-23 is controlled at both transcriptional and posttranscriptional levels.

The 4T1 tumor is an excellent mouse model for breast cancer research because its tumor development is well characterized both oncologically and immunologically (28). Tumor growth and metastatic spread of 4T1 tumor closely mimic stage IV breast cancer (29). 4T1 tumors are poorly immunogenic in that immunization with irradiated 4T1 cells provides only slight delays in tumor growth that are not sufficient to protect the animal (30). Our previous work demonstrated that administration of IL-12 to 4T1 tumor-bearing mice resulted in a substantial reduction in tumor size and decreased spontaneous metastases to the lungs, as well as significantly prolonged survival time (31, 32). 4T1 tumor cells secrete many cytokines such as TGF-β and IL-6, as well as PGE2, that may affect the host immune response to tumors. Our recent work demonstrates that the PGE2 secreted by 4T1 tumor cells suppresses CCL5 production from activated macrophages (33). Overproduction of IL-23 was mediated by PGE2 secreted from 4T1 tumor cells into a T175 flask at a concentration of 0.6 × 10^6/ml with freshly prepared complete culture medium. Seventy-two hours later, the Culture supernatants were collected, filtered through a 0.45-μm filter, divided equally into small tubes, and stored at −20°C for future use. Normal mammary gland epithelial cell line, CommaD Bgeo, and FSK4 cells isolated from mammary glands of female BALB/c mice (34) were kindly provided by Dr. Daniel Medina (Baylor College of Medicine, Houston, TX) and maintained in DMEM supplemented with 5 ml HEPES buffer (per 500 ml), insulin (10 μg/ml), epidermal growth factor (5 ng/ml), and 2% FBS.

**Plasmids and reagents**

Mouse IL-23 p19 promoter was generated by cloning p19 promoter (1348 bp) into pGL2-basic luciferase vector (Promega) between KpnI and XhoI sites. Primers used for cloning p19 promoter were 5′-CAGGCAAGCCAGGGATACAGACGAGG-3′ for sense strand and 5′-GGCCAGGCCGAGCCCT GTG-3′ for antisense strand. A CRE–mutant IL-23 p19 promoter was cloned using Quikchange II site-directed mutagenesis kit (Stratagene). All plasmid DNAs for transfection were prepared with Qiagen Endo-free Maxi Prep kits (Qiagen, Valencia, CA). LPS from Escherichia coli 0217:B8 and epidermal growth factor were purchased from Sigma-Aldrich. NS-398, AH6809, AH23848, and SC51322 were purchased from Cayman Chemical (Ann Arbor, MI). H89 and Forskolin were purchased from Calbiochem.

**RT-PCR**

Reverse transcription reactions were carried out as described previously (35) with 1 μg total RNA for reverse transcription. The following primers were used for PCR amplification: mouse IL-23 p19 cDNA: sense, 5′-TGGACAGCGGGCAATA TGGA -3′; antisense, 5′-TGGTGTCCCTTGTCCTTGGGGTT-3′; mouse GAPDH cDNA: sense, 5′-AACCTTGGGATTGTGGAAGG-3′; antisense, 5′-ACACATTGGGTTAGAAACA-3′.

**Quantitative real-time PCR**

To determine the levels of mRNA expression by quantitative real-time PCR (qRT-PCR), we used a modified protocol. In brief, cDNA samples were diluted and studied at several concentrations. Diluted cDNA was mixed with a pair of primers (10 μM) targeting mouse IL-23 p19 or GAPDH cDNA sequences as described earlier, and with SYBR green PCR master mix (Applied Biosystem, Foster City, CA) in a 15-μl volume. PCR cycling was set as follows: 2 min at 50°C, 10 min at 95°C for 1 cycle, followed by 40 cycles at 15 s at 95°C, 1 min at 60°C.

**ELISAs**

Supernatants from murine Flt3L-induced DC and RAW cell cultures were harvested 24 h after stimulation and stored at −70°C. Mouse IL-23 was detected using the mouse CytoSet ELISA kit (Invitrogen) according to the manufacturer’s instructions. Mouse IL-12(p40) was detected using mouse IL-12(p40) ELISA set (BD, Pharmingen). Concentrations were calculated by regression analysis of a standard curve.

**Transfection assay**

Transient transfections were performed by electroporation as described previously (35).

**Primary transcript measurement**

cDNAs were synthesized with random primers with 1 μg total RNA generated from RAW cells treated with LPS or LPS plus TC to determine the primary transcript of mouse IL-23 p19 gene. The primers used for primary transcript were mouse IL-23 p19 exon 2 (sense): 5′-TGTGTTG CTTGAGCC TCGTCC TGG-3′; and mouse IL-23 p19 intron 1 (antisense): 5′-AACCTTTCCGGACATTGGAAG-3′.

**Statistical analysis**

Student t test was performed wherever applicable. SD of the mean is shown unless otherwise indicated. *p < 0.05, **p < 0.01, ***p < 0.001.
**Results**

**Mammary gland tumor-bearing mice show increased Th17 cells**

To confirm whether Th17 cells were increased during breast tumor progression, we first induced mammary gland tumors in female BALB/c mice. Nineteen days after 4T1 cell injection, tumor-free and tumor-bearing wild type mice were sacrificed, and PBMCs, splenocytes, and mammary glands were collected for detection of CD4+Th1 and CD4+Th17 cells by FACS analysis (A). Percentages of Th1 and Th17 cells in PBMCs (B), spleens (C), and mammary glands (D) in tumor-free and tumor-bearing mice were summarized from the data collected from five mice.

**IL-23 is differentially overexpressed in tumors**

The increased number of Th17 cells in tumor-bearing mice compelled us to investigate whether the expression of IL-23 was also

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**FIGURE 1.** 4T1 tumor-bearing mice have increased Th17 cells. A total of $1 \times 10^5$ 4T1 tumor cells were injected s.c. in the abdominal mammary gland of 6- to 8-wk-old female BALB/c mice. Nineteen days after 4T1 cell injection, tumor-free and tumor-bearing wild type mice were sacrificed, and PBMCs, spleens, and mammary glands were collected for detection of CD4+Th1 and CD4+Th17 cells by FACS analysis (A). Percentages of Th1 and Th17 cells in PBMCs (B), spleens (C), and mammary glands (D) in tumor-free and tumor-bearing mice were summarized from the data collected from five mice.

**FIGURE 2.** IL-23 expression is increased in breast cancer. Total RNA was extracted from tumor-surrounding tissues and breast cancer tissues from human patients (A–C) and tumor-bearing mice (D–F). Quantitative mRNA expression of human IL-23 p19 (A), human IL-12 p40 (B), and human IL-12 p35 (C) in human breast tumor tissues were compared with normal adjacent tissue of the same individual ($n=11$). Quantitative mRNA expression of mouse IL-23 p19 (D), mouse IL-12 p40 (E), and mouse IL-12 p35 (F) in mouse normal mammary gland tissues were compared with 4T1 tumor tissues ($n=10$). qRT-PCR data were normalized relative to GAPDH mRNA expression levels in each respective sample and further normalized to the sample from the nontumor surrounding tissues from the same subject, which was set as 1.
enhanced because IL-23 is a critical cytokine for Th17 cell survival and expansion. We directly isolated total RNA from breast tumors obtained from human patients and tumor-bearing mice, and measured IL-23 p19 and p40 mRNA expression as well as IL-12 p35 mRNA by qRT-PCR. As shown in Fig. 2, IL-23 p19 (Fig. 2A, 2D) and p40 (Fig. 2B, 2E) mRNA expression were significantly increased, whereas the IL-12 p35 mRNA expression (Fig. 2C, 2F) was only slightly increased in tumor tissues from both humans and mice, suggesting that IL-23 is differentially overexpressed in the tumor microenvironment that could facilitate the expansion and survival of Th17 cells.

**Soluble factors secreted from tumor cells increase IL-23 production**

Because DCs and macrophages are major producers for IL-23 and the former are potent APCs critical for T cell differentiation and activation, we wanted to know whether tumor-secreted factors could enhance IL-23 production from DCs. We injected s.c. B16 melanoma cells overexpressing Flt3L into C57B6 mice, purified the DCs from spleens 12 d after, and applied different amounts of TCM collected from 4T1 tumor cells in the presence of LPS stimulation. As we reported previously, LPS induced IL-23 production from DCs (24). Addition of TCM dose dependently enhanced IL-23 (Fig. 3A) but suppressed IL-23/IL-12 p40 (Fig. 3B) production in LPS-stimulated DCs. In line with protein production, IL-23 p19 mRNA expression (Fig. 3C) was enhanced, whereas p40 (Fig. 3D) and p35 (Fig. 3E) mRNA expression were reduced by TCM in a dose-dependent manner in DCs stimulated with LPS. Similar IL-23 induction by TCM was also shown in activated macrophages (data not shown). Because the p40 subunit is always produced in large quantity compared with the p19 subunit, the levels of the p19 expression determine the amount of biologically functional IL-23 production from the activated cells.

To exclude the possibility that soluble factors secreted from normal mammary gland epithelial cells may affect IL-23 induction, we collected conditioned medium (CM) from CommaD Bgeo and FSK4 cells (normal mammary gland epithelial cells isolated from BALB/c mice), and applied those CM to macrophages treated with LPS, followed by measurement of p19 mRNA expression. CM from CommaD (Fig. 3F) and FSK4 (Fig. 3G) cells did not induce but rather suppressed IL-23 p19 mRNA expression, indicating that soluble factors secreted from tumor cells uniquely enhanced IL-23 expression. In addition, to determine whether TCM-enhanced p19 expression happened only to TLR4 signaling, we stimulated macrophages with TNF-α in the presence of different amounts of 4T1 TCM. 4T1 TCM also enhanced TNF-α–induced p19 mRNA expression in a dose-dependent manner (Fig. 3H), indicating that soluble factors secreted from breast tumor cells can enhance IL-23 expression induced by different activation pathways.

**FIGURE 3.** TCM increases IL-23 production in DCs and macrophages. A total of $1 \times 10^6$ Flt3L-induced immature DCs were purified and seeded in each well of a 24-well culture plate. Different amounts of 4T1 TCM as indicated were added to the culture in the absence or presence of LPS (1 μg/ml) for 24 h to measure mouse IL-23 (A) and mouse IL-23/IL-12 p40 (B) protein levels by ELISA. (C) A total of $3 \times 10^6$ Flt3L-induced DCs were stimulated with LPS (1 μg/ml) plus different amounts of 4T1 TCM as described earlier for 4 h, followed by collection of total RNA to measure mouse IL-23 p19 (C), IL-23/IL-12 p40 (D), and IL-12 p35 (E) mRNA expression by qRT-PCR. The same amount of RAW cells was stimulated with LPS (1 μg/ml) in the absence or presence of different amounts of culture supernatants collected from the CommaD Bgeo (F) and FSK4 (G) cells as indicated to detect p19 mRNA expression (4 h after treatment). (H) A total of $3 \times 10^6$ RAW cells were stimulated with TNF-α (25 ng/ml) in the absence or presence of different amounts of 4T1 TCM as indicated to detect p19 mRNA expression (8 h after treatment) by qRT-PCR. qRT-PCR data were normalized relative to GAPDH mRNA expression levels in each respective sample and further normalized to the sample from the untreated group, which was set as 1. Statistical analyses were performed between LPS- or TNF-α–treated group and LPS or TNF-α plus TCM or CM groups. *p < 0.05, **p < 0.01, ***p < 0.001, between two groups.
Tumor-secreted PGE₂ mediates IL-23 induction through EP2 and EP4 receptors

Our previous work indicated that 4T1 tumor cells secrete many cytokines and lipid molecules, including PGE₂ (36). To determine whether PGE₂ secreted by tumor cells was responsible for IL-23 induction, we collected TCM from 4T1 tumor cells treated with NS398, a specific COX2 inhibitor that can effectively block PGE₂ synthesis, applied these PGE₂-lacking TCM to RAW cells stimulated with LPS, and then measured p19 and p40 mRNA expression. TCM-enhanced p19 expression was almost completely abolished after blocking PGE₂ synthesis in 4T1 tumor cells (Fig. 4A), whereas TCM-mediated p40 mRNA reduction was almost completely reversed (Fig. 4B), indicating that PGE₂ is involved in IL-23 production in DCs treated with LPS (Fig. 4C). To further verify whether tumor-secreted PGE₂ mediated IL-23 induction in vivo, we injected NS398 into tumor-bearing mice and then challenged the mice with LPS, followed by measuring p19 mRNA expression in spleens. Blocking PGE₂ synthesis by NS398 significantly reduced p19 (Fig. 4D) and IL-17A (Fig. 4E) mRNA expression in tumors. The number of Th17 cells in tumors was also reduced after blocking PGE₂ synthesis by NS398 (Fig. 4F). Furthermore, blocking PGE₂ synthesis by NS398 in 4T1 tumor cells also completely abrogated TCM-induced p19 promoter activation (Fig. 4G). Taken together, these data indicate that tumor cell–secreted PGE₂ enhances IL-23 production and Th17 cell development in the tumor microenvironment.

To further characterize the receptors involved in tumor PGE₂-mediated IL-23 induction, we applied various PGE₂ receptor antagonists to block PGE₂ signaling and tested whether the inductive effects of 4T1 TCM were affected. Because there are four prostanoid receptors (EP1–4) involved in PGE₂ signaling, we blocked these PGE₂ receptors individually with SC-51322 (a selective EP1 antagonist), AH-6809 (an EP2 receptor antagonist), and AH-23848 (a selective antagonist for EP4) before LPS and 4T1 TCM stimulation. EP1 antagonist had no effect on TCM-mediated p19 induction, whereas EP2 and EP4 antagonists each

![FIGURE 4.](http://www.jimmunol.org/)

**FIGURE 4.** Tumor-secreted PGE₂ enhances IL-23 production through EP2 and EP4 receptors. A total of 1 × 10⁶ RAW cells were cultured with normal media (NM), 400 µl/ml 4T1 TCM, or 400 µl/ml TCM collected from 4T1 cells treated with NS398 in the presence or absence of LPS (1 µg/ml) for 4 h. Note that in the fifth and sixth bar from the left, NS398 was added to the macrophage culture, not to the 4T1 culture. IL-23 p19 (A) and p40 (B) mRNA expression were measured by qRT-PCR. (C) A total of 1 × 10⁶ bone marrow–derived DCs were generated from bone marrow cells isolated from femurs of B6 mice under IL-4 (10 ng/ml) and GM-CSF (40 ng/ml) treatment for 6 d and then treated with different amounts of PGE₂ as indicated in the absence or presence of LPS (1 µg/ml) for 24 h. The supernatants were collected for measurement of IL-23 levels by ELISA. (D and E) T17 cells were generated as described previously in Fig. 1. Seven days later, NS398 (10 mg/kg) and an equal amount of DMSO were given i.p. every 3 d for a total of four times. Nineteen days after 4T1 cell injection, splenocytes were isolated and used to extract total RNA for detection of p19 (D) and IL-17A (E) mRNA expression by qRT-PCR. (F) Tumor-bearing mice were treated with NS398 and DMSO as indicated earlier, and tumors were used to generate single cells to detect tumor-infiltrating Th17 cells by FACS analysis. (G) A total of 5 µg p19 promoter was transiently transfected into RAW cells by electroporation. The transfected cells were stimulated with 400 µl 4T1 TCM or TCM collected from 4T1 cells treated with NS398 in the presence of LPS (1 µg/ml) for 4 h. The luciferase activity was measured in cell lysates. (H) A total of 1 × 10⁶ RAW cells were pretreated with 10 mM SC51322 (EP1 antagonist), 3 µM AH6809 (EP2 antagonist), and 30 mM AH 23848 (EP4 antagonist) or AH6809 plus AH23848 for 30 min, then stimulated with LPS (1 µg/ml) and/or 400 µl 4T1 TCM for 4 h to detect p19 mRNA expression qRT-PCR. Data shown are mean + SD of three to four experiments. qRT-PCR data were normalized relative to GAPDH mRNA expression levels in each respective sample and further normalized to the sample from the untreated group, which was set as 1. *p < 0.05, **p < 0.01, ***p < 0.001, between two groups as indicated.
Tumor-secreted PGE2 promotes p19 expression at the transcriptional level through binding to the CRE site in the p19 promoter

To investigate the molecular mechanisms of TCM-mediated p19 induction, we measured primary transcript rates of the p19 gene in response to TCM in RAW cells, with primers corresponding to two different regions of the p19 gene. The use of primers specific for an intron/exon boundary region allowed us to assess the primary transcript rate of p19 inside the nucleus. As shown in Fig. 5A, p19 primary transcripts were induced by LPS within 30 min and kept increasing up to 3 h after LPS stimulation. Addition of TCM further increased the p19 primary transcript through all time points (Fig. 5A), indicating a transcriptional enhancement of the p19 gene by TCM. PGE2 showed the same inductive effect as TCM on p19 primary transcript (Fig. 5B). To further confirm whether TCM activated p19 gene transcription, we transiently transfected mouse p19 promoter-luciferase constructs into RAW cells by electroporation, followed by stimulating the transfected cells with different amounts of TCM and LPS. Luciferase activity was measured in cell lysates. The p19 promoter activity was enhanced by TCM (Fig. 5C) and PGE2 (Fig. 5D) in a dose-dependent manner, further confirming that TCM-induced p19 gene expression is regulated at the transcriptional level.

To elucidate the molecular basis of TCM-mediated p19 transcriptional induction, we decided to localize the functional TCM/PGE2 response element in the p19 promoter. By searching the p19 promoter, we noticed that there is a putative CRE between -1009 and -1004. We mutated this putative CRE binding site and transiently transfected the wild type and CRE mutant into RAW cells, and stimulated these cells with either TCM or PGE2 in the presence of LPS. Mutation of the CRE site in p19 promoter completely abolished responses to TCM (Fig. 5E) and PGE2 (Fig. 5F), indicating that this putative CRE binding site is critical for the responsiveness of p19 promoter to tumor-secreted PGE2 stimulation.

**TCM-enhanced p19 expression is mediated through cAMP/PKA signal transduction pathway**

TCM enhanced p19 transcription through the CRE site in the p19 promoter (Fig. 5F), suggesting that the inductive effect of TCM on p19 expression may be mediated by cAMP/PKA signaling pathway. To confirm this, we first blocked PKA function with the inhibitor H89 before 4T1 TCM and LPS stimulation, followed by measurement of p19 expression. Blocking PKA with H89 dose-dependently abolished the inductive effects of 4T1 TCM on LPS-induced p19 mRNA expression (Fig. 6A). H89 could also dose-dependently abrogate PGE2-induced p19 mRNA expression (Fig. 6B). In addition, Forskolin, a cAMP active analog, enhanced LPS-induced p19 mRNA expression (Fig. 6C) to similar levels when comparing it with 4T1 TCM, further supporting the involvement of cAMP/PKA signaling in TCM-enhanced p19 expression. Furthermore, TCM-enhanced p19 promoter activation was completely abolished after blocking PKA with H89 (Fig. 6D). Taken together, these results indicate that PGE2 secreted from breast tumor cells enhances LPS-induced p19 expression through the cAMP/PKA signal transduction pathway.
Discussion

The link between chronic inflammation and tumorigenesis has been noted for a long time; however, the mechanisms of the causal relationships between these two events are still largely unknown. Th17 cells have been found to be directly involved in the pathogenesis of several autoimmune disorders, such as experimental autoimmune encephalomyelitis, rheumatoid arthritis, and Crohn’s disease, by secreting proinflammatory cytokines that lead to accumulation of neutrophils and other immune cells causing chronic inflammation (37). The close association between Th17 cells and autoimmune inflammation motivated us to explore the relationships between chronic inflammation, Th17 cells, and cancer. Recently, it has been reported that Th17 cells are increased in many solid tumors including breast cancer (5). We also found in this study that Th17 cells were increased in mammary gland tumor tissues (Fig. 1A, 1D). In addition, there were even greater increases of Th17 cells in spleens and blood from tumor-bearing mice (Fig. 1B, 1C), which has not been appreciated before. Not only the percentages but the absolute numbers of Th17 cells were also increased in tumor-bearing mice compared with tumor-free mice (data not shown). Along with tumor progression, the percentage of Th1 cells tended to decrease and Th17 cells increased (data not shown). The increased Th17 cells and decreased Th1 cells may contribute to tumor progression.

IL-23 induces chronic inflammation through stimulation of innate myeloid cells and stromal activation, whereas the Th17 cells are important for orchestrating inflammatory tissue destruction (18). Although initial differentiation of Th17 cells does not require IL-23, IL-23 is necessary for the maintenance and expansion of Th17 cells (37). Consistent with a previous report (17), our study confirms that IL-23 was overexpressed in breast tumor tissues. Because tumor cells secrete high amounts of TGF-β and IL-6 (36), along with the overexpression of IL-23 in the tumor microenvironment, it seems that all of these cytokines required for Th17 cell development are readily presented in the tumor microenvironment. Because the p40 subunit is a shared subunit between IL-12 and IL-23, expression of the p35 and p19 subunits determines the levels of biologically activated IL-12 and IL-23, respectively. Our results indicate that IL-23 and IL-12 expression were differentially regulated in tumors, with increased expression of the p19 subunit and little change of the p35 subunit (Fig. 2A–F). Considering the critical roles for IL-12 and IL-23 in Th1 and Th17 cell development, this differential expression may explain why there were increased Th17 cells, but not Th1 cells, in the tumor microenvironment.

Different from tumor tissues that expressed high levels of both p19 and p40 subunits (Fig. 2A–F), DCs and macrophages showed a reduced p40 mRNA expression in response to TCM (Fig. 3B, 3D). This difference in p40 expression pattern between tumor tissues and DCs/macrophages could be because of the fact that endogenous ligands in the tumor microenvironment may use different signaling pathways other than LPS/TLR4 pathway to acti-
vate p40 expression. Indeed, 4T1 TCM not only enhanced LPS-induced p19 mRNA expression, but also increased TNF-α-stimulated p19 expression in macrophages (Fig. 3H). IL-23 p19 expression was induced only by tumor-secreted factors, but not by normal mammary gland epithelial cell–secreted molecules. In contrast, molecules secreted from normal epithelial cells suppressed LPS-induced p19 expression (Fig. 3F, 3G), suggesting that tumor cells acquire the ability to enhance IL-23 production in the tumor microenvironment after transforming into malignant cells.

Blocking PGE2 synthesis by NS398 in 4T1 cells abolished the ability of 4T1 TCM to enhance p19 expression (Fig. 4A), indicating that tumor cell–secreted PGE2 enhances LPS-induced IL-23 production. This is consistent with previous observations that PGE2 induced IL-23 in bone marrow–derived DCs (38) and with our own data (Fig. 4C). The Th17 cell–promoting effects of PGE2 are not only attributed to enhancement of IL-23 production as shown in this article and by others (38), but can also be attributed to increased expression of IL-23Rs and IL-1Rs. Overexpression of RAR-related orphan receptor γt, IL-17, and CCR6 expression in response to PGE2 stimulation can also contribute to Th17 cell development (39). It has been recently reported that less than nanomolar concentrations of PGE2 can promote Th1 cell differentiation, whereas higher concentrations of PGE2 lead to Th1 cell suppression (40). Our results also indicate the dual effects of PGE2 on IL-23 expression, with higher amounts of PGE2 suppressing and lower amounts of PGE2 enhancing IL-23 production (data not shown). Nevertheless, our study indicates, for the first time to our knowledge, that breast cancer cell-secreted PGE2 enhanced IL-23 production and tumor-associated Th17 cell development (Fig. 4D–F). Given that inhibition of PGE2 synthesis by NS398 in vivo only partially reduced p19 expression in tumor-bearing mice (Fig. 4D), other factors secreted by tumor cells may also be involved in activation of IL-23 during tumor development. It is of interest to investigate the endogenous molecules that induce p19 expression in tumor-bearing hosts. It appears that both EP2 and EP4 receptors are involved in TCM-mediated p19 expression. EP2 has major effects on TCM-mediated p19 induction, whereas EP4 mediates both TCM- and LPS-induced p19 expression, as LPS-induced p19 mRNA expression was also completely abrogated by blocking EP4 receptor (Fig. 4H). This differential involvement of EP2 and EP4 signaling in tumor-associated IL-23 production could be used to develop potential targets for tumor immunotherapy. The transcriptional induction of the p19 subunit by TCM and PGE2 (Fig. 5A–D) suggests that the p19 subunit could be targeted for control of IL-23 production during tumor development. Identification of the CRE site in the p19 promoter essential for control of TCM-induced p19 transcription (Fig. 5E) and clarification of the cAMP/ PKA pathway involved in p19 expression induced by TCM (Fig. 6) will further help us to design more detailed specific molecules targeting only the p19, but not p40, gene transcription.

In conclusion, our study highlights the molecular mechanisms of breast tumor cell-secreted PGE2 in promoting IL-23 expression and Th17 cell expansion. Our findings also shed light on considering different molecules and pathways involved in promoting tumor-associated Th17 cell development as potential targets for future development of tumor treatments.

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Disclosures
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