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RECEIVED 27 June 2025

ACCEPTED 28 July 2025

PUBLISHED 20 August 2025

CITATION

Zhang C, Liu W, Yang P, Lin R, Pu L and
Zhang H (2025) Dual roles of innate immune
cells and cytokines in shaping the breast
cancer microenvironment.
Front. Immunol. 16:1654947.
doi: 10.3389/fimmu.2025.1654947

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Dual roles of innate immune cells and cytokines in shaping the breast cancer microenvironment

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Breast cancer remains the most frequently diagnosed malignancy and a leading cause of cancer-related mortality among women worldwide. Increasing evidence underscores the pivotal yet paradoxical roles of innate immune cells and their associated cytokines in orchestrating the dynamic landscape of the breast tumor immune microenvironment (TIME). Innate immune effectors, including tumor-associated macrophages (TAMs) and natural killer (NK) cells, exert dual functions by either initiating robust antitumor responses or facilitating immune evasion, metastatic dissemination, and therapeutic resistance. For instance, MDSCs suppress T and NK cell activity via STAT3/NF- κ B signaling and modulate the cytokine milieu through IL-10 and TGF- β . Similarly, M2-polarized TAMs promote angiogenesis, epithelial–mesenchymal transition, and chemoresistance via IL-10/STAT3/Bcl-2 pathways. In contrast, NK cells and CD103⁺ DCs mediate tumor cell cytotoxicity and prime antigen-specific immunity, though their activity is frequently compromised in advanced disease. Moreover, key cytokines and chemokines, including IL-6, IL-10, IL-8, TNF- α , TGF- β , and CCL2/5, demonstrate subtype-specific and context-dependent effects, acting as both tumor-promoting and tumor-suppressing agents through complex signaling networks. This review highlights the dualistic nature of innate immune components in breast cancer, discusses their prognostic and therapeutic implications, and proposes novel intervention strategies, such as TAM repolarization, and cytokine modulation, to reprogram the TIME and restore effective immune surveillance, particularly in aggressive subtypes like triple-negative breast cancer.

KEYWORDS

breast cancer, tumor immune microenvironment, innate immune cells, immunomodulatory factors, immune surveillance, prognostic biomarkers

1 Introduction

Breast cancer is the most prevalent malignancy and primary cause of cancer-related death in women worldwide (1, 2). Recent advances in immunotherapy have shown significant potential in improving treatment outcomes and survival rates (3, 4). A comprehensive analysis of the tumor immune microenvironment could optimize immunotherapeutic approaches for breast cancer (5). Studies indicate that immune cells and mediators within this microenvironment not only combat tumors but also promote immune evasion, facilitating cancer progression (6, 7). Shared signaling pathways between immune and oncogenic processes regulate cell proliferation, apoptosis, and angiogenesis (8–11). Early in tumor development, malignant cells manipulate immune components to avoid detection, while advanced tumors establish an immunosuppressive niche, resisting immune-mediated destruction (12).

Effector T cells play a critical role in antitumor immunity, yet their function is often suppressed in breast cancer (13). Meanwhile, innate immune cells including macrophages, natural killer (NK) cells, and myeloid-derived suppressor cells (MDSCs), and mediators exhibit remarkable functional plasticity, exerting either tumoricidal or tumor-promoting effects depending on microenvironmental cues (14–16). The diversity of these immune components varies by tumor subtype and stage, offering diagnostic and prognostic value (17, 18). This review explores the mechanisms of innate immune cells and mediators in breast cancer progression, highlighting their clinical implications.

2 Innate immune cells in the breast cancer immune microenvironment

2.1 NK cells mediate direct antitumor cytotoxicity

NK cells are glycolipid-reactive lymphocytes with intrinsic cytotoxic capacity against tumor cells. Studies have demonstrated that activation of NK cells enhances antitumor immunity and survival in murine models of postoperative metastatic breast cancer (19, 20). Chemotherapeutic agents such as gemcitabine and cyclophosphamide may facilitate NK cell recruitment to the primary tumor site, and in combination with NK cell activation, significantly improve antitumor efficacy and reduce recurrence rates (21–23). In HER2-positive patients receiving adjuvant chemotherapy, the tumor microenvironment exhibited increased infiltration of NK cells and regulatory T cells, with this population showing reduced chemotherapy-related pathological responses (24–26). The increase in regulatory T cells may be associated with NK cell-mediated inhibition of tumor stem cell proliferation, reversal of MDSC-induced immunosuppression, and restoration of T cell proliferation (27, 28). Moreover, distinct NK cell subsets are associated with different stages of breast cancer progression. For instance, CD56^{bright}CD16⁺ and CD56^{dim}CD16[−] NK cell populations are significantly elevated in the peripheral blood of

patients with progressive invasive breast cancer (29). Intratumoral CD56⁺ NK cell density is positively correlated with tumor grade and stage, and although a lower level of CD56⁺ NK cells is generally indicative of favorable prognosis, no clear association has been established with overall survival (30). However, the cytotoxic activity of NK cells is often impaired in advanced-stage breast cancer due to multiple tumor-induced immunosuppressive mechanisms (31). Notably, transforming growth factor-beta (TGF- β), abundantly present in the tumor microenvironment, downregulates the expression of key NK cell-activating receptors such as NKG2D and NKp30, thereby compromising tumor cell recognition and cytolytic function (32–36). Additionally, MDSCs inhibit NK cell cytotoxicity by producing reactive oxygen species, particularly hydrogen peroxide, and immunosuppressive cytokines like TGF- β , which further dampen NK cell activation and IFN- γ production (37, 38). These suppressive pathways collectively lead to NK cell exhaustion, reduced granzyme B/perforin secretion, and impaired tumor control (39, 40). Understanding the mechanisms behind their functional impairment, particularly receptor downregulation and MDSC-mediated suppression, may yield valuable insights for diagnostic and therapeutic innovation.

2.2 Dendritic cells present tumor antigens to activate antigen-specific T cells

DCs, as pivotal antigen-presenting cells in adaptive immunity, play a central role in antitumor responses by promoting the expression of both exogenous and endogenous major histocompatibility complex (MHC) class I and II molecules (41, 42). They facilitate tumor antigen trafficking to draining lymph nodes, cross-present antigens to activate cytotoxic T lymphocytes (CTLs), and orchestrate T cell differentiation and activation (43–45). Among DC subsets, CD103⁺ conventional type 1 dendritic cells (cDC1s) are uniquely equipped for antigen cross-presentation, a process by which exogenous tumor-derived antigens are processed and presented on MHC class I molecules (46, 47). This activation relies on key components such as the Sec22b vesicle trafficking protein, the BATF3 transcription factor, and cross-priming signals via the STING and type I interferon pathways (48–50). Upon migration to lymph nodes, CD103⁺ DCs engage CD8⁺ T cells through MHC-I–peptide complexes and co-stimulatory molecules such as CD80/CD86, ultimately inducing tumor-specific cytotoxic responses (51). However, the frequency and functional competence of CD103⁺ DCs are often reduced in advanced breast cancer, leading to impaired priming of effector CD8⁺ T cells (52, 53). Tumor-derived suppressive cytokines such as IL-10, and TGF- β , as well as hypoxic conditions, inhibit CD103⁺ DC differentiation and antigen-presenting capacity (54, 55). Additionally, elevated expression of PD-L1 on dysfunctional DCs can further suppress T cell activation. These alterations in CD103⁺ DC function contribute to ineffective antitumor immunity, enhanced immune evasion, and poor therapeutic outcomes. Recent studies have shown that CD103⁺ DCs are capable of delivering intact tumor antigens to peripheral lymph nodes, thereby priming tumor-specific CD8⁺ T

cells and locally suppressing PD-L1 activity (52, 56). However, current research on DCs in the breast cancer context remains limited, and further mechanistic studies are warranted.

2.3 MDSCs promote breast cancer progression and affect prognosis through multiple signaling pathways and immunomodulatory factors

MDSCs comprise a heterogeneous population of myeloid progenitor cells, including immature granulocytic (G-MDSC) and monocytic (M-MDSC) subsets (57, 58). Clinical data indicate a close association between MDSC levels and breast cancer stage, tumor burden in metastatic disease, and chemotherapy efficacy (59). Elevated MDSC levels are linked to increased risk of postoperative recurrence and metastasis, whereas patients with lower MDSC counts demonstrate higher rates of pathological complete response (60, 61). In stage IV breast cancer patients, high levels of HLA-DR^{neg/low}, CD33⁺, CD11b⁺ MDSCs are associated with significantly reduced survival (62). Furthermore, MDSCs can promote the production of IL-1 β and IL-17, reducing the efficacy of chemotherapeutic agents such as 5-fluorouracil and gemcitabine, thereby adversely affecting prognosis (63, 64). Mechanistically, MDSCs in the breast tumor microenvironment promote invasion and metastasis via pathways such as STAT3-NF- κ B-IDO, STAT3/IRF-8, and PTEN/Akt (65), involving both inhibitory and stimulatory cytokines. These pathways drive MDSC expansion and lead to downstream functional consequences that impair antitumor immunity. For instance, activation of STAT3 induces expression of arginase-1 and iNOS, resulting in depletion of L-arginine and accumulation of reactive oxygen species (ROS), which in turn inhibit CD8⁺ T cell receptor ζ -chain expression and induce T cell anergy (66–68). Concurrently, IL-2 production suppression further impairs T cell proliferation and effector function (69). The PTEN/AKT axis supports MDSC resistance to apoptosis and enhances their immunosuppressive capacity through sustained IL-10 and TGF- β secretion (65). Collectively, these mechanisms contribute to immune evasion, tumor progression, and treatment resistance.

On one hand, cytokines such as TGF- β and Flt3L induce CD11b⁺ MDSC differentiation, while IL-6 and IL-18 promote CD33⁺ MDSC proliferation (70). Chemokines including CXCL5/CXCR2 are essential for MDSC recruitment in 4T1 BALB/c murine tumor models, while CCL1, CCL2, CCL5, GM-CSF, and G-CSF facilitate MDSC expansion and aggregation in the tumor milieu (71–73). On the other hand, MDSCs suppress antitumor immune responses by modulating the cytokine environment and cellular interactions. For example, MDSCs induce Th17 differentiation, mediate crosstalk between macrophages and tumor cells, and reshape the local microenvironment to favor tumor cell growth and metastasis (74). They also secrete IL-10 and TGF- β to promote regulatory T cell expansion, and enhance Treg activation through arginine metabolism

and TGF- β -mediated pathways, contributing to immune suppression (75, 76). Additionally, MDSCs downregulate NK cell activation by producing TGF- β and hydrogen peroxide, which suppress the expression of NK cell-activating receptors such as NKG2D, NKp46, and NKp44 (76). Some MDSC subsets, particularly under hypoxic conditions, upregulate PD-L1 expression via HIF-1 α activation; however, this phenomenon is not universal across all MDSC populations (77). In summary, MDSC accumulation in the breast cancer microenvironment may compromise surgical and chemotherapeutic efficacy. Targeting MDSC recruitment and immunosuppressive functions via multiple regulatory pathways holds promise for enhancing therapeutic outcomes.

2.4 TAMs mediate broad immunosuppressive effects through multiple mechanisms

Tumor-associated macrophages (TAMs) originate from circulating monocytes that infiltrate the tumor microenvironment and subsequently undergo polarization into either classically activated M1 or alternatively activated M2 phenotypes (78). The recruitment of TAMs is driven by chemokines such as CCL2 and cytokines like CSF-1 and VEGF, which establish a permissive environment for macrophage infiltration (79–81). Once recruited, macrophage polarization is largely dictated by local signals. Hypoxic conditions, IL-4, IL-10, and TGF- β collectively promote the differentiation of macrophages into the M2 phenotype, which is closely associated with immunosuppressive and tumor-promoting functions (82–85). M2-polarized TAMs play key roles in tumor angiogenesis, epithelial–mesenchymal transition (EMT), metastasis, and tissue remodeling (86). The S1PR1 gene in TAMs inhibits pulmonary metastasis and lymphangiogenesis in murine breast cancer models by downregulating inflammatory component NLRP3 (87). COX2⁺ TAMs induce MMP-9 expression and promote EMT in the breast tumor microenvironment. The COX2/PGE2 axis also enhances IL-6 secretion from macrophages, exacerbating inflammation and further promoting tumor progression (88). Under hypoxic conditions, TAMs upregulate VEGF and HIF-1 α expression to stimulate tumor angiogenesis (89). In triple-negative breast cancer, TAMs are recruited from peripheral circulation and, upon classical or alternative activation, contribute to tumor progression by suppressing cytokine production, impairing TILs function, promoting Treg expansion, and modulating PD-1 expression in the tumor milieu (90). Regarding chemoresistance, paclitaxel efficacy has been linked to M2 TAM depletion (91). Moreover, TAM-induced resistance is mediated by increased expression of Bcl-2 and STAT3, enhancing IL-10 secretion via the IL-10/STAT3/Bcl-2 signaling cascade to suppress antitumor immunity (85). In conclusion, TAMs exert multifaceted immunosuppressive effects within the breast cancer microenvironment by promoting angiogenesis, metastasis, immune evasion, and therapeutic resistance (Figure 1).

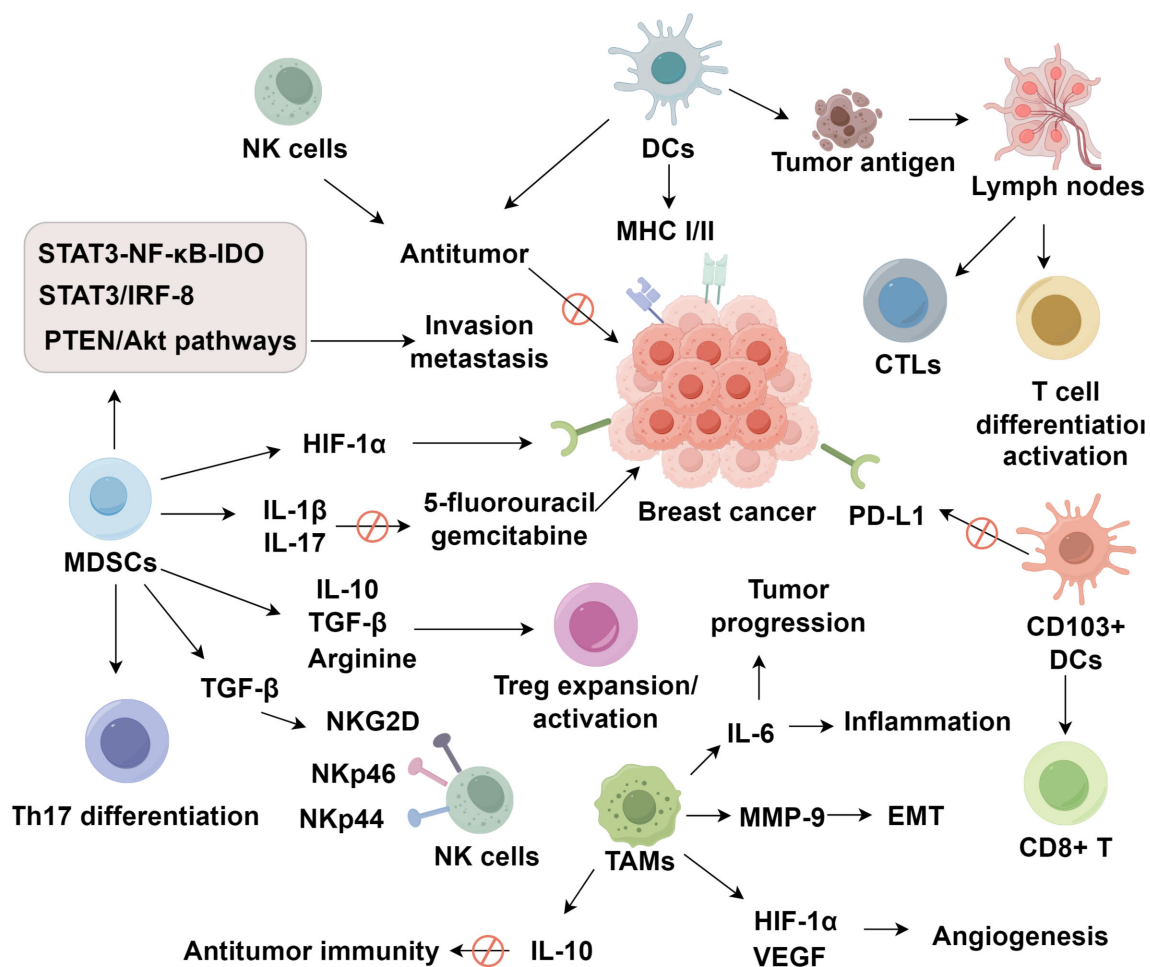


FIGURE 1
Roles of innate immune cells and cytokines in shaping the breast cancer microenvironment.

3 Innate immune factors in the tumor immune microenvironment of breast cancer

3.1 Dual roles of interleukins in breast cancer

Interleukins comprise a diverse family of lymphokines with pleiotropic biological activities. Their roles in breast cancer are highly context-dependent and vary by subtype. IL-6, for instance, is upregulated in over half of breast cancer patients, with elevated levels particularly noted in early-stage or high-grade tumors (92). In estrogen receptor (ER) positive breast cancer cell lines, IL-6 generally exhibits tumor-suppressive properties, while no significant effect has been observed in ER-negative cell lines (93, 94). Mechanistically, IL-6 promotes phosphorylation of JAK/STAT3 via interaction with its homodimeric or heterodimeric receptor complexes, thereby activating transcriptional programs. The feedback loop further enhances IL-6 expression via activated STAT3, rendering IL-6 less effective in breast cancer cells with low

STAT3 expression (95). IL-8, a proinflammatory chemokine-like cytokine, is associated with poor survival in ER-negative patients (96). It promotes lymph node metastasis and is elevated in advanced-stage tumors. Nonetheless, some studies suggest its involvement in immune activation under certain conditions, illustrating its duality (97–99). IL-10 is generally considered an immunosuppressive cytokine and is associated with poor prognosis in breast cancer. Its expression is regulated primarily through the STAT3 and SOCS3 pathways, where STAT3 silencing markedly reduces IL-10 levels, while SOCS3 silencing enhances its expression (100). The IL-10/STAT3/Bcl-2 axis plays a pivotal role in mediating TAM-induced breast cancer cell survival and paclitaxel resistance. Inhibition of IL-10 receptor signaling enhances CD8⁺ T cell responses and upregulates IL-12 and intratumoral dendritic cells, thereby improving chemotherapy efficacy (101).

IL-11 exerts its effects through binding to IL-11 receptor alpha (IL-11Ra) and gp130, activating JAK kinases and downstream STAT3 and SOCS3. These pathways regulate tumor cell proliferation, survival, motility, and invasion (102). In breast cancer patients with bone metastases, elevated IL-11 mRNA and increased expression of p38, p-c-Jun, and p-STAT3 have been

observed, highlighting its predictive value for bone metastatic potential (103). IL-15 primarily exerts indirect antitumor effects in the TIME. Through activation of PI3K signaling, IL-15 selectively stimulates T lymphocytes and enhances vaccine-like antitumor responses in combination with MEK inhibitors (104). It also potentiates NK cell-mediated cytotoxicity against CD44⁺CD24⁻ breast cancer stem-like cells and augments cetuximab efficacy (105). In a study by Gillgrass et al. (106), C57BL/6 mice receiving IL-15 via intravenous injection or harboring IL-15 transgenes exhibited a tenfold reduction in breast cancer metastasis compared to controls, likely due to enhanced NK cell cytotoxicity. Collectively, ILs exert tumor-promoting or tumor-suppressing effects in breast cancer primarily through engagement with specific receptors and activation of downstream signaling cascades. Deciphering their mechanistic roles may offer prognostic biomarkers and therapeutic targets (Supplementary Table S1).

3.2 Chemokines promote breast cancer cell invasion and metastasis

A growing body of clinical evidence supports the pivotal role of chemokines in breast cancer metastatic dissemination, and prognosis (107, 108). CCL2 and CCL5 are among the most extensively studied chemokines in the breast cancer microenvironment. In estrogen-rich conditions, both enhance tumor cell dissemination (109). Notably, levels of CCL2 and CCL5 are significantly elevated in the blood of breast cancer patients, particularly those with ER-positive tumors, and positively correlate with TAM infiltration (110). Persistent expression of CCL2 by mammary epithelial cells promotes chronic low-grade inflammation, increases glandular density, and elevates cancer risk (111). CCL2 may also modulate monocyte-macrophage crosstalk within the tumor niche (112). ELISA results indicate genotype-dependent differences in CCL2 expression across breast cancer cell suspensions, with an inverse correlation to ER and PR status. Kaplan-Meier analysis further associates low CCL2 levels with favorable prognosis (112). CCL5 enhances GLUT1 expression on tumor cells, promoting glucose uptake and metabolic reprogramming to support proliferation (113). In CCL5-deficient mice, both primary tumor burden and pulmonary metastases are markedly reduced. This may be attributed to CCR3 activation, Gfi1 expression, and Th2 polarization, which collectively establish a pre-metastatic niche conducive to myeloid cell recruitment (114). CCL18, CCL20, and CCL25 similarly contribute to prognosis prediction and promote TAM infiltration, angiogenesis, and metastatic progression (115–117). Serum CCL18 levels are significantly higher in breast cancer patients than in those with benign tumors or healthy controls, correlating with advanced clinical stage and poor survival (118). CCL20 facilitates tumor invasion and MMP-2/9 secretion in basal-like TNBC, with high CCL20 expression predicting reduced metastasis-free and overall survival (119). CCL25 promotes EMT via the CCL25/CCR9 axis, enhancing invasiveness and metastatic potential (120). Besides, CXCL1 expression in the tumor stroma is associated with tumor grade and recurrence, likely due to its negative

regulation by TGF- β (121). CXCL13 transcription correlates with pathological complete response rates and favorable immune responses in breast cancer, possibly through activation of TFH13 cells and differentiation of germinal center memory B cells, thereby shifting from regulatory T cell-mediated suppression toward effective humoral immunity (122, 123).

3.3 TNF- α : a double-edged sword in breast cancer progression

TNF- α , a proinflammatory cytokine, orchestrates tissue homeostasis by regulating cytokine production, cell survival, and apoptosis (124). On one hand, TNF- α induces cell cycle arrest in ER-positive breast cancer cells at the G0/G1 phase, impeding DNA synthesis and exerting tumor-suppressive effects. On the other hand, it activates the NF- κ B pathway and facilitates RIP1 ubiquitination, thereby stimulating JNK/ROS signaling and promoting tumor cell proliferation, enhancing the cytotoxic effects of chemotherapy and radiotherapy both *in vitro* and *in vivo* (125). Clinical data suggest that TNF- α levels are negative associated with breast cancer progression risk (126). However, TNF- α can also promote tumor growth, migration, and invasion, potentially through activation of the Wnt pathway and establishment of a tumor-permissive niche (127). Notably, the interpretation of TNF- α 's dual roles is limited by heterogeneity in immune status, inflammation levels, and disease stage across studies, necessitating further investigation (128).

3.4 TGF- β promotes breast cancer cell proliferation and metastasis

TGF- β , primarily synthesized by platelets, monocytes/macrophages, lymphocytes, fibroblasts, and epithelial cells, plays a central role in tumor progression, with TGF- β 1 as the predominant isoform (129). TGF- β 1 stimulates angiogenesis and enhances tumor cell affinity, invasiveness, and adhesion, while inhibiting normal mammary epithelial cell proliferation (130). Current research implicates the Smad signaling pathway as a major mediator of TGF- β -induced distant metastasis in breast cancer (131). TGF- β also suppresses IL-2 production and impairs T cell antitumor activity (132, 133). Additionally, it upregulates local cytokine expression, activates infiltrating immune cells, inhibits granzyme and perforin expression, downregulates MHC class I on tumor cells, and diminishes NK cell-mediated cytotoxicity (134). Importantly, TGF- β signaling has been shown to facilitate EMT and endow breast cancer cells with stem cell-like properties (135, 136). This dual role not only promotes tumor invasion and metastasis but also contributes to immune evasion through induction of an immunosuppressive microenvironment. Mechanistically, TGF- β activates EMT through canonical Smad-mediated transcriptional reprogramming and MAPK signaling pathways (137). Recent studies demonstrate that FAP/VCAN enhances the expression of EMT-associated transcription factors, further driving mesenchymal

transition and increasing tumor cell plasticity (138). Moreover, TGF- β -induced PI3K/Akt activation promotes the expression of stemness markers like ALDH1 and CD44^{high}/CD24^{low}, enabling tumor-initiating capacity and resistance to chemotherapy (139). This signaling crosstalk between PI3K/Akt and Smad pathways orchestrates both immune suppression and cellular reprogramming, allowing breast cancer cells to evade immune surveillance while acquiring aggressive phenotypes. Through PI3K/Akt signaling, TGF- β can further induce EMT, thereby enhancing tumor growth and dissemination (140, 141).

4 Conclusion

The breast cancer immune microenvironment is profoundly shaped by the dual roles of innate immune cells and cytokines, which can either support antitumor immunity or promote immune evasion and disease progression. MDSCs and TAMs are central mediators of immunosuppression through pathways such as STAT3/NF- κ B and IL-10/STAT3/Bcl-2, while NK cells and dendritic cells retain critical, yet often impaired, antitumor functions. Additionally, cytokines such as IL-6, IL-8, IL-10, TNF- α , and TGF- β demonstrate context-dependent activities, intricately regulating immune responses, tumor growth, and metastasis. The functional plasticity of these innate components highlights both the complexity and therapeutic potential of targeting the innate immune axis in breast cancer. Particularly in subtypes like triple-negative breast cancer, which lack effective targeted therapies, strategies aimed at reprogramming innate immune cells, blocking suppressive cytokines, or restoring cytotoxic activity could significantly enhance clinical outcomes. A deeper mechanistic understanding of innate immunity will not only advance prognostic biomarker development but also enable the design of rational combination therapies that synergize immunomodulation with conventional and emerging treatment modalities.

Author contributions

CZ: Writing – original draft. WL: Writing – original draft. PY: Writing – original draft. RL: Writing – original draft. LP: Writing –

original draft, Writing – review & editing. HZ: Writing – original draft.

Funding

The author(s) declare financial support was received for the research and/or publication of this article. This work was supported by Research Project of Sichuan Provincial Research Center for the Development of Primary Health Care (No: SWFZ24-W-20) and Nanchong Science and Technology Project (Grant No.22YYJCYJ0088).

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Supplementary material

The Supplementary Material for this article can be found online at: <https://www.frontiersin.org/articles/10.3389/fimmu.2025.1654947/full#supplementary-material>

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