

Review Article

Receptor tyrosine kinases in breast cancer treatment: unraveling the potential

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Abstract: Breast cancer is a multifactorial disease driven by acquired genetic and epigenetic changes that lead to aberrant regulation of cellular signaling pathways. Receptor tyrosine kinases (RTKs), a class of critical receptors, are involved in the initiation and progression of breast cancer. RTKs are cell surface receptors with unique structures and biological characteristics, which respond to environmental signals by initiating signaling cascades such as the mitogen-activated protein kinase (MAPK) pathway, Janus kinase (JAK)/signal transducer, activator of transcription (STAT) pathway, and phosphoinositide 3-kinase (PI3K)/AKT pathway. The critical role of RTKs makes them suitable targets for breast cancer treatment. Targeted therapies against RTKs have been developed in recent years, evaluated in clinical trials, and approved for several cancer types, including breast cancer. However, breast cancer displays molecular heterogeneity and exhibits different therapeutic responses to various drug types, leading to limited effectiveness of targeted therapy against RTKs. In this review, we summarize the structural and functional characteristics of selected RTKs and discuss the mechanisms and current status of drug therapy involving different protein tyrosine kinases in breast cancer progression.

Keywords: Receptor tyrosine kinases, breast cancer, tyrosine protein kinase inhibitors, anti-RTK therapy, drug resistance, targeted therapy

Introduction

Breast cancer (BC) is the most prevalent and highly fatal tumor among women worldwide [1]. It can be classified into five distinct subtypes: luminal A/B, HER2-positive (HER+), basal-like, claudin-low, and normal breast-like, based on the expression levels of estrogen receptor (ER), progesterone receptor (PR), HER2, cytokeratin 5/6 (CK5/6), and claudins 3/4/7 [2-4]. Among these, triple-negative breast cancer (TNBC) accounts for 15-20% of breast cancer and shares remarkable similarities with basal-like breast cancer. TNBC lacks the expression of ER, PR, and HER2, and is characterized by its high metastatic capacity [5, 6].

Breast cancer is a consequence of dysregulation in multiple signaling pathways within the epithelial cells of the breast. The activation of growth factors and chemokines disrupts diverse signaling cascades in the tumor micro-

environment, thereby contributing to cancer progression [7, 8]. Playing a crucial role in this process, receptor tyrosine kinases (RTKs) are a vital family of receptors that regulate essential biological processes, including cell proliferation, differentiation, metabolism, and survival [9]. They achieve this by initiating downstream signaling pathways.

RTKs are single-pass transmembrane proteins expressed in various cell types. Multiple RTKs, such as epidermal growth factor receptors (EGFRs), vascular endothelial growth factor receptors (VEGFRs), platelet-derived growth factor receptors (PDGFRs), insulin-like growth factor receptors (IGFRs), and fibroblast growth factor receptors (FGFRs), are expressed in different types of tumors, including breast cancer [9-11]. Elevated levels of RTKs have been associated with increased invasiveness of breast cancer and decreased overall and disease-free survival rates [12]. Ligand binding induces conforma-

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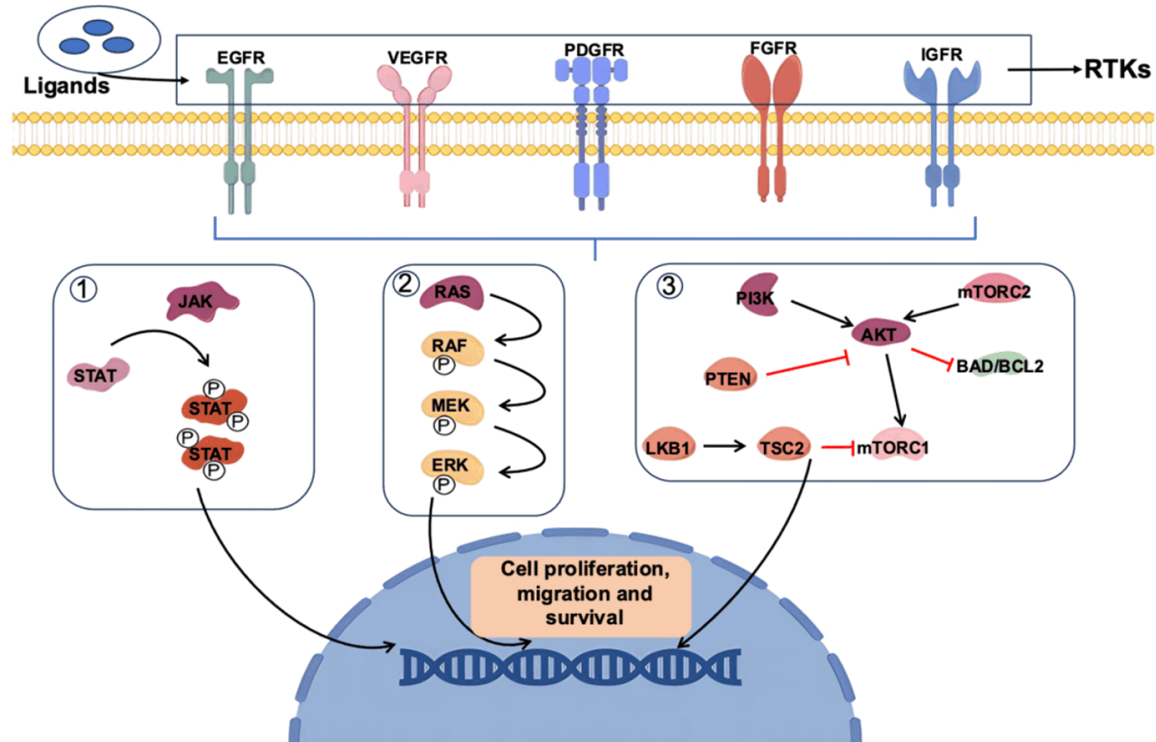


Figure 1. RTK-regulated important signaling in breast cancer progression. (1) Once a ligand binds to the receptor, two STAT proteins are phosphorylated by JAK forming a dimer that enters the nucleus, causing the transcription of target genes. (2) After the TKR is activated by a ligand, Ras dimerizes and binds Raf, promoting Raf activation. Active Raf phosphorylates and activates MEK1/2 which induces ERK1/2 activation, leading to transcription activation. (3) PI3K phosphorylates phosphatidylinositol-bisphosphate (PIP2) to PIP3, a process that can be reversed by the action of PTEN. PIP3 causes the activation of Akt in the plasma membrane, thereby activating the mTOR complex, one of the major pathways involved in tumorigenesis. The above have represented the interaction between various signaling pathways activated through RTKs and involved in tumor proliferation.

tional changes in RTKs, subsequently activating downstream signals. Key pathways known to be activated by RTKs include the mitogen-activated protein kinase (MAPK), Janus kinase (JAK)/signal transducer and activator of transcription (STAT), as well as phosphoinositide 3-kinase (PI3K)/AKT pathway [13-17]. These RTK-activated pathways play pivotal roles in various aspects of breast cancer progression (Figure 1).

Due to the significant role of RTKs in breast cancer progression, targeting RTKs may contribute to cancer treatment. Over the years, targeted therapies against RTKs, including small molecule inhibitors and monoclonal antibodies, have demonstrated efficacy in cancer treatment [18, 19]. Among them, drugs such as lapatinib, trastuzumab, and bevacizumab have gained approval from the U.S. Food and Drug Administration (FDA) for the clinical management of breast cancer. Furthermore, RTK

inhibitors have shown promise in overcoming multidrug resistance and improving disease-free survival rates in patients with metastatic breast cancer [20]. Despite the clinical benefits of anti-RTK therapy for breast cancer, the primary and acquired resistance significantly limits the effectiveness of RTK-targeted treatments. Therefore, further research is essential to overcome this challenge and enhance the efficacy of RTK-targeted therapies [21]. In this review, we have delved into the intricate signaling cascades of EGFR, VEGFR, PDGFR, FGFR, and other key receptors implicated in breast cancer. Our exploration of the role of RTK inhibitors in breast cancer treatment offers valuable insights into the potential for targeted therapy. Understanding the underlying mechanisms and the potential benefits of RTK inhibitors can contribute to more effective and personalized treatment strategies for breast cancer patients, ultimately improving their clinical outcomes.

Functions and targeted drugs of RTKs

Features of RTKs

RTKs, integral membrane proteins, are activated through specific ligand interactions. These receptors consist of distinct domains, including extracellular ligand-binding regions, a transmembrane domain, and intracellular kinase domains [22]. Remarkably, each receptor class exhibits unique structural and sequence characteristics within their extracellular domains, defining their ligand specificity. Various protein motifs, such as immunoglobulin-like (Ig) domains, leucine-rich domains (L domains), cysteine-rich domains (CR domains), or fibronectin type III (Fn3) domains, are specifically present in different receptors. Conversely, the intracellular domains encompass the tyrosine kinase domain and the C-terminal region [23]. Some receptors possess insertions that separate the kinase domain when varying lengths of sequences are inserted [24]. Additionally, the C-terminal domains of RTKs differ among the family members, contributing to the specificity and diversity of downstream signaling. Their catalytic activity enables tyrosine residue phosphorylation, which is triggered by ligand binding to the extracellular domains of RTK proteins, thereby stabilizing the active state [25, 26].

Mechanism of RTK activation

RTKs, a superfamily of 58 members into 20 subfamilies [27, 28], share two key features: ligand-induced dimerization and auto-phosphorylation of tyrosine residues [29]. As for the first one, conformational changes occur in the monomeric or self-inhibited receptors. This enables the receptors to form dimers, which facilitates the enhancement of tyrosine kinase activity. Subsequently, the kinase domain and the C-terminal region of RTKs undergo auto-phosphorylation at specific tyrosine residues. This auto-phosphorylation plays a crucial role in the assembly of signaling molecules comprising Src homology 2 (SH2) and phosphotyrosine-binding domains [30].

RTKs primarily interact with soluble ligands, such as growth factors, cytokines, and hormones, to initiate signal transduction pathways [25, 27]. These ligands engage a repertoire of downstream signaling components, including kinases like PI3K and SRC, adaptor proteins

like SHC and GRB2, transcription factors like STAT, ubiquitin ligases, and phospholipases such as phospholipase C-gamma (PLC- γ) [13-17]. These signaling cascades activate various pathways, including MAPK, PI3K/AKT/mammalian target of rapamycin (mTOR), PLC- γ /protein kinase C, and JAK/STAT pathways. It is important to note that RTK signaling can occur both intracellularly and at the cell surface, with distinct signaling pathways depending on the subcellular localization of the receptors [31]. Ultimately, the activation of RTKs leads to diverse biological responses, including cell growth, survival, inhibition of apoptosis, stimulation of angiogenesis, and promotion of cell motility (**Figure 2**) [32].

Development of RTKs-targeted drugs

RTKs have emerged as central players in regulating critical cellular processes, including cell growth, survival, organ morphogenesis, angiogenesis, and tissue regeneration [33, 34]. While RTK activity is intricately regulated in normal cells, dysregulated or constitutive activation of RTKs has been observed across a wide variety of cancers. Aberrant activation can stem from functional mutations, gene rearrangements, amplification, overexpression, or abnormal autocrine, endocrine, as well as paracrine signaling between receptors and ligands. Notably, these aberrations have been found to correlate with the progression of various human cancers [35-37].

Targeting RTKs has shown promising therapeutic benefits. In colorectal cancer, for instance, alterations in EGFR ligands [38], dual mutations in associated proteins, epidermal regulatory protein irregularities, and transforming growth factor-alpha (TGF- α) have been established as predictive biomarkers and prognostic indicators for the response to anti-EGFR antibodies, such as cetuximab or panitumumab [39]. Similarly, EGFR mutations, anaplastic lymphoma kinase (ALK) and ROS proto-oncogene 1 (ROS1) translocations in non-small cell lung cancer (NSCLC), ret proto-oncogene (RET) mutations in medullary thyroid carcinoma (MTC), and HER2 amplification in breast cancer have been identified, paving the way for targeted therapeutic strategies [40, 41]. In fact, over the last decade, RTK-targeted therapies have demonstrated significant improvements in the

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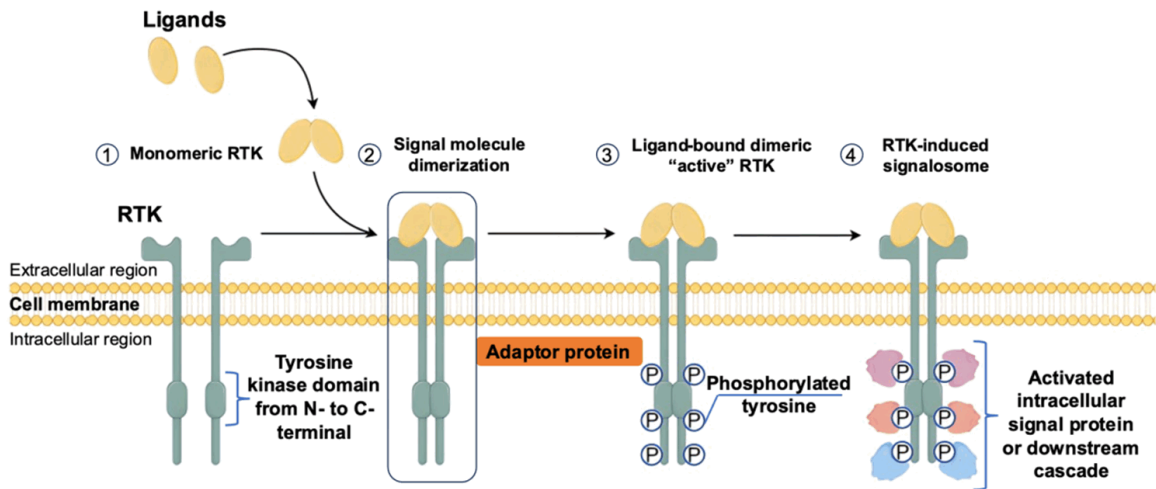


Figure 2. Classical Structure of receptor tyrosine kinase and activation mechanism. (1) At first, RTKs reside at the cell membrane as a monomer. (2) Upon ligand binding, RTKs are activated through the formation of inter-molecular dimerization in the presence of ligands, resulting in kinase activation and phosphorylation of the receptor C-terminal tail. (3) Phosphorylated RTK either serves as a docking site for adaptor proteins or may directly phosphorylate signaling molecules.

treatment of selected cancer patients [42-46]. Their ability to selectively inhibit constitutively activated RTKs within tumor cells holds promise as a novel approach for cancer treatment [47].

In summary, gaining insights into the mechanisms that drive the activation of RTKs, particularly within the context of specific RTKs, helps us understand crucial cellular processes with significant implications in cancer (Table 1) [48-52]. Moreover, advancements in targeting these aberrant signaling pathways have opened new possibilities for therapeutic interventions, bringing hope for improved outcomes in the treatment of cancer.

The drugs targeting tyrosine kinases can be categorized into antibody-based therapies and small molecule inhibitors. Currently, there are 87 approved small-molecule kinase inhibitors worldwide, with the majority of the 71 small molecule kinase inhibitors approved by the FDA being tyrosine protein kinase inhibitors (TKIs), which find their primary application in oncology [53-58] (Table 2).

In breast cancer, overexpression of HER2 occurs in approximately 25% of patients and is associated with lower survival rates [59, 60]. Similarly, EGFR is frequently upregulated in solid tumors and plays a role in various malignant characteristics such as proliferation,

apoptosis resistance, and tumor cell mobility. These discoveries have paved the way for the development of antibodies targeting HER2 and EGFR, and the success of drugs like trastuzumab and cetuximab validates the efficacy of targeting these growth factor receptors [61, 62]. Moreover, successful interventions using RTK inhibitors include imatinib for the treatment of gastrointestinal stromal tumors harboring c-Kit mutations and gefitinib as well as erlotinib for NSCLC patients with EGFR mutations [49]. In addition to its inhibition of BCR-ABL and SRC, sunitinib also targets multiple RTKs such as PDGFR and VEGFR on endothelial cells, both of which play roles in tumor angiogenesis and proliferation [63].

Based on clinical trial data for small molecule kinase inhibitors (SMKIs) [64], there are currently approximately 110 novel kinases being investigated as potential targets [51, 52, 55, 56, 65-67]. The approved kinase inhibitors only cover around 30% of the human kinase, indicating that there are still numerous untapped areas within this kind of drugs waiting to be explored.

The role of RTK signaling in breast cancer progression

Under normal physiological conditions, the activity levels of RTKs are tightly balanced through the mechanisms mentioned above, as

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Table 1. Classification and therapeutic applications of RTKs

Receptor family	Receptor	Applications
Epidermal growth factor receptor, EGFR	HER1, HER2, HER3, HER4	Non-small cell lung cancer, head and neck tumors, colorectal cancer, pancreatic cancer, breast cancer, ovarian cancer, cervical cancer
Insulin receptor, INSR	IGF-I, IGF-II, INSR, INSRR	Breast cancer, hematological malignancies, colorectal cancer, lung cancer, cervical cancer
Platelet-derived growth factor receptor, PDGFR	PDGFR α , PDGFR β , CSF-1R, SCFR, FLK2, FLT3	Hypereosinophilic syndrome, mastocytosis, gastrointestinal stromal tumor, epithelial cell tumor, leukemia
Fibroblast growth factor receptor, FGFR	FGFR1, FGFR2, FGFR3, FGFR4	Angiogenesis
Vascular endothelial growth factor receptor, VEGFR	VEGFR1, VEGFR2, VEGFR3, VEGFR4	Hepatocellular carcinoma, lung cancer, ovarian cancer
Hepatocyte growth factor receptor, HGFR	HGFR, MSPR	Breast cancer, colorectal cancer, gastric cancer, prostate cancer, renal cell carcinoma
Angiopoietins receptor of Tie family	Tie1, Tie2, TEK	Hemangioblastoma, epithelial cell tumor, gastric cancer, hepatocellular carcinoma

Table 2. List of FDA-approved TKIs

Targeted kinase	Name of the drugs
ALK	Alectinib, Crizotinib, Brigatinib, Lorlatinib, Ceritinib
Bcr-Abl	Bosutinib, Dasatinib, Nilotinib, Ponatinib, Imatinib
BTK	Acalabrutinib, Ibrutinib, Zarubrutinib
C-Met	Crizotinib, Cabozantinib
EGFR	Erlotinib, Afatinib, Gefitinib, Dacomitinib, Osimertinib, Neratinib
JAKs	Ruxolitinib, Baricitinib, Tofacitinib
PDGFR	Lenvatinib, Nintedanib, Ponatinib, Regorafenib, Imatinib
RET	Lenvatinib, Regorafenib, Sunitinib, Vandetanib
SRC	Dasatinib, Bosutinib, Ponatinib
VEGFR	Axitinib, Lenvatinib, Regorafenib, Pazopanib, Nintedanib, Sorafenib, Sunitinib
FGFR	Nintedanib, Erdafitinib
c-Kit	Pexidartinib, Avapritinib
FLT3	Gelretinib, Sunitinib

well as interactions with other molecules, including tyrosine phosphatases [68]. RTKs acquire activating capabilities through various mechanisms, such as gain-of-function mutations, genomic amplification, chromosomal rearrangements, and autocrine activation [9], ultimately resulting in the disruption of the balance between cell proliferation and cell death [22]. Moreover, when considering the intricate regulation of RTK signaling in terms of time and space, the dysregulation becomes even more intricate [69]. Constitutive activation of RTKs can endow normal cells with oncogenic properties, initiating tumorigenesis driven by these receptors [70].

The RTK pathway exhibits diverse mechanisms and clinical significance across different subtypes of breast cancer [25]. In HR+ (hormone

receptor-positive) breast cancer, RTK pathways such as EGFR and HER2 contribute to tumor progression by promoting cell proliferation and survival [49]. The interplay between hormone receptor activation and RTK signaling pathways further enhances cellular dependence on hormones [71]. In HER2+ breast cancer, overexpression of HER2 leads to the activation of downstream signaling pathways, including PI3K/AKT and MAPK, thereby fostering cell proliferation and anti-apoptotic effects [72]. The RTK pathway plays a pivotal role in this subtype, and targeted therapies against HER2, like trastuzumab, have achieved remarkable success in improving patient outcomes [73].

TNBC (triple-negative breast cancer), characterized by the absence of HR and HER2 expres-

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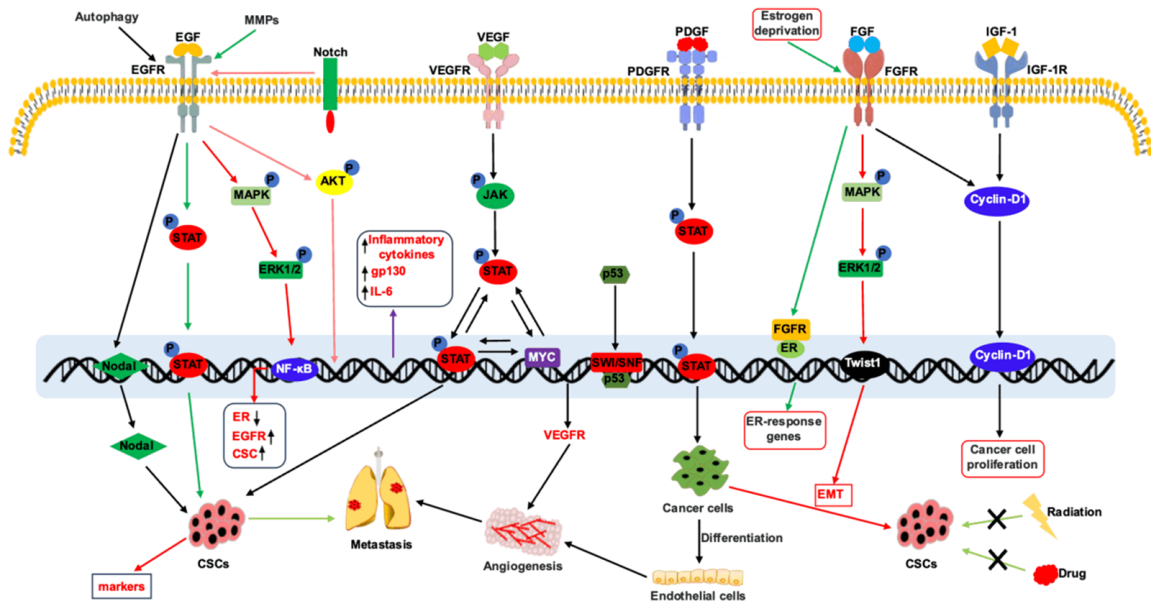


Figure 3. RTK-regulated signaling in breast cancer progression. (1) EGFR regulates the activation of JAK/STAT and MAPK signaling pathway to induce expression of stem cell markers leading to enrichment of cancer stem cells. EGFR induces Akt phosphorylation to promote inflammation. EGFR-regulated signaling also plays pivotal role in angiogenesis and metastasis. (2) VEGFR activates JAK/STAT signaling pathway to induce cancer stem cell phenotype through MYC expression. Mutant p53 induces the expression of VEGFR through the interaction with SWI/SNF complex. (3) PDGFR is expressed on stromal cells such as fibroblasts and is a marker of fibroblast activation. PDGFR-regulated STAT activation is involved in the differentiation of cancer cells to endothelial cells leading to angiogenesis. (4) FGFR-activated MAPK pathway induces EMT and CSC phenotype. (5) Cooperation between the FGFR and IGF-1R regulates nuclear translocation of Cyclin D1 leading to enhanced cancer cell proliferation.

sion, may see RTK pathways like EGFR and FGFR facilitate tumorigenesis and progression through distinct signaling mechanisms [74-77]. The absence of specific targets renders TNBC treatment challenging, yet ongoing research into RTK pathways is exploring novel targeted therapeutic strategies [78-80]. Heterogeneity in mutations and expression levels of RTK pathways across different breast cancer subtypes influences tumor biology and treatment responses [81, 82].

Next, we delve into the specific mechanisms of RTK pathways across different breast cancer subtypes (**Figure 3**), as an understanding of these mechanisms holds the potential to enhance prognosis and quality of life for breast cancer patients [25, 73, 75, 77, 83-91].

EGFR: key regulator of cancer stem cell phenotype and metastasis

EGFR, a member of the ErbB family, is an RTK comprised of four closely related receptors: EGFR1 (EGFR, HER1, c-ErbB1), HER2 (EGFR2,

c-ErbB2), EGFR3 (c-ErbB3, HER3), and EGFR4 (c-ErbB4, HER4). These receptors are situated on the cell membrane and consist of an extracellular ligand-binding domain, a transmembrane hydrophobic region, and an intracellular RTK domain [92, 93]. Activation of EGFR occurs upon binding with its ligand. Ligand binding induces conformational changes in the receptor, facilitating the formation of either homodimers or heterodimers with other ErbB receptors [94]. Dimerization leads to cross-phosphorylation of conserved tyrosine residues within the kinase domain, resulting in the activation of downstream signaling pathways such as MAPK/ERK1/2 and PI3K/AKT. These pathways regulate vital cellular processes including proliferation, survival, migration, differentiation, and metastasis [95, 96].

The EGFR signaling pathway is meticulously regulated in normal cells. However, alterations in EGFR expression and ligand overexpression in tumor cells can disrupt the balance, leading to abnormal autocrine or paracrine stimulation and increased activation of the tyrosine kinase

domain [97]. Consequently, this aberrant signaling promotes cell proliferation, differentiation, angiogenesis, and apoptosis suppression, ultimately facilitating tumor growth and metastasis [98]. Overexpression of EGFR is commonly observed in breast cancer tissues and is associated with heightened invasiveness and poor clinical outcomes [99]. Studies have revealed that EGFR and HER-2 are overexpressed in approximately 30% of invasive breast cancers and are correlated with tumor recurrence and overall survival. Furthermore, EGFR overexpression is observed in over half of TNBC cases, accounting for 15% of all breast cancers [100]. Research has revealed a positive correlation between EGFR expression and tumor pathological grade, while a negative correlation exists between EGFR expression and ER expression in breast cancer. Additionally, ER levels negatively correlate with cancer stem cell phenotype. These findings suggest that ER-negative TNBCs exhibit higher levels of EGFR expression and harbor a population of stem cells [98].

Inflammatory breast cancer (IBC) is an aggressive, fatal type marked by a significant number of chemo- and radio-resistant CSCs. Approximately 30% of IBC cases exhibit EGFR expression, rising to 40-50% in ER- and PR-negative cases [98, 100, 101]. High EGFR expression predicts worse prognosis and higher recurrence risk in IBC. Studies have demonstrated that using EGFR antibodies effectively reduces SUM149 cell proliferation, indicating the potential of targeting EGFR in IBC [102-104]. EGFR-HER2 heterodimers boost breast cancer metastasis. Moreover, EGFR inversely correlates with HER2 and ER. Research has shown that EGFR-HER2 heterodimers can promote the metastasis of breast cancer cells. In TNBC patients, EGFR expression is markedly elevated. Therefore, EGFR holds great potential as a therapeutic target in TNBC, warranting further investigation and development of targeted therapies [105, 106]. Recent studies conducted on various cell lines have highlighted the critical role of EGFR in promoting epithelial-mesenchymal transition (EMT). EMT involves cellular morphological changes, wherein epithelial cells transition to a mesenchymal fibroblast-like phenotype. This process is considered crucial for tumor infiltration and metastasis. While EMT is also implicated in normal

mammary gland development, its significance becomes more prominent in breast cancer progression [107]. Multiple growth factors, including EGFR, hepatocyte growth factor, fibroblast growth factor, and insulin-like growth factor 1 or 2, have been shown to induce EMT in different epithelial cell lines. Among these, EGFR is particularly influential in EMT induction. For instance, EGFR activates the Ras-ERK pathway, which regulates EMT, thereby impacting tumor infiltration and metastasis. In cancer cells, the activation of RSK through ERK enhances mesenchymal activity and invasiveness [108-110]. Studies have explored the role of erlotinib, an EGFR-tyrosine kinase inhibitor, can inhibit cell viability, invasiveness, and the transition of IBC cells from a mesenchymal phenotype to an epithelial phenotype. Treatment with erlotinib resulted in increased expression of E-cadherin, an epithelial cell marker, and decreased expression of elastin, a component of the extracellular matrix. These findings suggest that erlotinib may exert its anti-metastatic effects by suppressing EMT [102-106]. Therefore, the strong correlation between EGFR and EMT indicates their potential as critical targets for inhibiting tumor metastasis. Further research in this area holds promise for providing valuable insights into the development of targeted therapies.

VEGFRs: key node in tumor angiogenesis and lymphatic genesis

VEGF, also known as vascular permeability factor or vasculotropin, plays a crucial role in regulating angiogenesis by exerting specific effects on vascular endothelial cells. The VEGF family comprises six homologues, including VEGF-A, -B, -C, -D, -E, and the placenta growth factor. Within the VEGF family, three receptors have been identified. VEGFR-1, encoded by the Flt-1 gene; VEGFR-2, encoded by the Flk-1/KDR gene; and VEGFR-3, encoded by the Flt-4 gene. These receptors are classified as transmembrane receptor tyrosine kinases [111]. VEGF expression varies among different tissues, including the heart, lymph nodes, placenta, and tumor tissues, during body development. The discovery of VEGF and its receptors in breast cancer cells indicates the presence of specific autocrine signaling pathways. These pathways can mediate the phosphorylation of VEGFR-1/2 or induce NRP1/2 signaling, pro-

moting tumor cell proliferation, survival, and migration. Understanding these pathways is crucial in developing strategies to target VEGF signaling for therapeutic intervention in breast cancer [111-113].

Numerous studies have demonstrated the involvement of VEGF-A in promoting the survival of breast cancer cells. Blocking VEGF-A transcription, either through using VEGF siRNA or neutralizing antibodies, has been shown to induce apoptosis in tumor cells under both normal and low oxygen conditions [114]. This apoptotic effect in breast cancer cells involves downregulation of Bcl-2 expression, increased protein misfolding, and disruption of the PI3K pathway [115]. Moreover, VEGF binding to VEGF-R1 and VEGF-R2 sustains cancer cell survival. In cell models such as MCF-7 or MDA-MB-231, downregulating VEGF-R2 or NRP-1 inhibits AKT phosphorylation, suppressing VEGF-R1 and decreasing cancer cell survival [116]. These findings shed light on the complex interplay between VEGF-A and its receptors in breast cancer cell survival and provide crucial insights for the development of therapeutic strategies aimed at targeting the VEGF signaling pathway. VEGF-A, -C, and -D are simultaneously expressed in various types of tumor cells and bind to receptors VEGFR-1, VEGFR-2, and VEGFR-3. This binding serves to protect lymphatic endothelial cells from apoptosis induced by the immune system while promoting the growth, proliferation, and migration of these cells. Consequently, lymphatic vessel formation is stimulated, leading to lymphatic metastasis in tumors [117-120]. Notably, VEGF-C and VEGF-D exhibit specific affinity for VEGFR-3, which triggers receptor phosphorylation. VEGF-C demonstrates a high affinity for lymphatic endothelial cells, thus inducing their proliferation and the formation of lymphatic sinuses. In different cancer types, VEGF-A binds to VEGFR-1 and VEGFR-2 to induce tumor angiogenesis, while VEGF-C and VEGF-D interact with VEGFR-3 to promote lymphatic vessel generation [121]. Recent studies involving 50 breast cancer patients focused on investigating the expression of VEGF-C, VEGFR-3, and angiopoietin-1 in cancerous tissue, along with their associations with different clinical and pathological characteristics, including metastasis [122]. The results revealed a robust correlation between microlymphatic vessel formation and both

lymph node metastasis and VEGFR-3 expression [123]. Moreover, microvessel and microlymphatic vessel densities in breast cancer are crucial for tumor progression and lymph node metastasis. Notably, microlymphatic vessel density in adjacent tissues independently predicts lymph node metastasis. VEGF-C expression in lymphatic endothelial cells strongly correlates with lymphatic vessel formation and metastasis, highlighting its role in promoting lymphatic metastasis in breast cancer [124, 125]. It is worth noting that although VEGF plays a vital role in promoting tumor angiogenesis, lymphangiogenesis, and immune modulation, the vessels and lymphatic vessels formed exhibit characteristics such as immaturity, leakiness, and inadequate support from the surrounding vasculature [126]. Targeting VEGF-C, VEGF-D, and their corresponding receptor VEGFR-3 shows promise in inhibiting tumor metastasis and improve prognosis in breast cancer [127, 128]. These targeted interventions can suppress tumor vessel growth or promote apoptosis [129], holding potential for managing metastatic breast cancer and enhancing patient outcomes.

PDGFR: crucial role in tumor-stroma interaction

PDGFRs, belonging to the RTK superfamily, consist of PDGFR- α and PDGFR- β . These receptors share similar functions and play significant roles in early hematopoiesis, blood vessel formation, and organ development [130]. Both PDGFR α and PDGFR β are crucial in both physiological and pathological conditions. The diverse binding patterns of PDGF to its receptors involve five different homodimeric or heterodimeric forms: PDGF-AA, PDGF-BB, PDGF-AB, PDGF-CC, and PDGF-DD. PDGF-AA specifically activates PDGFR α , while PDGF-BB activates PDGFR α , PDGFR α/β , and PDGFR β [131]. PDGF-AB and PDGF-CC activate PDGFR α and PDGFR α/β , whereas PDGF-DD selectively activates its receptor, PDGFR- β . The interaction between PDGF and its receptors leads to the assembly of PDGFR subunits into dimers, which activates the intrinsic tyrosine kinase activity of the receptors [132]. Upon activation, PDGFR phosphorylates tyrosine residues on its substrates, initiating downstream signaling cascades that regulate cellular responses. These downstream signaling pathways can be divided

into three categories based on their specific effects: (1) regulation of cell survival and growth, (2) regulation of cell invasion, blood vessel formation, and metastasis, and (3) regulation of EMT [133-135].

PDGF is derived from the stromal stem cells of the local tumor microenvironment. These stem cells generate various cytokines that interact with tumor cells, playing a crucial role in tumor initiation and progression [136]. PDGFs and PDGFRs are key regulators of cell growth and division, exerting significant impacts on malignant cells and the tumor microenvironment [124]. Dysregulation of PDGF signaling has been observed in various human malignancies, including prostate, lung, kidney, ovarian, brain, and pancreatic cancers. Overexpression of PDGF has been detected in the stromal cells of breast cancer, accompanied by the activation of the PI3K-AKT-mTOR signaling pathway [137]. Promising results have been demonstrated through combined treatment employing PDGFR tyrosine kinase inhibitors and mTOR inhibitors, showing potential in reducing stromal reactions and tumor proliferation, offering a novel therapeutic strategy for breast cancer [134]. PDGF plays a vital role in breast tumor invasion. Enhanced expression of PDGF promotes cell proliferation, inhibits apoptosis, and induces the expression of the CXCR4, thereby facilitating tumor growth and lymph node metastasis. Effective elimination of PDGF-induced lymph node metastasis can be achieved through blocking CXCR4 signaling pathway [138]. In breast cancer cells, there exists an interplay between PDGF, Notch, and NF- κ B signaling pathways. Overexpressed PDGF leads to elevated NF- κ B/Jagged-1 expression, where NF- κ B activation influences Notch signaling, EMT, and tumor invasion. Downregulation of PDGFD can inhibit Notch and NF- κ B pathways, partially reverse EMT, suppress cell growth, and induce apoptosis [135]. The interactions between tissue-resident stem cells and the cancer microenvironment also contribute to tumor progression. These stem cells secrete PDGF in a paracrine manner, inducing EMT in cancer cells. This PDGF-dependent mechanism promotes the expansion of cancer stem cell populations and facilitates tumor growth [139]. In summary, PDGF represents a promising therapeutic target for the treatment of breast cancer. The dysregulation of PDGF signaling in the

tumor microenvironment and its interaction with tumor cells contribute to tumor initiation, progression, invasion, and metastasis [140]. Understanding the role of PDGF in breast cancer opens up opportunities for targeted therapeutic interventions aimed at disrupting PDGF signaling pathways and preventing tumor progression. Unveiling the crosstalk between PDGF, Notch, and NF- κ B signaling pathways provides valuable insights into the mechanisms behind tumor invasion, EMT, and the regulation of cancer stem cells.

FGFR: aberrant expression in breast cancer

FGFRs are members of the RTK family. Encoded by the FGFR1, FGFR2, FGFR3, and FGFR4 genes, these receptors are primarily composed of single-chain glycoproteins [141]. Structurally, FGFRs consist of three main regions: an extracellular region, a transmembrane region, and an intracellular region with tyrosine kinase activity. FGFRs play a crucial role in regulating cell growth and division [142]. Upon binding with their specific ligands, FGFRs undergo receptor dimerization, leading to the activation of their tyrosine kinase activity. Activated tyrosine kinases serve as connection points between upstream signaling pathways and transmit signals to the intracellular environment, triggering various downstream signaling pathways [143]. These pathways include the MAPK, PI3K/AKT, STAT, and PLC- γ pathway. These pathways regulate gene expression and modulate cellular processes such as cell differentiation, proliferation, and the formation of tumors [144, 145]. Numerous studies have demonstrated that FGFs and FGFRs play a crucial role in promoting cancer progression through diverse mechanisms. These mechanisms encompass inducing mitotic and survival signals, promoting EMT, invasion, and angiogenesis. The dysregulation of FGFR signaling has been implicated in various types of cancer, highlighting its potential as a viable therapeutic target for cancer treatment [145-148].

FGFRs and FGFs play a crucial role in breast development and tissue homeostasis regulation. An array of studies have identified a close association between ectopic expression of the FGFR family and the development of breast cancer [147]. Notably, approximately 10% of breast cancer patients exhibit amplification of

the FGFR1 gene, a genetic alteration that has been linked with early recurrence and poor prognosis, particularly in ER-positive breast cancer [149]. Intriguingly, FGFR1 amplification is rarely observed in HER2-amplified breast cancer, suggesting a mutually exclusive activation of similar downstream signaling pathways between FGFR1 and HER2 [150]. FGFR1 amplification has been linked to endocrine therapy resistance. High rates of FGFR1 amplification are observed in breast cancer subtypes characterized by a high Ki-67 proliferation index and luminal B phenotype, emphasizing the significance of FGFR1 overexpression in predicting unfavorable outcomes. These findings provide a strong rationale for exploring targeted endocrine therapies against FGFR1 [151]. Recent research has increasingly associated FGFR2 with breast cancer, identifying it as one of the key non-inherited susceptibility genes, particularly in TNBC. Studies have reported FGFR2 gene amplification and overexpression in a specific subtype of TNBC, demonstrating its activation of the PI3K/AKT signaling pathway and subsequent inhibition of apoptosis. These findings underscore the potential of FGFR2 as a promising therapeutic target, especially in TNBC cases with FGFR2 amplification [152]. Besides, FGFR3 mutations have been implicated in various malignancies, such as multiple myeloma, cervical cancer, and bladder cancer, but their association with breast cancer remains limited [153]. Moreover, compelling evidence has pointed towards FGFR4 ectopic expression in human breast cancer, which is linked to chemoresistance in breast cancer. By using mouse breast cancer models has substantiated the role of FGFR4 in promoting tumor progression and metastasis [154]. Analyses of breast cancer cells that survived doxorubicin treatment have revealed an upregulation of FGFR4 expression, while interference with FGFR4 using antagonistic antibodies has demonstrated increased chemosensitivity in breast cancer cells expressing FGFR4. Collectively, these findings underscore FGFR4 as a significant factor influencing chemotherapy resistance and a promising therapeutic target for overcoming drug resistance [155]. Collectively, it is evident that FGFRs are mechanistically interlinked with the function and resistance of other RTKs, providing potential targets for breast cancer treatment.

IGFR: a high-risk factor for breast cancer

As a member of the IGFR family, IGF-1R is a ubiquitously expressed type 1 transmembrane heterotetrameric receptor consisting of two ligands, an extracellular α subunit and two β subunits, and ligand binding induces transphosphorylation of tyrosine within the TK domain by the dimeric subunit partner [156]. Phosphorylated residues act as docking sites for other signaling molecules, such as insulin receptor substrates 1 to 4 (IRS1 to IRS4) and adaptor protein SHC, which lead to the activation of the PI3K and MAPK pathways [157, 158]. Under normal physiological conditions, the IGF system is tightly regulated, allowing for homeostatic growth. In tumor cells, these molecules are activated by mutations, chromosomal translocations, abnormal stimuli (autocrine, endocrine, or paracrine), or loss of genomic imprinting [159]. IGF-1R gene amplification has been reported in a variety of malignancies [160]. High concentrations of IGF-1 are present in several common cancers, including prostate cancer and premenopausal breast cancer, and higher blood concentrations of IGF-1 are associated with a higher risk of breast cancer in nonmenopausal women [161]. Therefore, IGF-1R can be a promising protein for specific and targeted therapeutics.

Current application of tyrosine kinase inhibitors in breast cancer treatment

Breast cancer is a heterogeneous disease which has been characterized molecularly into different subtypes depending on expression of ER, PR and HER2. For hormone receptor-positive breast cancer (luminal A and B), hormone therapy consists of selective estrogen receptor modulators (tamoxifen and raloxifene) is routinely used as adjuvant therapy [32, 162]. Since TNBC or basal like and HER-enriched breast cancer do not express hormone receptors so that hormone therapy is not effective in these subtypes [53]. However, due to the prominent expression of RTKs in TNBC and HER2-enriched subtypes, blocking the functions of RTKs is one of the promising approaches for management of TNBC and HER2-enriched breast cancer [42]. So far, various strategies have been adopted for inhibition of RTK-dependent signaling, and some are currently used in clinics (**Table 3**) [38, 39, 50, 55, 56, 66, 76, 77, 87, 163-178].

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Table 3. Current anti-RTK therapy of breast cancer

Molecule	Type	Target	Phase of study	Mechanism
Trastuzumab	Humanized mAb	HER	In clinical use	Inhibits HFR2 and HER3 dimerization, induces ADCC
Cetuximab	Chimeric mAb	EGFR	Phase I, II	Induces NK cell mediated ADCC
Panitumumab	Humanized mAb	EGFR	Phase II	Enhances sensitivity to DNA-damaging agents in TNBC
Nimotuzumab	Humanized mAb	EGFR	Phase I	Induces NK cell mediated ADCC
Necitumumab	Humanized mAb	EGFR	Phase II	Inhibits downstream targets in EGFR pathway, induces ADCC
Gefitinib	Reversible TKI	EGFR	Phase I, II	Reverses TAM resistance by up-regulating the ER α
Erlotinib	Reversible TKI	EGFR	Phase I, II	Suppresses CDK2 activity
Lapatinib	Reversible TKI	EGFR, HER2	In clinical use	Used as an alternate therapy in HER2 positive breast cancer
Afatinib	Irreversible TKI	EGFR, HER2	Phase II	Inhibits EGFR and HER2 signaling irreversibly
Varlitinib	Reversible TKI	EGFR, HER2, ErbB4	Phase II	Inhibits HER/MAPK signaling in TNBC
Dacomitinib	Irreversible TKI	EGFR, HER2, ErbB4	Phase I, Solid tumors	Inhibits HER2, EGFR, HER4, Akt and ERK phosphorylation
Sapitinib	Reversible TKI	EGFR, HER2, ErbB3	Phase I, Solid tumors	Showed higher inhibitory potential in tamoxifen resistant breast cancer
Vandetanib	TKI	EGFR, VEGFR2-3, RET	Phase I, II	Targets angiogenesis by inhibiting VEGFR2 and 3 signaling along with EGFR pathway
Neratinob	Irreversible TKI	EGFR, HER2, ErbB4	Phase I, II, III	Irreversibly blocks EGFR and HER2 pathway
BMS-690514	Irreversible TKI	EGFR, HER2, ErbB4, VEGFR1-3	Phase I, Solid tumors	Irreversibly blocks EGFR and HER2 pathway
AEE788	Reversible TKI	EGFR, ErbB2, VEGFR	Phase I	Targets angiogenesis by inhibiting VEGFR2 and 3 signaling along with EGFR pathway
Lucitanib	TKI	FGFR1-2, PDGFR α/β , VEGFR1-3	Phase II	Show anti-angiogenic and anti-tumoral activity by targeting FGFR and VEGFR

Tyrosine kinase plays a pivotal role in tumor formation and progression. TKIs, which specifically target these kinases, have emerged as a focal point of cutting-edge research in molecular targeted therapy for combating tumors worldwide [47]. By effectively suppressing the biological activity of tyrosine kinases, TKIs disrupt the reparative mechanisms employed by tumor cells, leading to cell cycle arrest at the G1 phase, induction of apoptosis, inhibition of neovascularization, and the manifestation of anti-tumor effects through diverse signaling pathways [179, 180]. Currently, TKIs utilized in breast cancer treatment can be classified into three main groups based on their specific targets: EGFR-targeting TKIs, VEGFR-targeting TKIs, and non-receptor TKIs.

Inhibitors of tyrosine kinase targeting EGFR

EGFR tyrosine kinase inhibitors (EGFR-TKIs) are small-molecule compounds that specifically target the EGFR [181-186]. Currently, there are

two main classes of drugs used to target the EGFR pathway in cancer treatment: 1) EGFR monoclonal antibodies, represented by trastuzumab, which targets HER2. Trastuzumab interferes with ligand binding to HER2, inhibiting receptor dimerization [187-189]. Trastuzumab has achieved significant breakthroughs in breast cancer treatment and is considered the standard therapy for HER2+ breast cancer. However, some patients develop primary or acquired resistance to trastuzumab, still posing significant challenges in clinical management [190]; 2) EGFR-TKIs can penetrate cells and competitively repress the tyrosine kinase domain of EGFR. By binding to ATP, they inhibit autophosphorylation of EGFR, thereby blocking downstream signaling pathways mediated by EGFR, ultimately exerting anti-tumor effects [191]. Currently, several EGFR-TKIs are being studied for breast cancer treatment, including lapatinib, afatinib, gefitinib, erlotinib, and neratinib [192].

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Inhibitors of tyrosine kinase targeting VEGFR

VEGFR Tyrosine Kinase Inhibitors (VEGFR-TKIs) are small-molecule compounds designed to specifically target the tyrosine kinase domain of VEGFR. Since angiogenesis plays a crucial role in tumor growth, invasion, and metastasis, inhibiting tumor angiogenesis has emerged as a promising approach for cancer treatment [191]. Existing anti-angiogenic therapies primarily focus on inhibiting the VEGF pathway using strategies such as VEGF monoclonal antibodies like bevacizumab, as well as VEGFR-TKIs sorafenib, sunitinib, and others [192-200]. Notably, VEGF mRNA expression has been identified in various tumors, including breast cancer. Bevacizumab has demonstrated efficacy in treating breast cancer in previous studies. Several novel VEGFR-TKIs are currently under investigation and in different stages of clinical trials, which mainly include sorafenib, sunitinib, axitinib, pazopanib, vandetanib, and others [201, 202].

Non-receptor tyrosine kinase inhibitors

Among the non-receptor tyrosine kinase family, Src kinases have received significant attention. They could interact with various receptor proteins, regulating cell proliferation, differentiation, adhesion, motility, and angiogenesis. Blocking or regulating the binding of Src tyrosine kinases with these overexpressed receptors can keep tumor cell proliferation and invasion under control. Recently, TKIs such as dasatinib (BMS-354825), bosutinib (SKI-606), and saracatinib (AZD-0530) have emerged, working by competing for the ATP-binding site of Src tyrosine kinase. Numerous ongoing clinical studies hold the promise of offering a brighter future for targeted therapy in breast cancer [203].

Promising future development

Over the past two decades, a diverse range of RTKs targeted inhibitors have been developed and clinically evaluated to enhance cancer patient survival rates. In particular, the aberrant activation of RTKs has emerged as a potential therapeutic target, where molecular targeted inhibitors can hinder the activity of pathogenic tyrosine kinases. Further insights into genetics, cell biology, and structural biology have led to the development of novel treat-

ment approaches. Disease-causing RTK mutations, deletions, translocations, and amplifications have been identified in breast cancer. Currently, therapies targeting RTKs involve both small molecule inhibitors and monoclonal antibodies, with ongoing research. The potential applications of RTKs in breast cancer treatment hold significant prospects for future advancements.

Targeting RTKs in TNBC treatment

TNBC is a highly heterogeneous subtype of breast cancer with the highest rates of recurrence and distant metastasis. Due to absence of both hormone receptors (HR) and HER2 protein, effective treatment for TNBC remain limited. Even immunotherapy has shown modest response rates of around 10-20% in patients. Particularly for patients with advanced-stage TNBC, chemotherapy remains the primary clinical treatment method. Therefore, the search for more effective breast cancer targets and treatment methods is of utmost importance.

Currently approved or clinically tested antibodies for breast cancer treatment can be classified into three main categories: 1) Monoclonal antibodies targeting tumor-surface antigens; 2) Immune checkpoint inhibitors represented by PD-1 and PD-L1 antibodies; 3) Antibody-drug conjugates (ADCs) [204]. Monoclonal antibodies targeting tumor-surface antigens primarily work by blocking the signaling pathways that promote tumor cell growth through binding to HER2 or other antigens on the tumor surface. This inhibits tumor growth or facilitates the destruction of tumor cells through antibody-dependent cellular cytotoxicity (ADCC). Various cell factor receptors such as EGFR, VEGFR, and FGFR are included in this category [205].

Research has shown that EGFR protein is frequently overexpressed in TNBC and serves as an independent prognostic indicator for disease-free and overall survival. EGFR can potentially be targeted using cetuximab and small-molecule TKIs [184]. Similarly, compared to non-TNBC patients, TNBC patients exhibit significantly higher levels of VEGF expression and have shorter disease-free survival periods [206]. Since angiogenesis is considered a key component driving tumor cell proliferation and survival, VEGF has emerged as a promising target for TNBC treatment [207]. A study evaluat-

ing bevacizumab, a monoclonal antibody targeting VEGF-A, as an adjunct therapy for TNBC showed improved immunotherapeutic effects [208]. Aberrant FGFR signaling, fueled by various genetic alterations including point mutations, activating mutations, fusions, rearrangements, and amplifications, plays a vital role in tumor progression. Therefore, FGFR is regarded as a potential target for breast cancer treatment [209]. While FGFR1 amplification is associated with poor prognosis in HR-positive breast cancer, its role in TNBC remains controversial. FGFR2 expression is correlated with poorer overall survival [210]. FGFR inhibitors have gained attention as one of the promising drugs. If TNBC patients can also benefit from FGFR inhibitors, it would significantly improve their survival rates. However, drug resistance in breast cancer patients to FGFR inhibitors is currently the major obstacle hindering clinical approval. Preclinical data have also investigated the efficacy of anti-FGFR isoform antibodies and FGFR inhibitors, showing promising results in Phase I clinical trials for solid tumors, including breast cancer [211].

Overall, targeting RTKs offers a potential therapeutic avenue for the treatment of TNBC. Further research and advancements in targeted therapies are crucial for enhancing the outcomes and survival rates of TNBC patients.

Alterations in RTKs in ER+ breast cancer with endocrine resistance

RTKs, including EGFR, HER2, IGFR, VEGFR, and FGFR, are activated upon ligand binding. These receptors are primarily involved in growth factors, cytokines, or hormones, and their activation or overexpression is associated with endocrine therapy resistance in ER+ breast cancer [212].

HER2 overexpression reduces the sensitivity to antiestrogen therapy, partly through activation of the PI3K-AKT-mTOR and MAPK pathways [213]. Additionally, HER2 expression depends on the NF- κ B pathway, and in ER α -suppressed breast cancer circulating tumor cells, NF- κ B signaling can increase HER2 expression. Thus, inhibiting the NF- κ B pathway in combination with fulvestrant can restore the sensitivity of ER+/HER2- endocrine-resistant breast cancer cells to endocrine therapy [214]. The current treatment for ER+/HER2+ tumors involves

combining estrogen targeting with HER2 inhibitors [215]. HER2 mutations are linked to acquired endocrine resistance and have been found in non-HER2 amplification metastatic breast cancer within 5% of endocrine therapy-resistant patients. ER+ breast cancer cells and xenografts that express HER2 mutations are resistant to estrogen deprivation or fulvestrant treatment and show poor response to HER2 TKI, lapatinib [216]. However, studies suggest that co-blocking HER2 and ER expression in breast cancer cells has a synergistic effect. Therefore, for patients with ER+ breast cancer and concurrent HER2 mutations, the combination of lapatinib and fulvestrant is a favorable choice [217].

EGFR amplification accounts for approximately 1.7% of endocrine-resistant metastatic breast cancer and can promote fulvestrant resistance. Co-administration of EGFR inhibitors can reverse this resistance [218-220]. In a cohort of 60 patients diagnosed with metastatic ER+ breast cancer, both before and after initiation of endocrine therapy, the comparison of whole exome sequencing data and circulating DNA analysis revealed that FGFR1 amplification accounted for 15%, FGFR2 amplification accounted for 5%, FGFR2 activating mutations accounted for 3.3%, and FGF3 amplification accounted for 28.3%. Immunohistochemical (IHC) staining and fluorescence in situ hybridization (FISH) showed that besides its typical membrane-bound intracellular signaling function, FGFR1 can also participate in endocrine resistance by regulating gene transcription in ER+ breast cancer [221]. The combination of FGFR inhibitors with fulvestrant can inhibit the growth of ER+/FGFR1-amplified cell lines and tumors. It was reported almost two decades ago that approximately 30% of breast tumors demonstrate elevated FGFR4 expression in comparison to normal tissues. Experimental studies suggest that FGFR4 may mediate acquired endocrine resistance in metastatic breast cancer [222]. Therefore, endocrine therapy in combination with novel FGFR inhibitors may offer new strategies for treating metastatic breast cancer.

Conclusion

Breast cancer is a multifactorial disease characterized by dysregulation of cellular signaling

pathways due to genetic and epigenetic alterations. Numerous growth factors and their receptors, known as RTKs, are involved in the development and progression of cancer. Overexpression or dysregulation of RTKs in breast cancer cells activates downstream signaling pathways such as MAPK, PI3K/AKT, and JAK/STAT, promoting tumor growth, angiogenesis, and metastasis. The multifaceted role of RTKs makes them attractive targets for breast cancer treatment. In recent decades, significant progress has been made in understanding RTKs and targeted therapies through genomic technologies. Several drugs, including small molecule inhibitors and monoclonal antibodies, have been developed and approved for treating cancer by targeting RTK activation. While approved TKIs have led to tumor regression or prolonged survival, the lack of selectivity for individual targets and the drug resistance remain challenges. Furthermore, structural mutations, gene amplification, and alternative pathway activation pose challenges to anti-RTK therapy.

Despite research findings supporting the significance of RTK signaling as a therapeutic target in breast cancer, existing clinical trial data show modest efficacy of RTK inhibitors. The reasons for the lack of efficacy of RTK inhibitors in breast cancer patients are still inconclusive, whether it is due to drug ineffectiveness, insufficient patient selection, or a lack of oncogenic potential in RTK genomic variations. Before considering RTK signaling as a therapeutic target in breast cancer, the following issues need to be addressed: precise definition of RTK signaling abnormalities and identification of predictive biomarkers for response to RTK inhibitors; optimization of combinational strategies of RTK inhibitors with endocrine drugs or other targeted agents to enhance efficacy and reduce resistance; and development of more effective RTK inhibitors.

In conclusion, RTK signaling plays a crucial role in the pathogenesis of breast cancer, and targeted strategies against RTK signaling show promising prospects for treatment. However, further exploration is needed to appropriately block this signaling pathway in breast cancer patients to achieve optimal efficacy. Therefore, further research on acquired resistance in breast cancer is of great significance for devel-

oping novel therapeutic strategies against tumor recurrence.

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None.

Abbreviations

ADCC, Antibody-dependent cellular cytotoxicity; ADCS, Antibody-drug conjugates; ALK, Anaplastic lymphoma kinase; BC, Breast cancer; CXCR4, CXC chemokine receptor 4; EGFR, Epidermal growth factor receptor; EMT, Epithelial-mesenchymal transition; ER, Estrogen receptor; FDA, Food and Drug Administration; FGFR, Fibroblast growth factor receptor; FISH, Fluorescence in situ hybridization; HR, Hormone receptors; IBC, Inflammatory breast cancer; IGFR, Insulin-like growth factor receptor; IHC, Immunohistochemical; JAK, Janus kinase; MAPK, Mitogen-activated protein kinase; MTC, Medullary thyroid carcinoma; mTOR, Mammalian target of rapamycin; NSCLC, Non-small cell lung cancer; PDGFR, Platelet-derived growth factor receptor; PI3K, Phosphoinositide 3-kinase; PLC- γ , Phospholipase C-gamma; PR, Progesterone receptor; RTKs, Receptor tyrosine kinases; SH, Src homology; STAT, Signal transducer and activator of transcription; TGF- α , Transforming growth factor-alpha; TKI, Tyrosine kinase inhibitor; TNBC, Triple-negative breast cancer; VEGFR, Vascular endothelial growth factor receptor.

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