

Breast Cancer: Biochemical Insights and the Therapeutic Potential of Plant-Derived Bioactive Compounds

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ABSTRACT

Breast cancer is the most commonly diagnosed cancer and the leading cause of cancer-related mortality among women worldwide. This review examines the biochemical mechanisms underlying breast cancer development and progression and evaluates the therapeutic potential of plant-derived bioactive compounds, with emphasis on their molecular targets, anticancer activities, and translational prospects. Breast cancer is a heterogeneous and multifactorial disease driven by genetic and epigenetic alterations that disrupt cellular proliferation, differentiation, survival, and genomic stability. Molecular classification commonly includes hormone receptor-positive and HER2-positive tumours, as well as major subtypes such as luminal A, luminal B, HER2-enriched, and triple-negative breast cancer (TNBC). Breast cancer progression is associated with the hallmarks of cancer, including sustained proliferative signaling, evasion of growth suppression and cell death, replicative immortality, angiogenesis, invasion and metastasis, metabolic reprogramming, and immune evasion. Metabolic alterations support the energetic and biosynthetic demands of tumour cells. Plant-derived bioactive compounds, including polyphenols, flavonoids, isoflavones, catechins, and isothiocyanates, have emerged as promising candidates for breast cancer prevention and management. Compounds such as curcumin, resveratrol, genistein, sulforaphane, quercetin, epigallocatechin gallate (EGCG), and corn silk-derived constituents exhibit anticancer activities through interconnected mechanisms, including cell-cycle arrest, apoptosis induction, modulation of tumour suppressor and oncogenic signaling, and regulation of hormone receptor pathways. These compounds influence pathways involving p53, PTEN, PI3K/AKT/mTOR, MAPK, NF- κ B, ER, PR, and HER2. Overall, the evidence supports the potential of plant-derived bioactive compounds as promising candidates for breast cancer prevention and treatment. However, most evidence remains preclinical, highlighting the need for further mechanistic, pharmacokinetic, safety, and well-designed clinical studies.

Keywords: Breast Cancer; Plant-derived Bioactive Compounds; Corn Silk; Apoptosis;

1.0 INTRODUCTION

Globally, breast cancer is the most diagnosed cancer in women with more than 2.4 million cases and approximately 694,000 fatalities in 2024 (Sung et al., 2026). The late-stage presentation observed in Sub-Saharan Africa is due to late-stage presentation (Sung et al., 2021). Despite the relative breast cancer incidence is highest in the most developed countries of the globe, greater populations in less developed regions mean that more than 50% of all breast cancers are diagnosed in low- and middle- income countries (LMICs), devising a substantial burden of the disease (Wilkinson & Gathani, 2022). Over the past decades, the incidence of breast cancer has been dramatically increasing in transitioning countries such as Africa, Asia, and South America that were known to have low incidence before. This has been attributed to significant alterations in behavioral

factors, reproductive health, life expectancy increase, and socio-cultural environments altogether led to changes in risk factor profiles that are similar to those observed in transitioned countries. Consequently, the incidence of breast cancer rates have elevated and gradually moving toward the levels observed in transitioned countries (Arnold et al., 2022).

Breast cancer is a highly heterogeneous disorder that can be caused by a diversity of different genetic changes in mammary epithelial cells, leading to immensely distinct disease manifestations in the patients (Lüönd et al., 2021). About six different subcategories of breast cancer have been illustrated based on their gene expression profiles and their identification and categorization was fundamental significance to our comprehending of cancer origin and progression, they include , basal-like, claudin-low, normal breast-like, ,

luminal A and B, basal-like, and HER2/ERB2 overexpressing (Testa et al., 2020).

For localized cancers, surgery is still the based treatment approach, it success however can be limited based on metastasis, size, and location of cancer. Additionally, for patients with advanced disease, surgery may not be suitable due to inherent risks. As a result of genetic mutation, variations in signaling pathways or heterogeneity of cancer, hormone therapy and chemotherapy are often hindered by resistance mechanisms namely hormone resistance and chemoresistance (Zafar et al., 2025). Also, the intense shortcomings of conventional treatment of cancer treatments comprise of systemic toxicity, reduced quality of life, and severe adverse effects, raise great worries about these methods (Shokoohi et al., 2025).

Medicinal plants are widely distributed across diverse regions worldwide and have gained increasing recognition as valuable sources of therapeutic agents. Consequently, the continued investigation of plant-derived metabolites has led to the identification of numerous cytotoxic compounds with potential anticancer activity, expanding opportunities for the development of novel strategies for cancer prevention and treatment (Dehelean et al., 2021). In contrast to conventional pharmacological agents, natural products such as dietary phytochemicals, medicinal herbs, and naturally occurring bioactive constituents such as polyphenols, flavonoids, and terpenoids, represent promising candidates for investigation as complementary or alternative approaches to breast cancer management. Their therapeutic potential is largely associated with their antioxidant and anti-inflammatory activities, alongside preclinical evidence demonstrating growth-inhibitory effects across cellular models representing diverse breast cancer subtypes (Telang, 2025).

Plant-derived bioactive compounds have attracted considerable attention as potential sources of novel anticancer agents, particularly in view of the limitations and adverse effects associated with some conventional chemotherapeutic agents. Accordingly, this review examines the biochemical insights underlying breast cancer development and progression and critically evaluates the therapeutic potential of plant-derived bioactive compounds, with emphasis on their molecular mechanisms, anticancer activities, and prospects for translation into breast cancer prevention and treatment.

2.0 BREAST CANCER: FROM MOLECULAR INITIATION TO DISEASE PROGRESSION

2.1 Breast cancer initiation and carcinogenesis

Breast cancer is a heterogeneous and multifactorial disease that develops through the progressive accumulation of genetic and epigenetic alterations that disrupt the regulatory mechanisms governing normal mammary epithelial-cell proliferation, differentiation, survival, and genomic integrity. Its development reflects complex interactions between inherited genetic susceptibility and non-hereditary factors, including hormonal influences, environmental exposures, and other lifestyle-related determinants. These alterations can confer proliferative and survival advantages on affected cells, facilitating the transition from normal epithelium through premalignant lesions to benign or malignant neoplasms. Malignant breast tumours may subsequently acquire invasive and metastatic capabilities, enabling them to infiltrate surrounding tissues and disseminate to distant organs (Basingab et al., 2025; Samad et al., 2025).

2.2 Genetic and epigenetic alterations

Beyond genomic abnormalities, which play a fundamental role in the molecular pathogenesis and therapeutic management of breast cancer, epigenetic dysregulation provides an additional layer of biological complexity. Epigenetic alterations can dynamically modify gene expression and disrupt essential cellular processes involved in breast cancer development and progression. Unlike many genetic alterations, which are difficult to reverse, epigenetic modifications are potentially reversible, making dysregulated epigenetic pathways attractive targets for pharmacological intervention, including small-molecule inhibitors of key epigenetic regulators. Moreover, alterations in the tumour epigenome can influence the expression of immune-related genes and modify interactions between cancer cells and the immune system, providing a potential rationale for combining epigenetic therapies with immunotherapeutic approaches (Prabhu et al., 2024). Epigenetic dysregulation is characterized by aberrant DNA methylation patterns, alterations in histone post-translational modifications (PTMs), and changes in chromatin composition and organization (Baylin & Jones, 2016). These epigenetic modifications can influence the expression and activity of genes involved in critical processes such as cell growth, proliferation, and DNA repair. The distinct epigenetic patterns generated by these alterations may also serve as potential biomarkers for cancer diagnosis, prognosis, and disease stratification (Prabhu et al., 2024). Aberrant DNA methylation represents a distinct and potentially reversible epigenetic alteration implicated in breast cancer initiation through the dysregulation of gene expression (Prabhu et al., 2024).

2.3 Oncogenes, tumour suppressor genes and genomic instability

Oncogenes are genes that, when aberrantly activated or overexpressed, can promote cellular alterations that contribute to malignant transformation and cancer development (Osborne et al., 2004). Oncogenes are altered forms of proto-oncogenes, which normally regulate essential cellular processes such as growth and division. Genetic alterations that cause constitutive activation or dysregulated expression of these genes can promote uncontrolled cell proliferation and contribute to malignant transformation (Dakal et al., 2024). Several oncogenes, including ERBB2, PIK3CA, MYC, and CCND1, which encodes cyclin D1, are frequently dysregulated in breast cancer and contribute to tumour development and progression. Inherited pathogenic variants in BRCA1 and BRCA2 are associated with a substantially increased susceptibility to breast and ovarian cancers. In addition, rare germline mutations affecting TP53, which encodes the tumour suppressor protein p53, and PTEN are linked to a markedly elevated risk of developing several malignancies, including breast cancer (Lee & Muller, 2010).

Tumour suppressor genes are genes that normally regulate cellular growth, proliferation, cell-cycle progression, and programmed cell death, thereby helping to maintain tissue homeostasis and prevent uncontrolled cell growth (Dakal et al., 2024). Tumour suppressor genes regulate multiple processes that restrain tumour development, including cell-cycle progression, apoptosis, genomic stability, angiogenesis, and metastatic behaviour. Loss or functional inactivation of these genes can disrupt normal growth control and promote excessive cellular proliferation, thereby facilitating malignant transformation. In addition to genetic mutations and deletions, tumour suppressor genes may be inactivated through epigenetic mechanisms, particularly promoter hypermethylation, leading to transcriptional silencing. Well-characterized tumour suppressor genes implicated in cancer include RB1, TP53, NF1, and APC (Singh et al., 2025).

Genomic instability is an early feature of tumour development and may be detectable even in histologically normal tissues. Inherited cancer-predisposition syndromes can involve defects in this process; notably, BRCA1 and BRCA2 encode proteins that participate in DNA repair and are strongly associated with hereditary breast and ovarian cancer susceptibility. Genomic instability, whether inherited or acquired, can increase the likelihood of genetic alterations, including gene loss, amplification, point mutations, and chromosomal rearrangements. Although many such alterations are detrimental to cell survival, those affecting genes that regulate cellular survival, proliferation, invasion, motility, and therapeutic response can confer selective advantages and contribute to malignant progression (Osborne et al., 2004).

2.4 Molecular and clinical classification of breast cancer

The molecular classification of breast cancer has been extensively studied and is commonly grouped according to the expression of hormone receptors, including estrogen receptor-positive (ER+), progesterone receptor-positive (PR+), and human epidermal growth factor receptor 2-positive (HER2+) tumours (Shaath et al., 2021). Triple-negative breast cancer (TNBC) is characterized by the absence of expression of estrogen receptor (ER), progesterone receptor (PR), and human epidermal growth factor receptor 2 (HER2) (Ramamoorthy et al., 2021). Luminal A tumours are typically characterized by expression of estrogen receptors (ER) and progesterone receptors (PR) and are therefore generally classified as hormone receptor-positive breast cancers. Luminal B tumours are also ER-positive but may show variable PR expression and may be HER2-positive, with a higher proliferative activity than luminal A tumours. HER2-positive breast cancers are characterized by HER2 overexpression or amplification and may occur with or without hormone receptor expression (Carvalho et al., 2025). The molecular characteristics of major breast cancer subtypes are presented in Table 1.

Table 1. Molecular characteristics of major breast cancer subtypes

Breast cancer subtype	Molecular characteristics	Major receptors/features	Clinical/biological relevance	References
Luminal A	Generally hormone receptor-positive	ER+, PR+, usually lower proliferative activity	Hormone-dependent tumour subtype	(Carvalho et al., 2025; Shaath et al., 2021)
Luminal B	Hormone receptor-positive with higher proliferative activity	ER+, variable PR; may be HER2+	Higher proliferative activity than Luminal A	(Carvalho et al., 2025)
HER2-positive	HER2 overexpression or amplification	HER2+, may be ER/PR+ or ER/PR-	Driven substantially by HER2 signaling	(Shaath et al., 2021)

Breast cancer subtype	Molecular characteristics	Major receptors/features	Clinical/biological relevance	References
Triple-negative breast cancer (TNBC)	Lack of the three major receptors	ER-, PR-, HER2-	Distinct molecular phenotype with limited receptor-targeted treatment options	(Ramamoorthy et al., 2021)

2.5 Major hallmarks of breast cancer progression

The eight established hallmarks of cancer encompass the acquired capabilities of sustaining proliferative signaling, evading growth suppressors, resisting cell death, achieving replicative immortality, inducing or accessing the vasculature, activating invasion and metastasis, reprogramming cellular metabolism, and evading immune destruction (Hanahan, 2022).

3.0 METABOLIC REPROGRAMMING AND OXIDATIVE STRESS

Metabolic reprogramming is a fundamental hallmark of breast cancer, characterized by the adaptation and redistribution of metabolic pathways to meet the increased demands of tumour cells. These metabolic alterations provide not only ATP to support elevated energy requirements but also biosynthetic precursors, including nucleotides, amino acids, and lipids, required for rapid proliferation and survival. Rather than being a passive consequence of malignant transformation, metabolic reprogramming actively supports oncogenic signaling, maintains redox homeostasis, and contributes to tumour-cell evasion of immune surveillance (Garg et al., 2025). Cancer cells are known to undergo metabolic alterations that increase glucose uptake and favour glycolysis even under conditions of sufficient oxygen availability. This metabolic adaptation, which promotes aerobic glycolysis while reducing reliance on mitochondrial oxidative phosphorylation (OXPHOS), is known as the Warburg effect (El-Sahli & Wang, 2020). Elevated levels of reactive oxygen species (ROS) are observed across a wide range of cancers and can contribute to tumour initiation and progression. ROS are highly reactive chemical species, with free-radical forms characterized by the presence of an unpaired electron. They can broadly be classified into free-radical and non-radical species, both of which can influence cellular signaling and oxidative homeostasis (Adegoke et al., 2026).

Across the major breast cancer subtypes, nuclear receptor pathways interact with growth factor signaling networks, with these molecular features having diagnostic and prognostic relevance. Increasing evidence also indicates a close relationship between nuclear receptor signaling and oxidative stress in breast

cancer (Dong et al., 2025). Reactive oxygen species (ROS) contribute to multiple stages of cancer development, including tumour initiation, promotion, and progression. Elevated intracellular ROS levels can activate oncogenic pathways and signaling molecules, including mutant Ras, Bcr-Abl, and c-MYC, thereby promoting cellular proliferation. Excessive ROS can also contribute to the inactivation of tumour suppressor pathways, angiogenesis, and mitochondrial dysfunction, collectively facilitating malignant transformation and tumour progression (Kumari et al., 2018).

3.1 Major signaling pathways: PI3K/AKT/mTOR, and NF-κB

The phosphoinositide 3-kinase (PI3K)/AKT/mammalian target of rapamycin (mTOR) signaling pathway is a major regulator of diverse cellular processes, including proliferation, survival, metabolism, and cell motility (2015). Binding of extracellular ligands, such as insulin or insulin-like growth factors (IGFs), to cell-surface receptors including receptor tyrosine kinases (RTKs) and G-protein-coupled receptors (GPCRs) initiates intracellular signaling that activates PI3K. Activated PI3K phosphorylates phosphatidylinositol 4,5-bisphosphate (PIP2) at the 3' position of the inositol ring, generating phosphatidylinositol 3,4,5-trisphosphate (PIP3). PIP3 then recruits AKT (protein kinase B; PKB) and 3-phosphoinositide-dependent protein kinase-1 (PDK1) to the plasma membrane through their pleckstrin homology (PH) domains, facilitating subsequent AKT activation. Following recruitment to the plasma membrane, AKT is phosphorylated at Ser473 by mTOR complex 2 (mTORC2), inducing a conformational change that facilitates its subsequent phosphorylation at Thr308 by PDK1. Once fully activated, AKT phosphorylates substrates at the plasma membrane before dissociating from the membrane and acting on additional targets within the cytoplasm and nucleus, thereby regulating diverse cellular processes (Miricescu et al., 2020). Activation of phosphoinositide 3-kinase (PI3K) triggers a signaling cascade that regulates cancer-cell growth, survival, and metabolism.

AKT, a serine/threonine protein kinase activated downstream of PI3K, serves as a major effector of this pathway in cancer. Mammalian cells express three AKT isoforms, which may have both overlapping and distinct functions in tumour biology. Dysregulated AKT

signaling promotes cellular growth and survival, thereby contributing to cancer development and progression (Engelman, 2009). Nuclear factor- κ B (NF- κ B) is a ubiquitously expressed transcription factor family that plays an essential role in normal mammary gland development. Dysregulated NF- κ B signaling has also been associated with the development and progression of estrogen receptor-negative (ER-negative) breast cancer (Shrihastini et al., 2021). NF- κ B is a key transcription factor that connects inflammatory signaling with cancer development. Its dysregulation is presented in Figure 1.

Figure 1. Biochemical mechanisms involved in breast cancer development and progression.

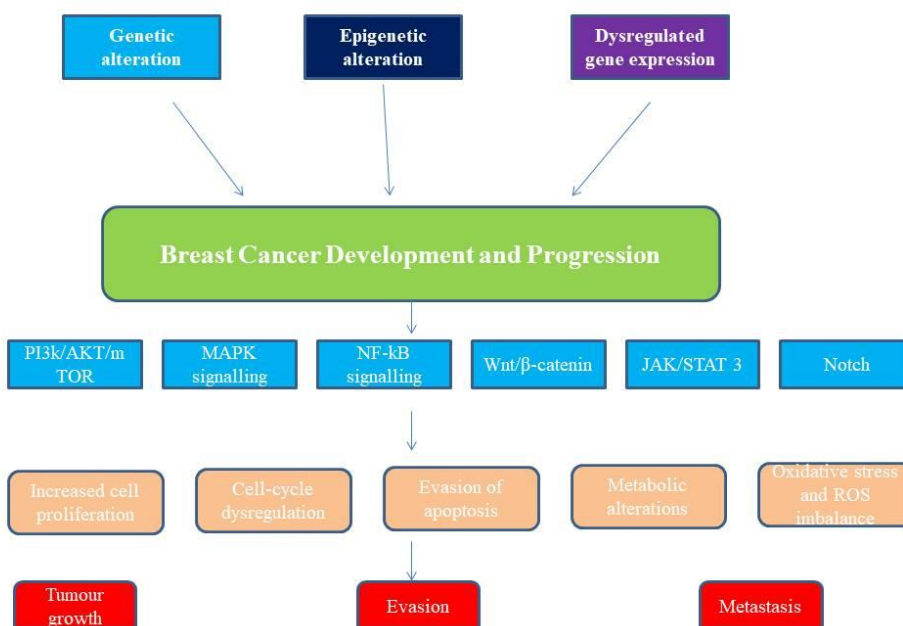
3.2 Invasion, metastasis and tumour microenvironment

The tumour microenvironment (TME) consists of the extracellular matrix (ECM) and basement membrane (BM), together with diverse cellular components such as endothelial cells, adipocytes, tumour-infiltrating immune cells, cancer-associated fibroblasts (CAFs), neuroendocrine cells, and pericytes. These components interact through a complex network of signaling molecules that collectively influence tumour development and progression (Neophytou et al., 2021).

has been implicated in breast cancer tumorigenesis and resistance to endocrine therapy (Pavitra et al., 2023). The p65 subunit mediates the transcriptional activity of NF- κ B by inducing the expression of target genes that suppress apoptosis and regulate cell-cycle progression. Sustained NF- κ B activation can also promote inflammation, tumour-cell invasiveness, tumorigenesis, and metastasis, while contributing to resistance to radiotherapy and chemotherapy (Pavitra et al., 2023). The biochemical mechanisms involved in breast cancer development and progression

4.0 PLANT-DERIVED BIOACTIVE COMPOUNDS AGAINST BREAST CANCER

Natural products have attracted considerable interest as potential sources of novel anticancer agents because of their diverse biological activities and established therapeutic value. They have played an important role in the discovery and development of lead compounds, with several natural product-derived agents, including vincristine, camptothecin, and paclitaxel, having demonstrated potent antitumour activity and entered clinical use. Consequently, natural products remain valuable sources for anticancer drug discovery, although many bioactive compounds require further characterization and evaluation to establish their mechanisms of action, efficacy, safety,



and clinical potential (Hu et al., 2018).

4.1 Curcumin

Curcumin ($C_{21}H_{20}O_6$) is the principal bioactive compound derived from *Curcuma longa*, commonly known as turmeric (Zhu et al., 2024). Curcumin has gained substantial interest for its potential anticancer activity because of its ability to modulate multiple biological processes involved in tumour development and progression. These processes include cellular proliferation, programmed cell death, angiogenesis, and metastasis, which are central to cancer biology. Curcumin acts on several molecular signaling pathways, including Wnt/ β -catenin, PI3K/AKT/mTOR, JAK/STAT3, MAPK, NF- κ B, and Notch, thereby inhibiting tumour growth and promoting apoptosis (Akter et al., 2025).

Curcumin has demonstrated potent antiproliferative activity against breast cancer cells in vitro, with inhibitory concentrations (IC_{50}) within the micromolar range. Its effects vary among breast cancer cell lines with different ER/PR/HER2 receptor profiles, with greater sensitivity observed in hormone receptor-positive cell lines such as T47D and MCF-7. Further investigation using these sensitive cell models indicated that curcumin induces G2/M cell-cycle arrest, suggesting that disruption of cell-cycle progression may contribute to its ability to inhibit breast cancer cell proliferation (Hu et al., 2018). Curcumin inhibited the phosphorylation and activation of the AKT/mTOR signaling pathway (Hu et al., 2018).

4.2 Resveratrol

Resveratrol is a stilbene-derived compound consisting of two phenolic rings linked by a styrene double bond, forming 3,4',5-trihydroxystilbene. It exists in two geometric forms, namely the *trans* and *cis* isomers, with the *trans* form being the predominant and most extensively investigated isoform. Exposure to heat or ultraviolet radiation can promote conversion of *trans*-resveratrol to the *cis* form, which has a structural configuration similar to that of the synthetic estrogen diethylstilbestrol (Ko et al., 2017). Resveratrol exhibits a broad range of pharmacological activities, including anti-inflammatory, antioxidant, antitumour, metabolic-regulatory, and immunomodulatory effects (Gao et al., 2025). Resveratrol can induce cell-cycle arrest by enhancing the activity of the tumour suppressor proteins p53 and PTEN, while simultaneously suppressing phosphatidylinositol 3-kinase (PI3K) signaling (Gao et al., 2025).

Resveratrol has been reported to suppress the proliferation of MCF-7 breast cancer cells in a concentration- and time-dependent manner. After 24 h

of treatment, significant cytotoxicity was observed at concentrations as low as 100 μ M. At this concentration, cell viability decreased to approximately 57.5% relative to untreated controls, with a reported IC_{50} of 51.18 μ M (Ribeiro & Vale, 2024).

4.3 Quercetin

Quercetin, a prominent flavonoid, is widely distributed in a variety of commonly consumed fruits and vegetables. Quercetin has been reported to modulate the expression of several genes, including AKT1, MAPK1, PGR, SGK1, and PTEN, through their upregulation, while the expression of ESR1 and MAPK3 may be downregulated. These genes are expressed across diverse tissues, with AKT1 and MAPK1 exhibiting broad expression in both normal and cancerous tissues, including those of the breast, prostate, and colorectum (Wu et al., 2025).

4.4 Epigallocatechin-3-gallate (EGCG)

Epigallocatechin-3-gallate (EGCG) is the most abundant catechin present in green tea. At concentrations ranging from 10 to 50 μ M, EGCG was reported to suppress the estrogen receptor (ER)-mediated estrogenic and proliferative effects of polychlorinated biphenyl PCB 102 in the estrogen-sensitive breast cancer cell line MCF-7/BOS. PCB 102 is an environmental carcinogen that may promote the growth of estrogen-responsive tumours, including breast cancer (Kuran et al., 2020). Signaling through ER, PR, and HER2 receptors is dysregulated across different breast cancer phenotypes, and EGCG has demonstrated inhibitory effects on these signaling pathways, reducing their activity (Marín et al., 2023). Alterations in epigenetic modifications of functionally relevant genes following EGCG treatment have been proposed as a molecular basis for its chemopreventive effects against breast cancer (Sheng et al., 2019).

4.5 Genistein and Sulforaphane

Genistein, a soy-derived isoflavone, has attracted considerable scientific interest because of its structural resemblance to 17 β -estradiol and its associated estrogenic activity. Its potent antioxidant, anti-inflammatory, and estrogenic properties have further highlighted genistein as a potential candidate for investigation in breast cancer prevention and therapy. Beyond its estrogenic activity, genistein exhibits anticancer effects through multiple mechanisms, including induction of apoptosis, inhibition of angiogenesis, and modulation of cell-cycle progression (Xiang et al., 2025).

Sulforaphane (SFN) is an isothiocyanate compound with potent histone deacetylase (HDAC) inhibitory activity, abundantly present in cruciferous vegetables such as broccoli sprouts, cabbage, cauliflower, and kale (Rahman et al., 2024). *In vitro* and *in vivo* evidence suggests that sulforaphane may inhibit the self-renewal capacity of triple-negative breast cancer (TNBC) cells by targeting the Cripto-mediated oncogenic signaling pathways (Castro et al., 2019).

In the context of breast cancer chemoprevention, sulforaphane (SFN) exerts multifaceted biological effects, including the enhancement of detoxification enzyme activity and suppression of cytochrome P450 enzymes such as CYP1A1 and CYP1A2. SFN may also reduce cancer-cell viability and proliferation by inducing cell-cycle

arrest, apoptosis, and autophagy, while targeting and reducing the population of cancer stem cells (CSCs) (Kuran et al., 2020). Low concentrations of SFN exhibit antitumour activity through mechanisms extending beyond direct inhibition of cancer-cell proliferation, including modulation of the tumour microenvironment (TME) and epithelial–mesenchymal transition (EMT). Consequently, these effects may contribute to tumour suppression and reduced metastatic potential (Pogorzelska et al., 2024). The tumour-inhibitory effects of genistein (GEN) and sulforaphane (SFN) may be mediated, at least in part, through modulation of epigenetic pathways and consequent alterations in epigenetic marks within cancer cells (Paul et al., 2018). The major plant-derived bioactive compounds and their molecular targets in breast cancer are illustrated in

Figure 2.

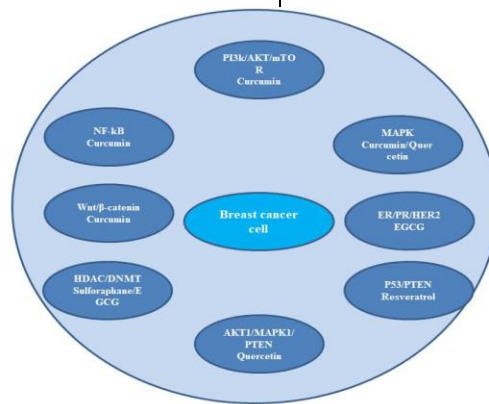


Figure 2. Major plant-derived bioactive compounds and their molecular targets in breast cancer.

5.0 CORN SILK-DERIVED BIOACTIVE COMPOUNDS

Corn silk (*Stigma maydis*) is a medicinal plant traditionally used in the management of various health conditions and has attracted increasing interest because of its antioxidant and potential anticancer properties (Manzanares et al., 2026). Corn silk is a rich source of diverse bioactive compounds, including maysin and its derivatives, terpenoids, vanillic acid, caffeic acid, and epicatechin monogallate, which have been associated with various biological activities, including antidiabetic, anti-obesity, and antimicrobial effects. Other constituents identified in corn silk, such as maysin, rutin, quercetin, apigenin, β -sitosterol, ascorbic acid, and chlorogenic acid, have also demonstrated potential anticancer activities by promoting apoptosis, enhancing

the expression of pro-apoptotic genes, and suppressing anti-apoptotic genes in cancer cells (Gulati et al., 2023). Corn silk extract (CSE) increased lipid peroxidation (LPO) and reactive oxygen species (ROS) production while reducing glutathione (GSH) levels in MCF-7 cells in a dose-dependent manner. The observed loss of mitochondrial membrane potential further indicates mitochondrial involvement in the cytotoxic effects of CSE. Moreover, CSE upregulated the pro-apoptotic markers p53, Bax, caspase-3, and caspase-9, while downregulating the anti-apoptotic protein Bcl-2, suggesting that CSE induces apoptotic cell death in human breast cancer cells through a ROS-mediated mitochondrial pathway (Al-Oqail et al., 2019).

Table 2. Major plant-derived bioactive compounds, sources and mechanisms

Compound	Plant source	Mechanisms	Evidence	References
Curcumin	<i>Curcuma longa</i> (turmeric)	Modulation of Wnt/ β -catenin, PI3K/AKT/mTOR, JAK/STAT3, MAPK, NF- κ B and Notch; G2/M cell-cycle arrest; inhibition of AKT/mTOR activation;	Preclinical	(Akter et al., 2025; Hu et al., 2018; Zhu et al., 2024)

Compound	Plant source	Mechanisms	Evidence	References
Resveratrol	Plant-derived stilbene sources	induction of apoptosis Antioxidant, anti-inflammatory, antitumour and metabolic-regulatory effects; p53/PTEN activation; suppression of PI3K signalling; cell-cycle arrest	Preclinical	(Gao et al., 2025; Ribeiro & Vale, 2024)
Quercetin	Fruits and vegetables	Modulation of AKT1, MAPK1, PGR, SGK1 and PTEN; downregulation of ESR1 and MAPK3	Preclinical	(Wu et al., 2025)
EGCG	Green tea (<i>Camellia sinensis</i>)	Suppression of ER-mediated proliferative signalling; modulation of ER, PR and HER2 pathways; epigenetic regulation including SCUBE2 methylation and DNMT activity	Preclinical	(Dong et al., 2025; Kuran et al., 2020; Marín et al., 2023)
Genistein	Soy	Antioxidant and anti-inflammatory activity; induction of apoptosis; inhibition of angiogenesis; modulation of cell-cycle progression; epigenetic effects	Preclinical	(Paul et al., 2018; Xiang et al., 2025) Xiang et al. (2025); Paul et al. (2018)
Sulforaphane	Cruciferous vegetables, including broccoli sprouts, cabbage, cauliflower and kale	HDAC inhibition; inhibition of Cripto-mediated signalling; cell-cycle arrest; apoptosis; autophagy; cancer-stem-cell suppression; modulation of EMT and tumour microenvironment	In vitro and in vivo	(Castro et al., 2019; Kuran et al., 2020; Paul et al., 2018; Rahman et al., 2024; Wu et al., 2025)
Corn silk-derived bioactive compounds	<i>Stigma maydis</i> (<i>Zea mays</i>)	ROS generation, lipid peroxidation, glutathione depletion, mitochondrial membrane-potential disruption; modulation of p53, Bax, caspase-3, caspase-9 and Bcl-2	Preclinical	(Al-Oqail et al., 2019; Gulati et al., 2023; Manzanares et al., 2026)

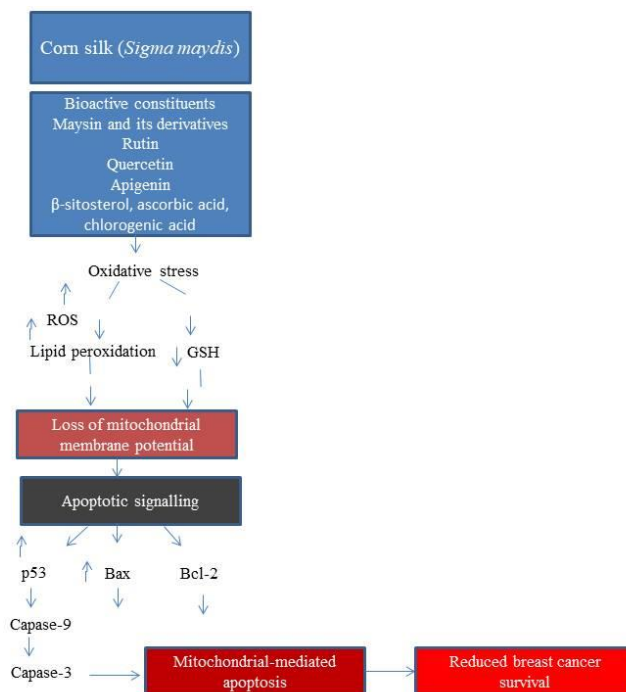


Figure 3 Proposed mechanisms by which corn silk-derived bioactive compounds may exert beneficial effect against breast cancer

6.0 CONCLUSION

Plant-derived bioactive compounds discussed in this review indicates that these compounds can exert anticancer effects through diverse and interconnected mechanisms, including cell-cycle arrest, modulation of tumour suppressor and oncogenic signaling, induction of apoptosis, and regulation of hormone receptor pathways. Compounds such as curcumin, resveratrol, genistein, sulforaphane, quercetin, EGCG, and corn silk-derived constituents have demonstrated the ability to influence molecular pathways involving p53, PTEN, PI3K/AKT/mTOR, MAPK, NF- κ B, ER, PR, and HER2, while also modulating genes such as AKT1, MAPK1, PGR, SGK1, ESR1, and MAPK3. Their biological effects may further involve modulation of epigenetic processes, enhancement of detoxification mechanisms, suppression of cytochrome P450 enzymes, and regulation of oxidative stress through alterations in ROS, lipid peroxidation, and glutathione levels. Altogether, these multifaceted activities highlight the potential of plant-derived bioactive compounds as sources of novel strategies for breast cancer chemoprevention and therapy. However, most available evidence remains preclinical, and further mechanistic, pharmacokinetic, safety, and well-designed clinical studies are required to establish their therapeutic efficacy and translational relevance.

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