Multidrug-resistant breast cancer: current perspectives

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Abstract: Breast cancer is the most common cancer in women worldwide, and resistance to the current therapeutics, often concurrently, is an increasing clinical challenge. By understanding the molecular mechanisms behind multidrug-resistant breast cancer, new treatments may be developed. Here we review the recent advances in this understanding, emphasizing the common mechanisms underlying resistance to both targeted therapies, notably tamoxifen and trastuzumab, and traditional chemotherapies. We focus primarily on three molecular mechanisms, the phosphatidylinositide 3-kinase/Akt pathway, the role of microRNAs in gene silencing, and epigenetic alterations affecting gene expression, and discuss how these mechanisms can interact in multidrug resistance. The development of therapeutics targeting these mechanisms is also addressed.

Keywords: PI3K/Akt, epigenetics, miRNA, ER, HER2, triple negative

Introduction

Breast cancer affects 1.38 million women worldwide per year, making it the most common cancer in women,1 and although the implementation of screening programs and the development of new therapeutics in the last 20 years have significantly reduced mortality rates in the Western world, resistance to these therapeutics is a growing problem.2 Resistance can be de novo but may also be acquired. Indeed, 30% of women with early-stage breast cancer have recurrent disease, and resistance to therapeutic agents can occur in at least a quarter of all cases.3,4 The incidence of resistance to therapeutics increases with disease progression,4 and this refractivity contributes to breast cancer having the highest mortality rate, 12.9/100,000 population in the USA in 2008, after lung cancer.1,5

Breast cancer is a heterogeneous disease and is divided clinically into three basic subtypes determined by the expression of hormone receptors (estrogen and progesterone), human epidermal growth factor receptor 2 (HER2), and triple-negative breast cancer, which expresses none of these receptors.6 Further subdivisions are now recognized, including luminal A, luminal B, basal-like, and HER2-enriched,7 and, recently, work has classified breast cancers into ten subtypes.8 However, to aid clarity, we will use the three basic clinical subtypes in this review. Each subtype has a different treatment strategy. For hormone receptor-positive breast cancer, the frontline treatment is endocrine therapy, whereas for HER2-positive cancers, it is trastuzumab (Herceptin; Roche, Basel, Switzerland). These specific therapies are often used in conjunction with traditional cytotoxic chemotherapeutics, such as taxanes and anthracyclines, which are the frontline therapies for triple-negative breast cancer.4 The mechanisms underlying resistance to these different therapeutics are multiple, complex, and not mutually...
exclusive, and have recently been excellently reviewed for each of the three subtypes individually. Here we will provide an overview of selected mechanisms underlying the drug resistance in each of these different groups, highlighting common mechanisms, specifically focusing on the role of the phosphatidylinositol 3-kinase (PI3K)/Akt pathway, miRNAs, and epigenetic alterations in drug resistance in breast cancer and how these interactions can contribute to a multidrug-resistant phenotype. The identification of potential targets for new therapies or as adjuvants to restore sensitivity to current treatments will be emphasized.

**Hormone receptor-positive breast cancer**

The predominant hormone receptor expressed in breast cancer is the estrogen receptor (ER), which is activated by the binding estrogens, predominantly estradiol. Hormone receptor-positive breast cancer also expresses progesterone receptors; however, these receptors have been somewhat neglected as therapeutic targets, as the first generation of antagonists had severe side effect profiles. Progesterone receptors have traditionally been considered as downstream targets of ERs, and their mechanistic roles in resistance to endocrine therapy underexplored. Consequently, we will limit our discussions here to ER-positive breast cancer (for further information on progesterone receptors in breast cancer we would like to draw the reader’s attention to the recent review by Brisker). Activation of the ER leads to a transcriptional response, both in genes with and without ER response elements, and also nontranscriptional cellular responses, all of which favor cell proliferation and survival (see Figure 1).

There are two ER forms, α and β. High expression levels of the latter have been correlated with good clinical prognosis, but as the role of this receptor in breast cancer has not been as widely studied as the ERα, we will focus on the former (we refer the reader to the recent review by Haldosén et al for further information). ERα-positive breast cancer accounts for approximately 70% of all breast cancer cases. The expression levels of ERα determine patient response to endocrine (antiestrogen) treatment and can be used as predictor of

**Figure 1** Estrogen, HER2 signalling, and the PI3K/Akt pathway in drug-resistant breast cancer. **Notes:** ER can activate gene transcription by nuclear translocation following ligand binding (1) or as a result of receptor phosphorylation in the absence of ligand (2). ERs may also be found associated with the plasma membrane in the presence of SRC and other adaptor proteins. Here, ligand binding triggers nongenomic effects via activation of signaling pathways, including the PI3K/Akt and the Ras/MAPK pathways (not shown) (3). These pathways are also activated by ligand binding to the GPR30 (4) and by growth factor binding to receptor tyrosine kinases, including HER2, inducing autophosphorylation and downstream signalling (5). The PI3K/Akt pathway (6) as indicated is a convergence point in the mechanisms implicated in drug resistance in the three types of breast cancer discussed here, as pathway hyperactivity frequently occurs with multiple downstream effects (7).

**Abbreviations:** BAD, Bcl-2-associated death promoter; DMNTs, DNA methyltransferases; E2, estrogen; ER, estrogen receptor; GF, growth factor; GPR30, G-protein coupled receptor 30; GSK3B, glycogen synthase kinase 3 beta; HER2, human epidermal growth factor receptor 2; IGF-1R, insulin-like growth factor receptor 1; MAPK, mitogen-activated protein kinase; mTORC1, mammalian target of rapamycin complex 1; P-gp, P-glycoprotein; PI3K, phosphatidylinositol 3-kinase; PTEN, phosphatase and tensin homolog; RTK, receptor tyrosine kinase; SRC, steroid receptor coactivator.
breast cancer is endocrine therapy, predominantly tamoxifen or fulvestrant, which are antagonists of ER in breast tissue (tamoxifen has agonist actions in other tissues). In premenopausal women, tamoxifen/fulvestrant is often used in conjunction with aromatase inhibitors (eg, anastrozole or letrozole) that reduce estrogen synthesis and lower the recurrence rate compared with tamoxifen alone. However, many patients with metastatic ER-positive disease develop resistance to endocrine therapy, so understanding the molecular mechanisms that lead to refractory disease may identify ways to circumvent resistance and restore responses to endocrine therapies. The mechanism of estrogen-induced cell responses (Figure 1) means there are many levels at which resistance to endocrine therapy can occur (excellently reviewed by Bianco and Gevry). Here we will explore those that mediate tamoxifen resistance, as this is the best studied, and many of these mechanisms apply to other endocrine therapies.

**Molecular mechanisms of tamoxifen resistance**

**Tamoxifen metabolism**

Tamoxifen itself is a prodrug that requires bioactivation to the major metabolite, endoxifen, to be active against ER. This process involves two members of the cytochrome P450 (CYP) family, CYP2D6 and CYP3A4. Both isoforms have several common polymorphisms. To date, none of the common CYP3A4 polymorphisms has been associated with altered tamoxifen metabolism. However, the CYP2D6 polymorphisms are well characterized and affect its catalytic activity. These polymorphisms are categorized into four groups, from the ultrarapid metabolizers with increased activity down to poor metabolizers with no CYP2D6 activity. Recent work has correlated CYP2D6 metabolizer status with response to tamoxifen treatment, with poor metabolizers having greater tumor progression than extensive metabolizers. Thus, determining CYP2D6 metabolizer status before tamoxifen treatment would be beneficial, allowing patients with poor metabolizer status to be treated with altered doses or other endocrine therapies, and consequently not categorized as resistant to endocrine therapy.

**ERα activity**

Phosphorylation is a common mechanism of post-translational modification to regulate enzyme activity, and has been linked with drug resistance in some cancers, including gemcitabine-resistant pancreatic cancer. Phosphorylation regulates ERα activity and plays a role in tamoxifen resistance, specifically phosphorylation of the serine 305 residue by protein kinase A or p21-activated kinase-1. Both of these kinases show enhanced activity in tamoxifen-resistant breast cancer. This phosphorylation changes the action of tamoxifen from antagonist to agonist; thus, the presence of tamoxifen now leads to the formation of an active transcription complex. The mechanisms underlying this change of response are not fully understood, but phosphorylation of S305 induces an altered orientation of binding between ERα and the steroid receptor coactivator-1, allowing the recruitment of RNA polymerase II and ERα-mediated gene transcription. This occurs without changes in the overall levels of binding; thus, in the presence of tamoxifen, estrogen-dependent gene transcription can be induced, and in patients with overactive protein kinase A or p21-activated kinase-1, treatment with tamoxifen could enhance tumor progression. To date, though, no studies have explored this mechanism in patient tissues.

Recently, a third isoform of ER has been identified, a 36kDa protein transcribed from an alternative start site and lacking the transactivation domains of the full-length (66kDa) ER, ER-α36. This isoform has a dominant negative effect on ERα activity, inhibiting both estrogen-dependent and independent effects, and levels are increased in tamoxifen-resistant MCF-7 cells and have been associated with poorer disease-free survival in ER-positive and ER-negative breast cancer. The binding of both estrogen and tamoxifen to ER-α36 stimulates activation of mitogen-activated protein kinase (MAPK)/extracellular signal regulated kinase (ERK) pathway, leading to cell proliferation and thus contributing to tamoxifen resistance.

In addition to the MAPK/ERK pathway, ERα can activate, by nontranscriptional mechanisms, the PI3K/Akt pathway (see Figure 1 for details), and alterations that increase the activity of this signaling pathway can lead to tamoxifen resistance. However, ERα is not the only receptor that can activate this pathway. It is also activated by a number of growth factor receptors, including fibroblast growth factor receptors (FGFR) 1 and 3 and insulin-like growth factor receptor 1 (IGF-1R). Both of these receptors have been shown to contribute to tamoxifen resistance via PI3K/Akt signaling and MAPK signaling. Recent work suggests that microRNAs (miRNAs) also have important roles in modulating the PI3K/Akt pathway in response to tamoxifen treatment. Sachdeva et al identified miR-101 as being able to confer tamoxifen-resistant and estrogen-independent growth on MCF-7 cells by suppressing membrane-associated guanylate kinase inverted 2 expression and reducing the activity of phosphatase and tensin homolog (PTEN), a negative
regulator of the PI3K/Akt pathway. Aberrations to the PI3K/ 
Akt pathway and the roles of miRNAs in drug resistance in 
breast cancer are discussed in more detail in the sections 
PI3K/Akt pathway and miRNA-mediated resistance.

Aberrant expression of ERα target genes can lead to 
tamoxifen resistance. For example, overexpression of cyclin 
D1 drives cancer cell proliferation, circumventing the normal 
cell-cycle control and deregulating ERα-dependent 
gene responses. Such alterations to the expression of ERα- 
dependent genes often arise from epigenetic changes, which 
occur in multiple formats (see section Epigenetic regulation 
for more details), the net effects of which are increased or 
decreased gene transcription. For example, transcription of the 
antiapoptotic gene BCL-2, an ERα target gene, is increased 
in tamoxifen-resistant cells, due to histone demethylation, 
thus favoring cell survival and disease progression.

HER2-positive breast cancer

HER2 is a receptor tyrosine kinase and a member of the ErBb 
family. Dimerization of HER2 as homo- or heterodimers with 
other ErBb family members, in both the presence and absence 
of ligand, leads to receptor activation and downstream signaling 
(see Figure 1). In mammary tissues, HER2 activation promotes 
cell survival and proliferation. Amplification of the HER2 
(ErbB2) gene occurs in approximately 20% of breast cancers, 
and 8% of ERα-positive breast cancers are also positive for 
HER2. ERα/HER2-positive breast cancer is associated with a 
poorer clinical outcome due to a tendency to display intrinsic 
resistance to endocrine therapy, which may result from interplay 
between the downstream signaling pathways.

The development of trastuzumab (Herceptin), a mono- 
clonal antibody that binds HER2, has improved clinical outcomes for patients with HER2 amplification. Trastuzumab 
induces a cytostatic signal, G1 arrest, and induction of an 
immune response to destroy the cancer cell. However, 
de novo resistance to trastuzumab occurs in approximately 
65% of cases, and resistance develops in approximately 70% 
of patients who initially respond. A number of causative 
mechanisms have been proposed (for an in-depth review, 
please see Pohlmann et al and Vu and Claret), including 
altered binding, upregulation of downstream pathways, and 
alterations to the immune response induced.

Molecular mechanisms 
of trastuzumab resistance

Epitope masking

Resistance to trastuzumab can occur due to epitope masking 
altering the binding to HER2. Two possible epitope 
masking candidates have been identified to date. Mucin 4, 
a large O-glycosylated membrane-associated protein, is one 
possible candidate, as it is upregulated in JIMT-1 cells that 
are trastuzumab resistant. The ratio of trastuzumab bind- 
ing to HER2 binding sites was a fifth of normal on these 
cells, and trastuzumab–HER2 binding was increased by 
RNAi knockdown of Mucin 4. The second candidate is 
the CD44/hyaluronan polymer complex, and, again, RNAi 
 knockdown of CD44 or chemical inhibition of hyaluronan 
synthesis resulted in increased trastuzumab–HER2 binding 
in JIMT-1 cells. This effect is postulated to be due to the 
bulky nature of the complex sterically hindering trastuzumab 
binding and alterations to trastuzumab internalization, 
thus conferring resistance, as trastuzumab cannot suppress HER2 
signaling.

HER2 signaling

Blockade of HER2 signaling with trastuzumab can be 
bypassed, to some degree, by the upregulation of other ErBb 
family members and increased heterodimer formation. In 
addition, in up to 30% of HER2-enriched breast cancers, 
an amino-terminal truncated form of HER2 is expressed, 
p95-HER2. This form of HER2 possesses constitutive kinase activity, triggering downstream signaling, but lacks 
the trastuzumab binding site, thus generating trastuzumab 
resistance. In these cases, treatment with another mono- 
clonal antibody, pertuzumab, which blocks dimer formation, 
or with lapatinib, which inhibits the tyrosine kinase activity 
of HER2 dimers, may restore clinical responsiveness to 
anti-HER2 therapy. However, even if HER2 signaling is 
effectively blocked, cancer proliferation may continue, as 
downstream pathways are activated by alternative routes, 
as described for tamoxifen resistance, again via IGF-1R, 
 which is often overexpressed in trastuzumab-resistant cells, 
and its inhibition can restore sensitivity to trastuzumab in 
SKBR3 cells. Signals from IGF-1R are transduced, in 
part, by the PI3K/Akt pathway, which is also activated by 
HER2 and ERα. Trastuzumab treatment can induce altera- 
tions to this pathway, giving rise to resistance via sustained 
Akt activation. One mechanism that may mediate this is the 
upregulation of c-Met, which physically interacts with HER2, 
enhancing growth in HER2-overexpressing cells. This effect 
is abrogated upon treatment with a c-Met inhibitor such as 
SU11274. Trastuzumab treatment also induces upregulation 
of a number of miRNAs, notably miR-21, that can influence 
the PI3K/Akt pathway by inhibiting PTEN. In trastuzumab-
resistant cells, overactivity of the PI3K/Akt pathway leads 
to epigenetic changes, including repression of FoxO, and
subsequently the increased transcription of the antiapoptotic gene survivin.\textsuperscript{46} It can also downregulate p27\textsuperscript{kip1}, which has been proposed as a critical downstream effector of trastuzumab, leading to increased cyclin-dependent kinase 2 expression and cell proliferation.\textsuperscript{42} The aberrations in this pathway contributing to multidrug-resistant breast cancer are discussed further in the section PI3K/Akt pathway.

**Altered immune response**

As a monoclonal antibody, trastuzumab-induced cell death is partially mediated by antibody-dependent cell-mediated cytotoxicity, a process by which natural killer cells/monocytes bind to the Fc region of trastuzumab with Fcγ receptors and initiate tumor cell death.\textsuperscript{47} FcγRIIIa has a well-known polymorphism at position 158, where either a valine or a phenylalanine is expressed, which has been linked to clinical prognosis. Indeed, the latter is less effective at inducing antibody-dependent cell-mediated cytotoxicity upon trastuzumab binding to HER2 and shows poorer clinical outcome than the valine/valine genotype in patients.\textsuperscript{48} This mechanism of resistance is specific to monoclonal antibody therapies and not related to the common mechanisms discussed in the section Common mechanisms leading to drug-resistant breast cancer.

**Triple-negative breast cancer**

Triple-negative breast cancer does not express ER\textalpha{} or progesterone receptors (PR) or show HER2 amplification, and accounts for 10%–20% of breast cancers.\textsuperscript{49} To date, there are no targeted therapies for this breast cancer subtype. Consequently, frontline treatments are limited to surgical approaches and chemotherapeutics, with the taxanes and anthracyclines being the chemotherapeutics of choice.\textsuperscript{30} Taxanes (eg, paclitaxel) act as mitotic poisons by stabilizing microtubules, leading to abnormal spindles and induction of apoptosis,\textsuperscript{51} whereas anthracyclines (eg, doxorubicin) act as DNA intercalators and topoisomerase II inhibitors and they can also generate reactive oxygen species via semiquinone formation.\textsuperscript{52} These chemotherapeutics are often given in conjunction with the targeted therapies for the other subtypes of breast cancer discussed previously, and thus cellular alterations induced by targeted therapies can contribute to chemotherapeutic resistance and vice versa.

**Molecular mechanisms of resistance to chemotherapeutics**

Resistance to both the taxanes and the anthracyclines predominantly arises from decreased drug intracellular concentrations due to increased efflux.\textsuperscript{12} This increased efflux is mediated by a small number of adenosine triphosphate (ATP)-binding cassette proteins that utilize ATP hydrolysis to translocate a variety of substrates, and increased expression of these correlates with poor clinical prognosis in breast cancer irrespective of subtype.\textsuperscript{53} The taxanes and anthracyclines are substrates for P-glycoprotein (P-gp), the best studied of the ABC transporters responsible for drug efflux and encoded by the \textit{MDR1} gene (\textit{ABCB1}), as well as other transporters, notably multidrug resistance-associated protein 2 (MRP2) and breast cancer resistance protein, that contribute to resistance to chemotherapeutics.\textsuperscript{54} We will focus on P-gp here as an example, as many of the mechanisms discussed may be applicable to MRP2 and breast cancer resistance protein. Resistance to one chemotherapeutic commonly means resistance to many, often structurally distinct compounds, as P-gp can transport a diverse range of molecular structures. Indeed, the tamoxifen metabolite endoxifen is a P-gp substrate.\textsuperscript{55}

**Alterations to drug efflux levels**

The primary mechanism underlying increased efflux is upregulation of the drug transporter proteins. This phenomenon occurs in a wide variety of cancers and has consequently been excellently reviewed by Chen and Sikic.\textsuperscript{12} Subsequently, we will cover this topic briefly here to highlight the commonalities with tamoxifen and trastuzumab resistance, specifically focusing on miRNAs, the PI3K/Akt pathway, and epigenetic alterations (discussed in more detail in the section Common mechanisms leading to drug-resistant breast cancer).

Recent work has identified miRNAs as having an important role in multidrug resistance, with over 50 different miRNAs linked to this phenotype (see Kutanzi et al\textsuperscript{56} for a review). A number of these miRNAs, including miR-19, miR-21, and miR-205, target PTEN, suggesting that the PI3K/Akt pathway is important in resistance to chemotherapeutics as well as for the more targeted therapies discussed previously. Indeed, use of the Akt inhibitor perifosine in multidrug-resistant MCF-7 cells improved response to doxorubicin treatment.\textsuperscript{57} It remains to be seen whether this is via a direct effect of the PI3K/Akt pathway on \textit{MDR1} expression or an indirect effect possibly via a reduction in cell survival signaling. In addition to altered miRNA levels, chemotherapeutic-resistant cancers, both in vitro and in patients, show diminished epigenetic repression of \textit{MDR1} with promoter hypomethylation and histone H3 lysine 9 acetylation.\textsuperscript{58–60}
Common mechanisms leading to drug-resistant breast cancer

As can be seen from these discussions, the three clinical subtypes of breast cancer have distinct therapeutic approaches, but the molecular mechanisms that give rise to refractory disease have common facets, notably alterations to the PI3K/Akt pathway, miRNA levels, and epigenetic modulation of gene transcription. These common facets will now be discussed in more detail, together with their potential as targets for adjuvant therapies to circumvent drug resistance and restore clinical responsiveness.

PI3K/Akt pathway

The PI3K/Akt pathway is an important signaling mechanism regulating many cellular responses, including cell proliferation and survival (Figure 1) in normal as well as neoplastic breast tissue. It forms a convergence point between all three clinical subtypes of breast cancer, and aberrations in this pathway occur in 70% of breast cancers irrespective of subtype. As highlighted previously, aberrations in this pathway are important in resistance to both tamoxifen and trastuzumab, especially as this pathway forms a crosslink between HER2 signaling and ERα-regulated gene transcription, and have also been linked to MDR1 upregulation and resistance to chemotherapeutics. Thus, understanding this pathway is paving the way for new adjuvant treatments in resistant breast cancer. A number of changes can occur, but all result in sustained pathway activity. Common aberrations include activating mutations or amplification of any of the PI3K subunits p110α, p110β, or p85α or loss of PTEN activity and its inhibition of PI3K, via inactivating mutations, overexpression of miRNAs, or promoter hypermethylation. Both of these scenarios result in increased Akt phosphorylation and sustained Akt activation, the net effects of which are inhibition of apoptosis, transcription of ERα-dependent genes, and cell proliferation. A major downstream effector of Akt activation that mediates a number of these responses is mammalian target of rapamycin complex 1 (mTORC1). mTORC1 also acts as a signaling integration node receiving inputs from the MAPK pathways that may be disrupted in drug-resistant breast cancer. Sustained PI3K/Akt/mTORC1 activity may also be due to alterations in miRNA expression and can induce a number of epigenetic changes that perpetuate drug resistance, which are discussed here.

miRNA-mediated resistance

In the last decade it has become clear that alterations to miRNA expression levels can contribute to cancer prognosis and outcome. miRNAs are small, noncoding RNAs or approximately 22 nucleotides, which bind to mRNA, preventing translation and accelerating mRNA deadenylation and subsequent degradation, thus having a gene silencing effect. Several miRNAs have been associated with drug resistance in breast cancer (see Table 1), and these target a variety of genes, including PTEN, ESR1 (ERα), FoxO3, and DNA (cytosine-5)-methyltransferases (DNMTs). The mechanisms that lead to miRNA upregulation in drug-resistant breast cancer are currently unclear, but they have powerful effects. One miRNA that is overexpressed

Table 1 miRNA associated with drug resistance in breast cancer

<table>
<thead>
<tr>
<th>miRNA</th>
<th>Expression change associated with resistance</th>
<th>Target genes</th>
<th>References</th>
</tr>
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<tbody>
<tr>
<td>Lin 28</td>
<td>Upregulated</td>
<td>CDKN1A (p21), RBL1, Let-7</td>
<td>91</td>
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<tr>
<td>miR-10a</td>
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<td>92</td>
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<td>miR-21</td>
<td>Upregulated</td>
<td>PTEN, PDCD4</td>
<td>92,93</td>
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<td>miR-22</td>
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<td>92</td>
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<tr>
<td>miR-29a</td>
<td>Upregulated</td>
<td>PTEN</td>
<td>92,94</td>
</tr>
<tr>
<td>miR-30c</td>
<td>Downregulated</td>
<td>TWFL</td>
<td>95</td>
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<tr>
<td>miR-31</td>
<td>Downregulated</td>
<td>PKC epsilon (PRKCE)</td>
<td>96</td>
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<td>miR-34a</td>
<td>Downregulated</td>
<td>NOTCH1</td>
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<td>miR-125b</td>
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<td>E2F3</td>
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<td>miR-128</td>
<td>Downregulated</td>
<td>BMI1, ABCC5</td>
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<td>YB-1 (P-gp indirectly)</td>
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<td>miR-181</td>
<td>Upregulated</td>
<td>Not stated</td>
<td>92</td>
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<tr>
<td>miR-181a</td>
<td>Downregulated</td>
<td>ABCG2 (BCRP)</td>
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<td>miR-200a and miR-200b</td>
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<td>ZEB1/2</td>
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<td>Downregulated</td>
<td>ZEB1, CDH1 (E-cadherin), PTEN, NTRK2 (TrkB), BMI1 (metadherin)</td>
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<td>miR-203</td>
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<td>miR-633</td>
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<td>HSPG2</td>
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</table>

Notes: A number of miRNAs have shown altered expression levels in drug-resistant forms of breast cancer in both cells and patients. The table contains those reported since 2011 (for prior studies we refer the reader to Kutanz et al46) together with their delineated target genes.

Abbreviations: BCRP, breast cancer resistance protein; miRNA, micro-RNAs; PDCD4, programmed cell death 4; P-gp, P-glycoprotein; PTEN, phosphatase and tensin homolog.
in both trastuzumab-resistant cells and cells resistant to chemotherapeutics is miR-21, which targets PTEN and results in sustained PI3K/Akt pathway activity as discussed previously.\textsuperscript{44,64} It also downregulates the apoptotic gene programmed cell death 4 (PDCD4), allowing cancer cells to evade apoptosis. This protein is also inactivated by phosphorylation by S6K1, a downstream effector of the PI3K/Akt pathway.\textsuperscript{65} Another prominent miRNA that appears to be important in drug resistance in both ER\textsubscript{α}-positive and triple-negative breast cancer is miR-221, which targets the cell-cycle inhibitory protein p27Kip1, among others.\textsuperscript{56,66} Thus, it can be seen that miRNAs have important roles in mediating drug resistance in breast cancer. However, the mechanisms leading to miRNA overexpression are not yet fully understood.

**Epigenetic regulation**

There are three main interlinked mechanisms by which epigenetic modulation leads to transcriptional regulation, chromatin remodeling, modification of nucleosome composition, and modification of epigenetic marks, all of which have been implicated in resistance to breast cancer therapies. ATP-dependent chromatin remodeling allows transcriptional complexes to access the highly coiled genomic DNA to initiate gene transcription. This can be achieved by selected transcription factors, known as pioneer factors. One such family, the Forkheads (Fox), is highly involved in breast cancer.\textsuperscript{65} Indeed, FoxA1 controls approximately 50% of ER\textsubscript{α} target genes,\textsuperscript{68} and its expression, along with that of FoxP1, has been correlated to a favorable response to tamoxifen treatment.\textsuperscript{69} In contrast, FoxM1 has a role to play in trastuzumab and paclitaxel resistance, as knockdown increases drug sensitivity in multidrug-resistant cell lines.\textsuperscript{70} FoxO1 expression is also associated with chemotherapeutic and tamoxifen resistance, as it regulates the transcription of both the MDR1 (P-gp) and ABC2 (MRP2) drug efflux pumps.\textsuperscript{71} The nuclear translocation of another FoxO isoform, FoxO3a, is inhibited by phosphorylation by Akt, which acts to drive cell proliferation and tamoxifen resistance, as FoxO3a has cytostatic actions via p27 upregulation and cell-cycle inhibition\textsuperscript{72} and by decreasing the expression of ER\textsubscript{α}-regulated genes.\textsuperscript{73} The biology of this complex family of transcription factors is not fully understood, but it has become clear that the balance of expression of the different isoforms is important, and further studies are needed to fully delineate their roles in drug-resistant breast cancer.

Nucleosomes are duplicates of the canonical histones H2A, H2B, H3, and H4 contained in a DNA loop, and modification by substitution with noncanonical histones regulates chromatin compaction and thus the transcription factor access to the genomic DNA.\textsuperscript{74} One such noncanonical histone implicated in ER\textsubscript{α}-positive breast cancer is H2A.Z, which stabilizes the nucleosome at the promoter of ER\textsubscript{α}-dependent genes. Overexpression of H2A.Z increased cell growth in MCF-7 breast cancer cells in the presence of tamoxifen and the absence of estrogen, suggesting that this histone can drive cell growth in an ER\textsubscript{α}-independent manner, and high expression levels of H2A.Z in patients have been associated with poor clinical prognosis.\textsuperscript{75} Post-translational modification of histone residues, predominantly by methylation and acetylation, also contributes to alterations in gene transcription. Methylation of lysine 27 of histone H3 governs the ligand dependency of ER\textsubscript{α}-mediated transcription of the BCL-2 gene, an important driver of the antiapoptotic response of breast cancer cells. Both tamoxifen-resistant and triple-negative breast cancer have been shown to have demethylation of H3K27 and consequently constitutive activation of BCL-2 and cancer cell survival.\textsuperscript{35,76} Changes to histone acetylation also occur in breast cancer, and hyperacetylation of histones H3 and H4 of the HER2 promoter may contribute to trastuzumab resistance by driving increased HER2 expression.\textsuperscript{77} Histone hyperacetylation is also involved in the overexpression of MDR1 (P-gp) in chemotherapeutic-resistant breast cancer, and the levels of acetylation of the lysine 9 residue of histone H3 are elevated by two orders of magnitude in drug-resistant MCF-7 cells.\textsuperscript{60}

In addition to histone residues, DNA bases can also be methylated, specifically at CpG sites, which are often found to be associated with gene promoter elements. The formation of methylated CpGs is catalyzed by the DNMT enzymes, and methylation levels are inversely correlated with gene transcription.\textsuperscript{78} Both hypermethylation and hypomethylation occur in drug-resistant breast cancer, as seen in Table 2. PTEN is frequently hypermethylated in drug-resistant breast cancer, and this silencing is maintained by a positive feedback as reduced PTEN levels lead to increased Akt activity and increased activity of DNMT1, the DNMT that methylates the PTEN promoter expression,\textsuperscript{79} thus bypassing HER2 or ER\textsubscript{α} induction of PI3K/Akt pathway activation. Hypermethylation of the ESR1 (ER\textsubscript{α}) promoter by DMNT3B contributes to tamoxifen resistance by reducing expression of tamoxifen’s target, ER\textsubscript{α}.\textsuperscript{80} In contrast, hypomethylation and increased expression
of MDR1 (P-gp) play an important role in resistance to chemotherapeutics.\textsuperscript{58} Thus, it is clear that DNA methylation status has important roles in mediating drug resistance in breast cancer and, to this end, Rhee et al\textsuperscript{81} have recently published an integrated analysis correlating DNA methylation status with gene expression data for the different subtypes of breast cancer. This study, together with the comprehensive molecular analysis of the subtypes compiled by the Cancer Genome Atlas Research Network,\textsuperscript{82} will allow other genes with altered methylation states to be identified and their roles in drug resistance explored, especially for drug-resistant HER2-positive breast cancer, as this area has not been explored in this subtype.

### Future perspectives for the treatment of drug-resistant breast cancer

The studies discussed here delineating the molecular mechanisms underlying drug resistance in breast cancer, in terms of both single and multidrug resistance, have identified

### Table 2 Genes with altered methylation status in drug-resistant breast cancer

<table>
<thead>
<tr>
<th>Gene</th>
<th>Protein</th>
<th>Hypermethylated/hypomethylated</th>
<th>References</th>
</tr>
</thead>
<tbody>
<tr>
<td>ABCB1 (MDR1) Upstream promoter</td>
<td>P-glycoprotein</td>
<td>Hypomethylated</td>
<td>57,58,111–114</td>
</tr>
<tr>
<td>ABCB1 (MDR1) Alternative Downstream promoter</td>
<td>P-glycoprotein</td>
<td>Hypermethylated</td>
<td>111</td>
</tr>
<tr>
<td>ACVR1</td>
<td>Activin A receptor</td>
<td>Hypomethylated</td>
<td>115</td>
</tr>
<tr>
<td>APC</td>
<td>Adenomatous polyposis coli</td>
<td>Hypomethylated</td>
<td>113</td>
</tr>
<tr>
<td>TUBA1A</td>
<td>(\alpha)-Tubulin</td>
<td>Hypomethylated</td>
<td>115</td>
</tr>
<tr>
<td>BAD</td>
<td>Cell death regulator Aven (PDCD12)</td>
<td>Hypermethylated</td>
<td>115</td>
</tr>
<tr>
<td>BRCA1</td>
<td>BRAC1</td>
<td>Hypermethylated</td>
<td>113</td>
</tr>
<tr>
<td>CDH1</td>
<td>E-cadherin</td>
<td>Hypermethylated</td>
<td>113</td>
</tr>
<tr>
<td>CDK10</td>
<td>Cyclin-dependent kinase 10</td>
<td>Hypermethylated</td>
<td>116</td>
</tr>
<tr>
<td>CXCR4</td>
<td>Stromal cell-derived factor I receptor</td>
<td>Hypermethylated</td>
<td>115</td>
</tr>
<tr>
<td>ESR1</td>
<td>ER(\alpha)</td>
<td>Hypermethylated</td>
<td>113,115</td>
</tr>
<tr>
<td>ESR2</td>
<td>ER(\beta)</td>
<td>Hypermethylated</td>
<td>117,118</td>
</tr>
<tr>
<td>FTH1</td>
<td>Ferritin heavy chain</td>
<td>Hypomethylated</td>
<td>115</td>
</tr>
<tr>
<td>FOXK1</td>
<td>Forkhead box protein k1</td>
<td>Hypomethylated</td>
<td>115</td>
</tr>
<tr>
<td>GSTP1</td>
<td>Glutathione S-transferase (\pi) 1</td>
<td>Hypomethylated</td>
<td>113</td>
</tr>
<tr>
<td>HIC1</td>
<td>Hypermethylated in cancer 1</td>
<td>Hypermethylated</td>
<td>113</td>
</tr>
<tr>
<td>IL2</td>
<td>Interleukin 2</td>
<td>Hypermethylated</td>
<td>115</td>
</tr>
<tr>
<td>LEP</td>
<td>Leptin</td>
<td>Hypermethylated</td>
<td>115</td>
</tr>
<tr>
<td>MGMT</td>
<td>6-O-methylguanine-DNA methyltransferase</td>
<td>Hypomethylated</td>
<td>57,119</td>
</tr>
<tr>
<td>NAT1</td>
<td>N-acetyltransferase 1</td>
<td>Hypermethylated</td>
<td>120</td>
</tr>
<tr>
<td>CDKN1A</td>
<td>p21</td>
<td>Hypermethylated</td>
<td>121</td>
</tr>
<tr>
<td>TP73</td>
<td>p73</td>
<td>Hypermethylated</td>
<td>115</td>
</tr>
<tr>
<td>PLAU</td>
<td>Plasminogen activator urokinase</td>
<td>Hypomethylated</td>
<td>57,113</td>
</tr>
<tr>
<td>PGR</td>
<td>Progesterone receptor</td>
<td>Hypermethylated</td>
<td>122</td>
</tr>
<tr>
<td>TFF1</td>
<td>p52 (trefoil factor 1)</td>
<td>Hypermethylated</td>
<td>123</td>
</tr>
<tr>
<td>ATP2B4</td>
<td>Sarcolemmal calcium pump</td>
<td>Hypermethylated</td>
<td>123</td>
</tr>
<tr>
<td>DUSP7</td>
<td>Dual-specific phosphatase 7</td>
<td>Hypermethylated</td>
<td>123</td>
</tr>
<tr>
<td>GDF15</td>
<td>Growth differentiation factor 15</td>
<td>Hypermethylated</td>
<td>123</td>
</tr>
<tr>
<td>PSAT1</td>
<td>Phosphoserine aminotransferase 1</td>
<td>Hypermethylated</td>
<td>124</td>
</tr>
<tr>
<td>PTEN</td>
<td>PTEN</td>
<td>Hypermethylated</td>
<td>78</td>
</tr>
<tr>
<td>RAB6C</td>
<td>WTH3</td>
<td>Hypermethylated</td>
<td>113,125,126</td>
</tr>
<tr>
<td>RASAL1</td>
<td>Ras protein activator-like 2 (GAP1)</td>
<td>Hypermethylated</td>
<td>113</td>
</tr>
<tr>
<td>ARHGEF2</td>
<td>Rho/roc GEF2</td>
<td>Hypermethylated</td>
<td>115</td>
</tr>
<tr>
<td>RASSF1</td>
<td>Ras association domain containing protein 1</td>
<td>Hypermethylated</td>
<td>113</td>
</tr>
<tr>
<td>RFC1</td>
<td>Replication factor C1</td>
<td>Hypermethylated</td>
<td>127</td>
</tr>
<tr>
<td>SDK2</td>
<td>Sidekick 2</td>
<td>Hypomethylated</td>
<td>115</td>
</tr>
<tr>
<td>SULF2</td>
<td>Sulfatase 2</td>
<td>Hypermethylated</td>
<td>113</td>
</tr>
<tr>
<td>TGM2</td>
<td>Tissue transglutaminase</td>
<td>Hypomethylated</td>
<td>113,115</td>
</tr>
<tr>
<td>UTRN</td>
<td>Utrophin</td>
<td>Hypomethylated</td>
<td>115</td>
</tr>
</tbody>
</table>

**Note:** Hypomethylation results in gene overexpression as DNA methylation reduces gene transcription; consequently, hypermethylation effectively leads to gene silencing.

**Abbreviations:** ER, estrogen receptor; PTeN, phosphatase and tensin homolog.

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number of pathways that offer potential routes to circumvent resistance to the current therapies.

The PI3K/Akt/mTORC1 signaling axis offers targets for therapeutic interventions, and a number of clinical trials are ongoing using PI3K, AKT, mTOR, or dual inhibitors in combination with endocrine or chemotherapies (Table 3). However, caution is required, as the clinical response may depend on the specific aberration and the subtype of breast cancer, as inhibition of Akt may induce apoptosis by release of Bcl-2-associated death promoter (BAD) inhibition, but Akt inhibition can also permit FoxO3a nuclear translocation, potentially leading to the transcription of ERα-dependent genes encouraging cell proliferation. Also, upregulation of growth factor receptors (eg, FGFRs and IGF-1R) may favor activation of other signaling cascades, such as the MAPK pathways, which could be exacerbated by inhibition of

<table>
<thead>
<tr>
<th>Table 3 Inhibitors of the PI3K/Akt pathway currently undergoing clinical trials</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Drug</strong></td>
</tr>
<tr>
<td>AZD5363</td>
</tr>
<tr>
<td>GSK2110183</td>
</tr>
<tr>
<td>GSK2141795</td>
</tr>
<tr>
<td>MK2206</td>
</tr>
<tr>
<td>HER2+</td>
</tr>
<tr>
<td>Not stated</td>
</tr>
<tr>
<td>Triciribine Phosphate Monohydrate</td>
</tr>
<tr>
<td>BAY 80-6946</td>
</tr>
<tr>
<td>BKM120</td>
</tr>
<tr>
<td>HER2</td>
</tr>
<tr>
<td>Trastuzumab-resistant HER2+</td>
</tr>
<tr>
<td>BYL719</td>
</tr>
<tr>
<td>GDC-0941</td>
</tr>
<tr>
<td>XL147</td>
</tr>
<tr>
<td>CC-223</td>
</tr>
<tr>
<td>Everolimus</td>
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<tr>
<td></td>
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<tr>
<td>Rapamycin</td>
</tr>
<tr>
<td></td>
</tr>
<tr>
<td>Temsirolimus</td>
</tr>
<tr>
<td></td>
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<td></td>
</tr>
<tr>
<td></td>
</tr>
<tr>
<td>Ridaforolimus</td>
</tr>
<tr>
<td>BEZ235</td>
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<tr>
<td></td>
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<td></td>
</tr>
<tr>
<td></td>
</tr>
<tr>
<td>GDC-0980</td>
</tr>
<tr>
<td>XL765</td>
</tr>
</tbody>
</table>

**Notes:** The alterations to the PI3K/Akt pathway are common factors in the different subtypes of breast cancer and also have important roles in mediating drug resistance (see text for details). Subsequently, this pathway is a promising therapeutic target to overcome drug resistance with a variety of compounds in clinical trials. Data obtained from the ClinicalTrials.gov database.

**Abbreviations:**  AI, aromatase inhibitor; ER, estrogen receptor; HER2, human epidermal growth factor receptor 2; mTOR, mammalian target of rapamycin complex 1.
PI3K/Akt/mTORC1. In addition, the effects of this pathway on transcription via epigenetic changes need to be considered to prevent the selection of tumor subpopulations that are resistant to therapy, especially the FoxO family, as targeting these transcription factors directly is not a viable option currently, due to their complexity. Thus, the combination of therapies needs to be carefully considered and appropriate for the cancer subtype.

Overcoming drug resistance that results from P-gp overexpression may require a different approach to that of the PI3K/Akt pathway, as several P-gp inhibitors have been trialed without satisfactory clinical outcomes. To this end, a number of compounds that are microtubule stabilizers, like the taxanes, but are not P-gp substrates have been trialed with promising clinical results (see Nobili et al for details). Other drugs that actually exploit P-gp overexpression are being considered, notably NSC73306, the cytotoxic capacity of which correlates with P-gp expression levels. The more P-gp expressed, the more toxic NSC73306 is. NSC73306 does not appear to be a P-gp substrate. Understanding the way this drug utilizes P-gp overexpression may help identify mechanisms to circumvent multidrug resistance involving P-gp.

As yet, no therapeutics targeting specific miRNAs have made it into the clinic. However, one antagonist to miR-122 is undergoing Phase II clinical trials for use in hepatitis C, suggesting that miRNAs could be valid therapeutic targets in breast cancer. To this end, therapeutics targeting miR-21 and miR-221, which are implicated in drug resistance in breast cancer, are being commercially developed for use in hepatocellular carcinoma and other cancers, and so it may not be too long before clinical trials of miRNA inhibitors for the treatment of multidrug-resistant breast cancer become a reality.

Reversing the deleterious alterations to epigenetic regulation that are associated with drug resistance in breast cancer is a challenging proposition. However, histone deacetylation inhibitors are showing promise in all subtypes of breast cancer, but caution is required, as these approaches may alter the expression of ERα, HER2, and MDR1, as discussed previously, which could actually enhance drug resistance. It will be interesting to see how the large volume of preclinical data available on this topic translates to clinical outcomes, as trials of a number of different histone deacetylation inhibitors are ongoing.

Other approaches to circumvent multidrug resistance in breast cancer, especially the triple-negative subtype, are being pursued and include inhibitors of angiogenesis, epidermal growth factor receptor, poly(adenosine diphosphate-ribose) polymerase, and FGFRs, which are outside the scope of this review (we refer the reader to Bayraktar and Glück).

Conclusion
Multidrug-resistant breast cancer is a complex clinical condition arising from a diverse range of molecular perturbations, yet several common mechanisms have been identified. The PI3K/Akt pathway discussed here is just one. By identifying these common mechanisms and developing therapeutics targeting them, an armory for overcoming drug resistance in different clinical situations can be created. It will be interesting to see how the PI3K/Akt/mTOR inhibitors perform in the ongoing clinical trials to ascertain whether such global approaches are useful for circumventing resistance to frontline therapies. Further studies are required before therapeutics targeting other common mechanisms highlighted here, miRNA upregulation and epigenetic alteration, may be targeted, as these are not yet as well understood.

Disclosure
The authors report no conflicts of interest in this work.

References


