

Non-Hodgkin's B-cell lymphoma: Advances in molecular strategies targeting drug resistance

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Abstract

Non-Hodgkin's lymphoma (NHL) is a heterogeneous class of cancers displaying a diverse range of biological phenotypes, clinical behaviours and prognoses. Standard treatments for B-cell NHL are anthracycline-based combinatorial chemotherapy regimens composed of cyclophosphamide, doxorubicin, vincristine and prednisolone. Even though complete response rates of 40–50% with chemotherapy can be attained, a substantial proportion of patients relapse, resulting in 3-year overall survival rates of about 30%. Relapsed lymphomas are refractory to subsequent treatments with the initial chemotherapy regimen and can exhibit cross-resistance to a wide variety of anticancer drugs. The emergence of acquired chemoresistance thus poses a challenge in the clinic preventing the successful treatment and cure of disseminated B-cell lymphomas. Gene-expression analyses have increased our understanding of the molecular basis of chemotherapy resistance and identified rational targets for drug interventions to prevent and treat relapsed/refractory diffuse large B-cell lymphoma. Acquisition of drug resistance in lymphoma is in part driven by the inherent genetic heterogeneity and instability of the tumour cells. Due to the genetic heterogeneity of B-cell NHL, many different pathways leading to drug resistance have been identified. Successful treatment of chemoresistant NHL will thus require the rational design of combinatorial drugs targeting multiple pathways specific to different subtypes of B-cell NHL as well as the development of personalized approaches to address patient-to-patient genetic heterogeneity. This review highlights the new insights into the molecular basis of chemorefractory B-cell NHL that are facilitating the rational design of novel strategies to overcome drug resistance.

Keywords: Drug resistance, NHL, B-cell lymphoma, mechanisms of drug resistance, Akt, apoptosis, NF κ B, oxidative stress, microRNAs, TGF β , cluster differentiation antigens, multidrug resistance, drug metabolism, MAP kinases, tyrosine kinases, p53, proteasome, epigenetics, microsatellite instability, stromal influences, stroma, sphingosine kinase, geranylation, zinc transporter, positive regulatory domain I protein, retinaldehyde dehydrogenase

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Introduction

The problem of multidrug resistance in non-Hodgkins lymphoma

Non-Hodgkins lymphoma (NHL) is a heterogeneous class of cancers displaying a diverse range of biological phenotypes, clinical behaviours and prognoses. The majority of NHL cases originate from B cells with about 10% arising from T cells.^{1,2} B cells that normally undergo clonal expansions at different stages of differentiation can give rise to the B cell type of NHL.³

The standard treatment for NHL is the anthracycline-based chemotherapy regimen, termed CHOP, which is composed of cyclophosphamide, doxorubicin, vincristine and prednisolone.⁴ The addition of rituximab (*monoclonal antibody to CD20*) to CHOP (*R-CHOP*) has provided the first

major improvement in therapy in over three decades and is now the new standard for treatment.⁵ Most NHL patients initially respond to chemotherapy yielding complete response rates of 40–50%.^{6–10} Regrettably, a substantial population of patients undergo relapse, resulting in disappointing 3-year overall survival rates of only about 30%.¹¹ The problem is compounded by the higher doses of CHOP administered to relapsed patients, which have resulted in severe side-effects and a response in only about one-third of relapsed patients.^{12–14} Relapsed lymphomas are not only refractory to subsequent treatments with the initial chemotherapy regimen but also can exhibit cross-resistance to a wide variety of anticancer drugs.

Acquisition of chemoresistance in B-cell lymphomas is due to the emergence of subpopulations of drug-resistant tumour cells, which leads to the failure of standard

CHOP therapies. Chemoresistance in NHL is not consistently associated with the upregulation of multidrug pump (i.e. P-glycoprotein; MDR1) expression indicating the existence of other drug-resistant mechanisms.^{15,16} Inherent genetic heterogeneity and instability of the tumour cells drive the acquisition of drug resistance in lymphoma.¹⁷

It is now apparent that a new generation of less toxic and more targeted approaches based on rational drug design is needed to prevent and/or reverse chemoresistant disease.¹⁸ The purpose of this article is to highlight the many new insights into the molecular basis of chemorefractory NHL, which are leading the way to the rational design of novel drugs to overcome chemoresistance. Due to the genetic heterogeneity of B-cell NHL, many different pathways leading to drug resistance have been identified. Successful treatment of chemoresistant NHL will thus require cocktails of combinatorial drugs targeting multiple pathways specific to different subtypes of NHL as well as the development of personalized approaches to address patient-to-patient genetic heterogeneity.

Innate and acquired drug resistance varies among subtypes of NHL

Aggressive NHL includes diffuse large B-cell lymphoma (DLBCL), mantle-cell lymphoma (MCL), Burkitt's lymphoma (BL), follicular lymphoma (FL) and peripheral T-cell lymphoma (PTCL). Each of these subtypes of NHL display a wide range of responses and outcomes to standard chemotherapeutic regimens due to genetic heterogeneities. Despite remarkable advances in chemotherapy, more than half of patients with aggressive B-cell NHL (B-NHL) are incurable.⁶ PTCL, in particular, remains a challenge for chemotherapy since there are no drugs that can prevent progression of the disease.¹⁹

The two most common types of NHL are DLBCL and FL, representing more than half of all patients with B-NHL.¹ The most common histological type is DLBCL and is classified as an aggressive subtype, but potentially is curable with chemotherapy.^{1,20–22} The second most frequent type of NHL is FL, which is usually incurable with conventional chemotherapy, and exhibits a median survival of 10 years postdiagnosis.²³ MCL is an aggressive disease with a 3–4-year median survival and poor responsiveness to conventional chemotherapy.^{24–27}

Drug-resistant DLBCL

Most DLBCL patients initially respond favourably to CHOP, but ~50% eventually relapse with CHOP-resistant disease that disseminates and is highly lethal without transplantation.²⁸ Even though CHOP-resistant DLBCL affects about 10,000 new cases in USA each year, the molecular features of CHOP-resistant DLBCL have not been adequately defined. Drug resistance can be inherent (innate) from the beginning²⁹ or develop from prior exposure to chemotherapy (acquired).^{30,31} The varied responses of DLBCL to chemotherapy are due to aberrations in multiple molecular pathways, which are attributed to the heterogeneous genetic nature of DLBCL.³² Gene expression profiling (GEP) of patient tumours has better defined the molecular

heterogeneity underlying the heterogeneous clinical behaviour of DLBCL. Patients with DLBCL have been classified into three groups according to their GEP patterns based on the three cell-of-origin signatures, activated B-cell-like DLBCL (ABC-DLBCL), germinal-centre B-cell-like DLBCL (GCB-DLBCL) and mediastinal.^{33–36} The GCB and ABC subcategories are characterized by distinct differences in survival, chemoresponsiveness and dependence on signalling pathways.³⁷ ABC-DLBCL resembles *in vitro* activated B cells. In a separate multiple clustering array analysis,³⁸ DLBCLs were categorized into Ox-phos, BCR/proliferation and host-response signatures. The BCR/proliferation subset displayed the upregulation of genes involved in B-cell activation and proliferation.

Mantle-cell lymphoma

Mantle-cell lymphoma (MCL) is an aggressive disease that has a poor response to conventional chemotherapy resulting in an overall survival of about 3–4 years.^{27,39} A major problem in treating MCL is the occurrence of relapse caused by resistance to chemotherapy. Many different drug combinations comprised of alkylating agents, anthracyclines and purine analogs have been tested in MCL patients.⁴⁰

One of the unique features of MCL is a cluster differentiation (CD) phenotype associated with a specific chromosomal translocation, t(11;14)(q13;q32), which translocates the cyclin D1 gene to be under the control of the immunoglobulin heavy chain gene enhancer, resulting in upregulation of cyclin D1.⁴¹ Overexpression of cyclin D1 plays a critical role in the pathogenesis and chemorefractoriness of MCL. However, accumulating evidence indicates that MCL frequently is dysregulated not only in cell-cycle regulation but also in apoptosis and DNA repair.^{42,43}

MCL frequently can also be innately resistant to anticancer agents.⁴³ A number of dysfunctional biochemical pathways have been identified that may contribute to the relatively high resistance of MCL to chemotherapy-induced apoptosis,⁴⁴ including the activation of NFκB pathway,^{45–47} overexpression of antiapoptotic proteins and the absence of proapoptotic proteins.⁴⁸ GEP has also identified the upregulation of genes associated with multidrug resistance in MCL.⁴⁹ The resistance of MCL to alkylating agents and to anthracycline can also result from the upregulation of the glutathione S-transferase (GST) gene, which is located in 11q13 and thus co-amplified along with the cyclin D1 gene⁵⁰ as well as the phosphoinositide 3-kinase/Akt pathway (PI3K/Akt).^{51,52} Despite the generation of several new therapeutic agents directed against PI3K/Akt, B-cell receptor signalling and Bcl-2, poor clinical outcomes continue to be a problem in a significant population of MCL patients.^{43,53}

Drug-resistance pathways in B-cell NHL

PI3K/Akt pathway in B-cell NHL drug resistance

The PI3K/Akt pathway plays a central role in promoting survival and chemoresistance in NHL.^{54–58} Dysregulation of the PI3K/Akt pathway is frequent in DLBCL and worsens prognosis.^{58–65} New drugs targeting this pathway have

shown encouraging results in treating relapsed NHL patients.⁶⁶⁻⁷¹ However, not all chemorefractory DLBCL patients show positive responses to current Akt pathway inhibitors, and many experience severe side-effects.^{72,73}

A primary mediator of PI3K signalling is the Akt/protein kinase B kinase, which acts to promote cell survival through direct phosphorylation of apoptotic regulators. Akt phosphorylation of proapoptotic substrates (including Bad, FOXO, GSK-3 β and ASK1) targets them for binding to 14-3-3 proteins,⁷⁴⁻⁸⁰ which effectively neutralizes their ability to induce apoptosis.

A role for the activation of the Akt pathway in promoting chemoresistance in NHL was shown by treatment with pharmacological inhibitor (LY-294002) and by Akt siRNA, both of which inhibited Bcl-xL expression and sensitized the cells to chemotherapeutics.⁸¹ Moreover, higher Akt activity was observed in CHOP-resistant DLBCL cells than in CHOP-sensitive cells, which was associated with the upregulation of 14-3-3 ζ .^{82,83} Chemical inhibition of Akt⁸² or shRNA-mediated knockdown of 14-3-3 ζ ⁸³ restored CHOP sensitivity to the resistant cells, indicating that CHOP resistance was mediated by these proteins, was reversible and might be targeted as a clinical strategy for CHOP resensitization.

mTOR in the Akt pathway is an important therapeutic target for DLBCL. Rapamycin inhibited mTORC1 in DLBCL lines and primary tumours with minimal cytotoxicity.⁸⁴ Clinical trials of the rapamycin analogs, temsirolimus and everolimus have demonstrated overall response rates of about 30% for relapsed DLBCL.⁸⁵⁻⁸⁷ However, only about half of relapsed patients respond to mTOR inhibitors. A critical focus needs to be on the development of new inhibitors of the PI3K/Akt pathway that bypass resistance mechanisms. As an example, addition of a histone deacetylase inhibitor reversed resistance to rapamycin.⁸⁴

Dysregulated apoptotic pathways

The germinal centre (GC) is the location of immune surveillance in the lymph node. B cells that express functional B-cell receptors and have a block to execution of an activated apoptotic program migrate to the GC.⁸⁸ One hallmark of germinal centre-derived B-cell NHL (GC-DLBCL) is resistance to apoptosis characterized by the dysregulation of apoptotic control mechanisms.^{37,89,90} In addition, dysregulation of genes involved in apoptotic pathways has also been reported to be associated with chemoresistance in activated B-cell-like DLBCL (ABC-DLBCL). Thus, a promising approach in both frontline and salvage therapeutic strategies in B-cell NHL is targeting altered apoptotic pathways. Strategies targeting the two main apoptotic pathways, extrinsic and intrinsic, are summarized below.

Extrinsic (death receptor) pathway

The tumour-necrosis factor receptor (TNFR) family of transmembrane proteins, including the death receptors for Fas (CD95) and tumour necrosis factor-related apoptosis-inducing ligand (TRAIL), induces cell death. TRAIL mediates apoptosis by binding to cell-surface transmembrane receptors, either death receptor 4 (DR4/APO2/TRAIL-R1) or

death receptor 5 (DR5/KILLER/TRAIL-R2/TRICK2),⁹¹ which recruit the death-inducing signalling complex composed of FADD and the inactive proenzymatic form of the apoptosis-initiating proteases caspase-8.^{92,93} Self-activation of caspase-8 by autoproteolysis leads to the activation of the executioner caspase-3 to carry out apoptosis.

TNFR family members can selectively induce apoptosis in some drug-resistant B-cell lymphomas.⁹⁴⁻⁹⁷ Twelve out of 22 primary lymphoma cell cultures derived from biopsied DLBCL samples were sensitive to TRAIL,⁹⁷ which included seven clinically chemoresistant lymphomas. TRAIL was found to induce apoptosis in DLBCL cells expressing the upregulation of prosurvival molecules, Bcl-2 and/or X-linked inhibitor of apoptosis (XIAP). Thus, TRAIL might be an effective therapy for drug-resistant DLBCL patients that show dysregulated extrinsic apoptosis pathways.^{96,98,99}

The Bfl-1 protein is required for the survival of malignant B cells and might be a potential target against drug-resistant B-cell lymphoma.¹⁰⁰ Bfl-1 is a direct transcriptional target of nuclear factor-kappa B (NF- κ B),¹⁰¹⁻¹⁰³ and its upregulation is associated with an increased resistance to tumour-necrosis factor (TNF)- α , anti-CD95, TRAIL and chemotherapeutic drugs.¹⁰²⁻¹⁰⁴ In DLBCL, downregulation of Bfl-1 occurs in tumour cells induced to undergo apoptosis by inhibition of the activated NF- κ B pathway.¹⁰⁵ Moreover, short-hairpin RNA silencing of Bfl-1 in DLBCL cell lines sensitized those cell lines to anti-CD20 (rituximab)-mediated cell death and chemotherapeutic agents. Thus, Bfl-1 will be a candidate target in the design of new strategies for drug-resistant cancer therapy.

Intrinsic pathway

The Bcl-2 family regulates an apoptotic pathway that is initialized at the mitochondrion known as the intrinsic apoptotic pathway. Bcl-2 family members function through mutual interactions with each other and the balance between the anti-apoptotic (Bcl-2, Bcl-xL, Mcl-1) and the proapoptotic (Bax, Bak; and the BH3-only Bid, Bim and PUMA protein) members are critical for preventing or initiating apoptosis.^{106,107} The BH3-only proapoptotic (Bid, Bim, PUMA) proteins act as molecular sensors of cellular stress or damage and are activated in response to DNA damage, growth factor withdrawal and oncogene activation.¹⁰⁸

Many chemotherapeutic drugs activate the intrinsic apoptosis pathway, leading to the release of proapoptotic molecules, including cytochrome *c*, from the intermembrane space of mitochondria into the cytosol. Cytochrome *c*, Apaf-1 and procaspase-9 complex together to form the apoptosome machinery in the cytoplasm. The apoptosome promotes oligomerization of Apaf-1, which then triggers the activation of the initiator procaspase-9. The active caspase-9, in turn, cleaves and activates downstream executioner caspases, including pro-caspase-3, which cleaves proteins, thus producing the characteristic apoptotic phenotype of blebbing, nuclear condensation and cell shrinkage.

Dysregulation of apoptosome formation and caspase activation has been associated with chemoresistance in B-cell lymphoma. BL cells commonly are resistant to

apoptosis induction by chemotherapeutic agents, which has been attributed to deficient levels of Apaf-1, thus leading to the failure of cytochrome *c* to promote apoptosome formation and caspase activation.¹⁰⁹

Overexpression of antiapoptotic family members in B-cell lymphomas is associated with the inhibition of apoptosis and chemotherapy resistance, resulting in lower clinical response rates and shortened survival.^{110–114} Bcl-2 was observed overexpressed in about 80% of FL and 20% of DLBCL as a result of the t(14;18) translocation and amplification of the Bcl-2 gene, respectively.^{115–117} Bcl-2 expression was also correlated with a higher relapse-rate, shorter disease-free survival and shorter overall survival.^{16,118–121} Antisense-mediated repression of Bcl-2 expression resulted in significant increases in the sensitivity of lymphoma cells to chemotherapeutic drugs.^{122–124} Oblimersen (Genta Inc.) is a phosphorothioate Bcl-2 antisense oligonucleotide, which in combination with rituximab, resulted in an overall response rate of 42% including 10 complete responses and 8 partial responses in relapsed B-cell NHL patients.¹²⁵ Median duration of response was 12 months with minimal toxicities. Thus, co-administration of Oblimersen and rituximab is a safe treatment that will be most beneficial in patients with refractory NHL.

IAP proteins

Inhibitor of apoptosis (IAP) proteins can block executioner caspases.¹²⁶ Overexpression of IAPs (XIAP) has been shown to result in resistance to agents that induce apoptosis pathways.^{127,128} XIAP is the most potent inhibitor of the apoptosis cascade and can repress apoptosis induced by TNF, TRAIL, Fas-L and conventional chemotherapeutics.^{127,128} In DLBCL, XIAP expression was associated with a poor prognosis.¹²⁹ A small-molecule XIAP antagonist re-activated the intrinsic apoptosis pathway in drug-resistant DLBCL cell lines.^{130,131} Peripheral blood mononuclear cells and tonsil germinal-centre B cells from healthy donors were not affected, validating the XIAP antagonist for possible development as a therapy for chemotherapy-refractory DLBCL. The sensitivity of DLBCL cells to the XIAP antagonist could be predicted from molecular markers, such as expression of XIAP, Bcl-2 and levels of constitutive caspase-9 activation,¹³¹ indicating a potential for selecting patients for XIAP therapy.

DNA damage response

Mutations in the DNA damage response (DDR) genes may promote tumour formation as well as drive emergence of drug resistance. The *Atm* gene product is a primary component of the DDR, which has a phosphatidylinositol-3-kinase-like protein kinase that phosphorylates many proteins upon DNA damage.¹³² *Atm* mutations have identified in hematologic malignancies.

An association between Myc activation and *Atm* inactivation has been identified during the progression of human B-cell lymphomas.¹³³ In mice, *Atm* loss collaborated with Myc activation to accelerate the development of lymphomas.^{134–136} Following anticancer therapy, *Atm* (DDR)-compromised lymphomas exhibited defects in ability to

undergo apoptosis and had a poorer long-term outcome as compared to DDR-competent lymphomas. *Atm* thus appears to prevent tumour progression by converting oncogenic signalling into apoptosis, resulting in selection against an *Atm*-dependent DDR and the emergence of drug-resistant lymphomas.

NFκB pathway

Activation of NF-κB is a driver in apoptosis resistance in a variety of B-cell malignancies leading to poor outcome in lymphoma patients.^{137,138} The NF-κB family has the capacity to regulate transcription of a diverse array of genes involved in cancer cell growth, including those involved in proliferation and resistance to apoptosis.^{139–142} Drug-resistant lymphoma cell lines have been sensitized by treatment with inhibitors of the NF-κB pathway.^{143,144}

Bfl-1 is a direct transcriptional target of NF-κB,^{101–103} and its upregulation is associated with decreased sensitivity in lymphomas to chemotherapeutic drugs and apoptotic stimuli, including TNF-α and anti-CD95.^{102–104} Inhibition of NF-κB pathway in DLBCL^{37,105} led to the downregulation of Bfl-1 expression and apoptosis. Knockdown of Bfl-1 in sensitized DLBCL cell lines to anti-CD20 (rituximab) and standard chemotherapeutics.¹⁰⁰

microRNAs

A microRNA, miR-21, has been shown to influence sensitivity of DLBCL cells to CHOP by impacting the PI3K/Akt-signalling pathway.¹⁴⁵ Mir21 targets PTEN for downregulation and NFκB upregulates miR-21. Knockdown of NFκB decreased miR-21 and sensitized DLBCL cells to chemotherapy.

A frequent genetic alteration that has been observed in MCL is chromosome 13q31–q32 amplification targeting a microRNA cluster termed miR-17–92.^{146–148} Upregulation of miR-17–92 activated the PI3K/AKT pathway and inhibited apoptosis induced by chemotherapeutics in MCL cell lines.¹⁴⁹ Downregulation of miR-17–92 repressed the PI3K/AKT pathway and inhibited tumour growth in a xenograft MCL mouse model.

TGFβ pathway

Members of the transforming growth factor-β (TGF-β) superfamily modulate proliferation, apoptosis and differentiation in many different cell types. TGF-β inhibits cell proliferation by arresting cells in the G1 phase of the cell cycle through the p15INK4b, p21Cip1/WAF1, p27 and c-Myc proteins.⁷⁰ Binding of TGF-β receptors to their ligands activates the serine/threonine kinase activity of the TGF-β receptors (TβRI and TβRII). The ligand-activated TβRII phosphorylates and activates the TβRI, which in turn transmits the TGF-β signal by phosphorylating and activating the Smad2 and Smad3 proteins. The activated Smads oligomerize with Smad4, and the complexes then translocate to the nucleus where they regulate transcription of TGF-β target genes.^{66,67,150}

Lymphoma cells can acquire resistance to TGF-β through promoter methylation of the TβRII gene.⁷¹ Promoter

analysis in lymphomas revealed CpG methylations at −25 and −140 of the *TβRII* promoter that correlated with the silencing of the *TβRII* gene.

Overexpression of BCL6 contributes to TGF-β resistance in B-cell lymphoma. BCL6 transcriptionally represses Smad4.⁷² B-cell lymphoma cells with upregulated BCL6 were refractory to TGF-β, whereas knockdown of BCL6 expression restored the response to TGF-β.

Oxidative stress pathways

Changes in oxidative stress pathways may explain the more aggressive tumour phenotype of drug-resistant lymphoma variants. In a murine lymphoma model, lymphoma cells transfected with catalase or selected for resistance to hydrogen peroxide were resistant to CHOP.^{151–153} Oxidative stress-resistant cells demonstrated an altered metabolic profile, including the ability to generate ATP from alternative carbon sources such as glutamine.^{154,155} When treated with glucocorticoids, the oxidative stress-resistant cells were better able to maintain ATP levels as compared to sensitive parental cells.¹⁵⁵ Experiments with an uncoupler of mitochondrial respiration showed that the oxidative stress-resistant cells produced more ATP from mitochondria than the sensitive cells.¹⁵⁴

Reactive oxygen species

Once inside the cell, anthracyclines in the CHOP cocktail kill lymphoma cells by DNA intercalation, topoisomerase II inhibition and reactive oxygen species (ROS) induction. The type of ROS generated can be critical; superoxide anion and hydrogen peroxide inhibited cancer cell migration and invasion, whereas hydroxyl radical promoted cell migration and invasion.¹⁵⁶ The Akt-survival pathway has been implicated in regulating ROS in lymphoma cells. Akt activation correlated with both decreased ROS and increased cell survival in lymphoma cells.¹⁵⁷

Chronic ROS exposure can generate lymphoma cells with upregulated antioxidant defense systems, which results in chemoresistance.¹⁵⁸ Oxidative stress-resistant variants expressed increased catalase and superoxide dismutase activities and increased phase 2 enzymes, NAD(P)H:quinone oxidoreductase and GSTs μ and π .

Proton pumps

The acidity of the tumour microenvironment due to hypoxic conditions, which influence ROS production, plays an important role in tumour progression, chemoresistance and metastatic behaviour.^{159,160} Cancers adjust to acidity by upregulating proton extrusion activity, thus allowing the tumour cells to survive.^{161–163} Tumour cells control intracellular pH through proton pumps like the vacuolar-type H⁺-ATPase (V-ATPase). Modification of cellular pH gradients by treatment with proton pump inhibitors (PPIs) sensitized B-lymphoma cells to chemotherapeutics through ROS production.¹⁶⁴ Neutralization of ROS by the antioxidant, N-acetylcysteine, delayed apoptosis. PPIs also inhibited the growth of B-cell lymphoma in SCID mice. Thus, PPIs

may provide for therapeutic approaches for drug-resistant B-cell lymphomas.

GSH

The glutathione-S-transferases (GSTs) multigene family of enzymes detoxify electrophilic xenobiotics, including alkylating agents, and reduce oxidative stress.^{165–171} Overexpression of the GST- π isoenzyme has been associated with alkylating agent and anthracycline resistance in lymphomas.¹⁷¹

CD antigens

CD20-rituximab. The coadministration of rituximab to CHOP chemotherapy has significantly increased the survival of DLBCL patients.^{172–179} Rituximab is a humanized monoclonal antibody that binds to the CD20 antigen on B lymphocytes.¹⁸⁰ CD20 is expressed by >99% of B-cell NHL,² which is not internalized following antibody binding¹⁸¹ or secreted into the circulation.¹⁸² However, given that it is also expressed by normally differentiated pre-B cells and B cells,^{183,184} normal B cells are also depleted during rituximab therapy, so that NHL patients have a prolonged B-lymphopenia following rituximab therapy.¹⁸⁵ Regrettably, many patients will relapse after rituximab/CHOP (R-CHOP) therapies.^{184,186–193}

Rituximab exerts its antilymphoma activity through multiple mechanisms, including growth inhibition, apoptosis, complement-dependent cell cytotoxicity (CDC) and antibody-dependent cellular cytotoxicity (ADCC).^{60,184} Although rituximab mediates CDC and ADCC of CD20-positive human B cells,¹⁹⁴ it can have direct apoptotic effects. Unfortunately, resistance to rituximab can eventually evolve in some patients during the course of disease, which is only explained in part by the loss of CD20 expression.¹⁹⁵

A variety of signalling events have been observed in lymphoma cells exposed to rituximab *in vitro*, including the activation of Src-family of protein tyrosine kinases, decreased NFκB activity and downregulation of Bcl-2 levels.^{196–201} Rituximab inhibited Akt in B-cell lymphoma cell lines, which contributed to the sensitization of drug-resistant cells to chemotherapeutic drugs.⁸¹

B-lymphoma cell lines resistant to rituximab have cross-resistance to multiple chemotherapeutic agents and exhibit downregulation of the Bcl-2 family proteins Bax and Bak.²⁰² Repeated exposure to rituximab generates a therapy-resistant phenotype by modulating the expression of Bax and Bak. The development of new inhibitors of the Akt and Bcl-2 pathways will now allow rationally designed clinical trials addressing Rituximab resistance that employ combinations of the new inhibitors and rituximab.

CD147. Upregulation of extracellular matrix metalloproteinase inducer (EMMPRIN or CD147) drives lymphoma progression and induces resistance to chemotherapeutic drugs.^{203–208} CD147 is a transmembrane glycoprotein of the immunoglobulin superfamily that is expressed on the surface of lymphoma cells. It functions as a regulator of matrix metalloproteinase (MMPs) expression in the local

lymphoma environment.²⁰⁴ High expression of MMPs has been correlated with tumour metastasis.²⁰⁹ Reduced CD147 expression led to reduced metastasis and sensitized drug-resistant cells to chemotherapeutics.²¹⁰

MDR proteins

The ability of cancer cells to resist the cytotoxic effects of chemotherapeutic agents is termed multidrug resistance (MDR), which is manifested by a decreased sensitivity to a wide range of nonhomologous drugs targeting multiple diverse pathways.²¹¹ Overexpression of the 170–180 kDa ATP-dependent pump, P-glycoprotein (P-gp transporter), is frequently associated with resistance against a wide range of chemotherapeutics^{212–215} and results in the MDR phenotype. P-gp transports or effluxes chemotherapeutics out of the cell, which reduces the intracellular concentration of the drugs, thus protecting cellular structures from damage and promoting cell survival. MDR due to the upregulated expression of P-gp product has been implicated as a critical factor in the prognosis and clinical outcome of refractory lymphoma patients.^{215–218} Expression of P-gp has been found in all histological types of NHL.²¹⁹ Clinical trials combining chemotherapy with resistance modifiers have provided evidence for the role for P-gp in drug resistance in NHL.^{220–222} However, some reports have indicated a lack of correlation between clinical response and P-gp expression,^{29,216,223–225} possibly because MDR is mainly implicated in acquired drug resistance in lymphomas.^{226,227} Thus, upregulation of P-gp is not consistently associated with chemoresistance in NHL, indicating the existence of additional drug-resistant pathways and mechanisms.^{15,16}

Upregulation of the PI3K/Akt pathway can influence MDR in lymphoma. PI3K/Akt inhibition correlates with downregulation of NFκB activity and reduced Pgp function.²²⁸ PI3K/Akt activity was higher in drug-resistant lymphoma cell lines than in sensitive cells, and PI3K/Akt inhibitors inhibited P-gp function and increased sensitivity to chemotherapeutics in drug-resistant cell lines.

Upregulation of the adenosine triphosphate-binding cassette drug transporter, ABCG2, in DLBCL correlated inversely with the disease-free survival.²²⁹ Activated hedgehog (Hh) signalling stimulated high-ABCG2 expression in DLBCL through direct upregulation of ABCG2 gene transcription.²³⁰ Activation of Hh signalling in DLBCL cell lines led to co-upregulation of Bcl-2 and ABCG2, which was associated with increased resistance to chemotherapeutics.

In addition to P-gp, the lung-resistance protein (LRP) is associated with MDR in lymphoma. LRP was first identified in a non-P-gp-multidrug-resistant lung cancer cell line.²³¹ LRP is the major protein component of vaults, which are complex ribonucleoprotein particles located primarily in the cytosol and nuclear membrane and mediate nucleocytoplasmic transport.^{232,233} Upregulation of LRP is associated with resistance to multiple chemotherapeutics.^{234,235} High LRP expression was associated with more aggressive lymphomas and a lower response rate to chemotherapy than LRP-negative patients.²³⁶

Drug metabolizing pathways

GSTs detoxify electrophilic chemotherapeutics, such as alkylating agents.^{166–171} GSTs act by promoting direct binding of drugs to alkylating agents and steroids and can also neutralize free radicals generated by anthracyclines.^{166,168,237–239} Drug resistance in lymphoma has been associated with an increase in glutathione content or GST activity.^{167,171,240–242} The GST-π isozyme is elevated in lymphoma cell lines resistant to anticancer agents.^{166–170} GST-π expression has been reported to have prognostic significance in DLBCL.²⁴³

Glutathione S-transferase P1-1 (GSTP1-1) is a phase II detoxifying enzyme and plays a role in resistance to chemotherapeutics. GSTP1-1 may be a prognostic factor in late-stage NHL,^{243,244} since survival times were 64 and 25 months for the low and high GSTP1-1 groups, respectively. One strategy to overcome drug resistance would consist of treating relapsed NHL patients concomitantly with chemotherapeutics and GSTP1-1-specific inhibitors.

MAP kinase pathway

The MAP kinase signalling pathway may influence the sensitivity of B-lymphoma cells to chemotherapeutics. The contribution of the MAP kinase pathway and mitochondrial apoptotic pathways was studied in a panel of human B lymphoma cell lines exhibiting varying degrees of drug resistance and Bcl-2/Bax expression.²⁴⁵ Mitochondrial dysfunction was induced in these cells by the mitochondrial toxicants, carbonyl cyanide *m*-chlorophenylhydrazone (mCICCP) and antimycin A. The drug-resistant lines had higher Bcl-2/Bax expression ratios and were less sensitive to mitochondrial toxicant-induced apoptosis than the sensitive cell lines. Treatment with mitochondrial toxicants led to the activation of the MAP kinase pathway in only the drug-sensitive lines. Specific inhibition of the MAP kinase pathway augmented baseline and mCICCP-induced apoptosis, indicating that differential sensitivity to mitochondrial toxicants in B lymphoma cells involved regulation by MAP kinases.

Tyrosine protein kinases

Oncogenic tyrosine kinases regulate multiple signalling pathways involved in both cell survival and resistance to chemotherapeutics.^{246–252} Binding of antigen to the B-cell receptor (BCR) activates phosphorylation of Src family kinases (SFK), which is followed by the activation of MAP kinase, PI3kinase and NFκB pathways²⁵³ resulting in B-cell activation and survival.^{254,255}

Over one-third of DLBCL patients tested expressed active SFKs in their tumours and thus may be candidates for treatment with the SFK inhibitor, dasatinib.²⁵⁶ Dasatinib is dual-kinase inhibitor that is currently approved for use in chronic myelogenous leukemia.²⁵⁷ In DLBCL cell lines, sensitivity to dasatinib varied by 400-fold, and resistance to dasatinib was associated with the dysregulation downstream of BCR activation.

The anaplastic lymphoma kinase (ALK) is a receptor tyrosine kinase involved in glucocorticoid-resistance in lymphomas.²⁵⁸ The glucocorticoids, prednisolone and

dexamethasone induce cell-cycle arrest and apoptosis in lymphoid cells and are included in chemotherapeutic regimens for lymphomas.^{259,260} Unfortunately, glucocorticoid resistance commonly occurs in lymphomas.^{261–264} In about two-thirds of anaplastic large-cell lymphoma (ALCL), a rare type of NHL, a fusion of the nucleophosmin and ALK genes by the t(2;5) chromosomal translocation, gives rise to a hybrid NPM-ALK protein.²⁶⁵ Dysregulation of ALK caused by fusion to NPM is a causative factor in both ALCL and DLBCL.^{266–270} Abnormal activation of ALK is the result of the fusion of the N-terminal NPM partner encoding an oligomerization motif to activate the kinase domain of the ALK protein, which is critical for resistance to glucocorticoids.^{271–273}

P53 tumor suppressor gene

P53 mutations are often associated with decreased sensitivity to chemotherapeutics,^{274,275} more aggressive clinical course²⁷⁶ and higher relapse.^{16,277–280} Lymphomas with a p53 mutation were more likely to be drug-resistant than those with normal p53 and to have a shorter progression-free survival.¹⁶

The BH3-only genes, Puma and Noxa, are direct transcriptional targets of p53. The combinatorial action of the p53 target genes, Puma and Noxa, is important for the induction of apoptosis by chemotherapeutics in lymphoma cells.²⁸¹ In nontransformed lymphoid cells, the loss of Puma and Noxa induced as much resistance to chemotherapeutics as loss of p53 itself.

Proteasome

The 26S proteasome complex is a large multisubunit catalytic complex that degrades ubiquitinated proteins.²⁸² Proteasome inhibition has emerged as a new therapeutic option in lymphoma.²⁸³ The pharmacological proteasome inhibitor (PI), bortezomib (PS-341, Velcade) has shown efficacy against NHL through disrupting the equilibrium between protein biosynthesis and degradation.^{282,284–286} Preclinical studies have demonstrated that proteasome inhibition potentiates the activity of other chemotherapeutics.^{287,288} However, not all lymphomas are bortezomib-sensitive, and acquired resistance to bortezomib can occur.²⁸⁴ Although bortezomib has single-agent efficacy in patients with relapsed or refractory MCL,^{289–292} about 40–50% of patients develop bortezomib-resistant disease. Bortezomib-resistant lymphoma cell lines exhibited residual proteasome activity in the presence of bortezomib,²⁹³ possibly due to increased expression of the b5, b2 and b1/b5 subunits of the proteasome. Alternative proteolytic systems may take the place of the proteasome leading to resistance to bortezomib.^{294–296} Targeting the PI3K/Akt signalling pathway may be a strategy to treat bortezomib-resistant MCL, since the dual PI3K and mTOR inhibitor NVP-BEZ235 overcame bortezomib resistance in MCL cells.

Activation of the endoplasmic reticulum (ER) stress pathway is correlated with resistance to doxorubicin-containing chemotherapy regimens, such as R-CHOP, in DLBCL patients. The 78-kDa glucose-regulated protein (GRP78), also known as immunoglobulin heavy chain

binding protein, is an ER stress sensor commonly overexpressed in DLBCL that plays a role doxorubicin- and bortezomib-resistance.²⁹⁷ Small-interfering RNA silencing of Bip/GRP78 overcame bortezomib resistance.²⁹⁸

Epigenetics

Epigenetics plays a critical role in many pathological processes of cancer.²⁹⁹ Histone deacetylases (HDACs) play a central role cancer epigenetics.³⁰⁰ HDACs catalyze the removal of acetyl groups from core histones, which leads to the compaction of chromatin and repression of transcription.³⁰¹

HDACs have been implicated in promoting drug resistance in B-cell malignancies.^{302,303} Thus, HDAC inhibitors (HDIs) are being investigated as a new therapeutic approach to treat B-cell lymphomas.^{304,305}

HDI-mediated inhibition of HDACs results in increased histone acetylation, which can reactivate silenced genes leading to the reversion of drug resistance.^{306–310}

Preclinical studies revealed synergistic interactions between proteasome inhibitors (PIs) and HDIs in lymphoma.^{311,312} Coadministration of subtoxic concentrations of PIs with HDIs (vorinostat) synergistically increased apoptosis in both GC- and ABC-DLBCL cells, suggesting that a strategy using irreversible PIs to enhance the activity of HDIs might be effective in DLBCL. In other examples, HDIs reversed mTOR (mammalian target of rapamycin) resistance through a phosphatase that antagonized mTORC2 activation,⁸⁴ suggesting a combination of HDI and mTOR inhibitors as a strategy for overcoming mTOR resistance in DLBCL. The coadministration of HDIs with rituximab may be a strategy to reverse rituximab resistance in B-cell lymphomas.³¹³ HDIs enhanced the cytotoxic activity of rituximab by upregulating expression CD20 antigen on lymphoma cells.

MSI instability

MSIs are repetitive DNA sequences. Within MSIs, DNA polymerases are subject to slippage, and misalignments can form between the template and nascent strands. Mismatch repair (MMR) corrects these strand misalignments during DNA replication. MSI is a sign of deficient MMR processes.^{314–318} In NHL, MSI may serve as a MMR biomarker that predicts lymphoma response to chemotherapy.³¹⁹ MSI was found in 14% of tumours in NHL patients. Response to chemotherapy and outcomes were significantly worse in those NHL patients with MSI tumours.

Stromal influences

Stromal cells are an essential component of the bone marrow microenvironment that influences and supports tumour growth and survival.^{320–323} Resistance to chemotherapy can result from cytokines and growth factors released from stromal cells.^{320,321} Bone marrow stroma can provide a protective 'sanctuary site' for lymphoma cells during chemotherapy,³²⁴ thus having an impact on the outcome of chemotherapy in DLBCL.³²⁵ Secretion of interleukin-4 and the integrin ligand VCAM-1 from stromal

cells increase survival and rescue B cells from chemotherapy-induced apoptosis.^{326,327} Another factor released from bone marrow stromal cells is the lymphoma cell adhesion-induced B cell-activating factor (BAFF) protein, a member of the TNF superfamily of cytokines, which promotes B-cell activation, proliferation and differentiation, thus enhancing B-lymphocyte survival.^{328–331} BAFF receptors are expressed on lymphomas originating from diverse subclasses of B-cell lineages.³³² Increased levels of BAFF were present in serum from NHL patients.³³² Small-hairpin RNA depletion of BAFF increased sensitivity of lymphoma cells to chemotherapy and overcame stroma-mediated drug resistance.

Stroma-produced survival signals can influence the expression, conformation and protein–protein interactions of Bax and Bcl-xL, which can then influence the sensitivity of a B-cell lymphoma to chemotherapeutics.^{76,333–337} Stroma-mediated activation of CD40 upregulated Bcl-xL protein levels via activation of NFκB. VCAM-1-mediated signals repressed conformational changes in Bax protein and prevented etoposide-induced formation of Bax–Bcl-xL complexes. Stromal upregulation of IL-6 may contribute to the intrinsic chemoresistance commonly found in both primary and metastatic malignancies.^{338,339} Additionally, tumour-directed inflammatory responses originating in the stroma that release IL-6 may reduce the efficacy of genotoxic agents.

Lymphocytes home into tissue stromas, which guide the lymphocytes by secreting chemokines and expressing ligands for lymphocyte adhesion molecules. In B-cell lymphomas, the tumour cells retain the trafficking and homing ability of their normal counterparts.^{340–343} Lymphoma cells are directed to supporting stroma by chemokine receptors and adhesion molecules, where they receive survival and drug-resistance signals.^{344,345} Stromal cells release chemokines, such as CXCL12 and CXCL13, which provide guidance for localizing B-cells within lymph-node compartments.^{323,346,347} Lymphocyte homing requires the cooperation between chemokine receptors and adhesion molecules, such as integrins, CD44 and L-selectins.³⁴⁸ Moreover, accessory cells, including CD68+ macrophages and T cells, in the lymphoma microenvironment can influence the clinical outcome,^{349–351} indicating that crosstalk between lymphoma and stromal cells plays an important role in lymphoma progression and chemoresistance.

FL patients frequently are initially sensitive to chemotherapy but then relapse. Highly tumorigenic FL cells exhibiting a cancer stem cell-like phenotype (FL-SC) were found to interact with follicular dendritic cells in a CXCL12/CXCR4-dependent manner to resist chemotherapeutics, indicating an important role for FL-SC and niche cell-signalling in maintaining drug resistance in FL.³⁵²

Other

Sphingosine kinase. Upregulation of sphingosine kinase 1 (SphK1) frequently occurs in lymphomagenesis. SphK1 is associated with resistance to chemotherapy and radiotherapy.^{353,354} SphK1 controls the 'sphingolipid rheostat' by catalyzing the formation of the survival molecule, sphingosine-1-phosphate, at the expense of the pro-

apoptotic molecule, ceramide.³⁵⁵ SphK1 protein and mRNA levels showed increasing expression with increasing clinical grade of NHL.³⁵⁶

Geranylation. Inhibition of protein prenylation (geranylgeranylation) can sensitize DLBCL to chemotherapeutics.³⁵⁷ Prenylation is a post-translational hydrophobic modification of proteins that facilitates the attachment of proteins to membranes. The lipid isoprenoid acts as a lipid anchor, which is essential for proper protein localization and biological function.^{358–360} Treatment with simvastatin, an inhibitor of protein farnesylation and geranylgeranylation, sensitized CHOP-resistant DLBCL cells to cytotoxic treatment.³⁵⁷ Coadministration of protein geranylgeranylation inhibitors and conventional chemotherapeutics thus may be a strategy for treating patients with CHOP refractory DLBCL.

Zinc transporter. Gallium nitrate is a clinically active agent in the treatment of lymphoma.^{361–365} Gallium binds to transferrin in the circulation, which targets it to transferrin receptors that are expressed on lymphoma cells.^{366–371} Gallium also acts on zinc metabolism pathways.³⁷² Unfortunately, resistance to gallium can occur, which is caused by the upregulation of metal-responsive transcription factor-1 activity and metallothionein expression.³⁷² Immunohistochemical staining of lymphomas showed that the metallothionein protein is variably expressed in different lymphomas.

PRDM-1. The positive regulatory domain I (PRDM1) protein regulates the differentiation of mature B lymphocytes to plasma cells.^{373,374} The *PRDM1* gene encodes 2 isoforms, PRDM1α and PRDM1β that are regulated by NFκB.^{375,376} Those DLBCL cases that expressed PRDM1 displayed more aggressive behaviour and a poorer patient outcome.³⁷⁷ PRDM1β expression thus might serve as a prognostic marker for drug resistance in some types of DLBCL.

ALDH. The intracellular enzyme retinaldehyde dehydrogenase (ALDH) promotes resistance of MCL to chemotherapeutics.^{378–380} ALDH is a cytosolic enzyme required for the biosynthesis of all-*trans*-retinoic acid and is highly expressed by normal hematopoietic and neural stem cells.^{381,382} ALDH is expressed in B-cell lymphomas^{383,384} and can induce cyclophosphamide resistance in lymphoma cell lines.^{385–389}

Summary and conclusions

Both intrinsic genetic alterations as well as chemoprotective microenvironments can play roles in the cellular response of B-cell lymphomas to chemotherapeutics. Given the genetic diversity of B-cell lymphomas and differential antigen expression patterns across lymphoma subtypes, it is unlikely that a single small molecule or antibody-based therapeutic will effectively treat all categories of NHL. Overcoming drug resistance to current chemotherapeutic regimes in B-cell lymphomas will require multitargeted combinatorial therapies to restore apoptotic pathways in

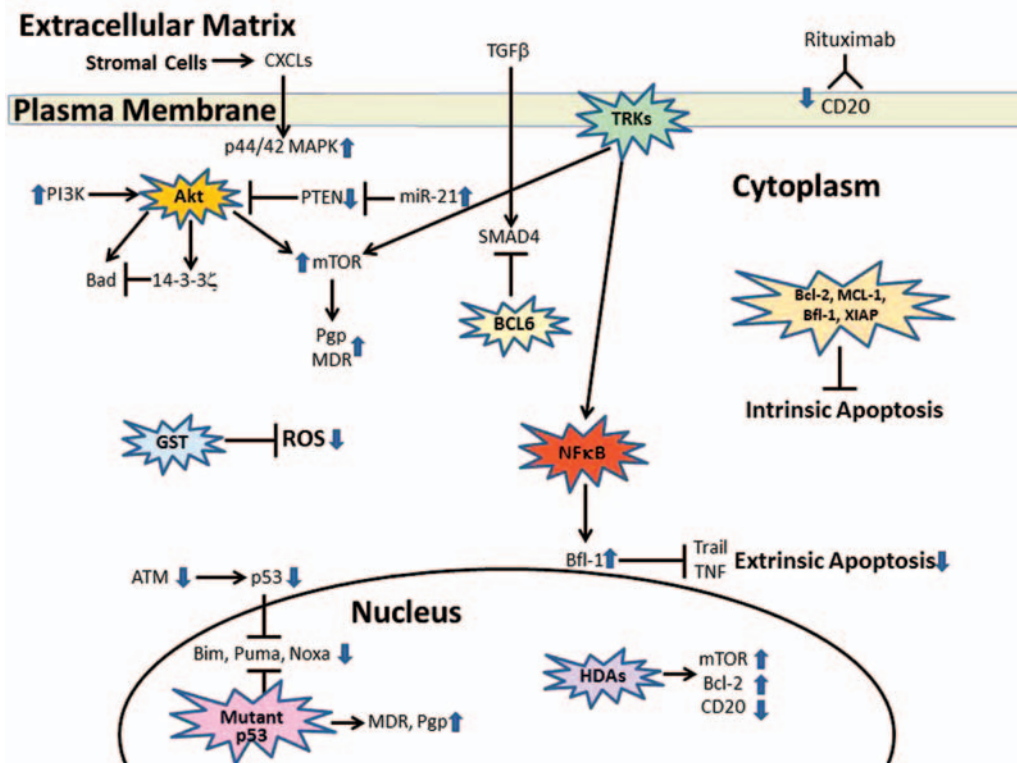


Figure 1 Schematic representation of drug resistance pathways in B-cell lymphomas. PI3K/Akt is frequently activated, which leads to increased mTOR activity stimulating upregulation of multidrug resistance pumps (MDR, Pgp). Akt phosphorylates Bad and 14-3-3 ζ , leading to binding and sequestration of the proapoptotic protein Bad and blocking to apoptosis. Upregulation of antiapoptotic proteins (Bcl-2, Mcl-1, XIAP, Bfl-1) can block chemotherapeutic-induced intrinsic apoptosis. The Akt pathway can be activated by upregulation of miR-21, which represses expression of the Akt-negative regulator, PTEN. Activation of tyrosine receptor kinases (TRKs) can induce drug resistance by activating Akt through mTOR. TRKs can also activate NF κ B, which upregulates Bfl-1 resulting in blocking of TNF- or Trail-induced extrinsic apoptosis. Upregulation of BCL6 blocks TGF β -signalling through SMAD4. Glutathione transferases (GSTs) can suppress oxidative stress caused by reactive oxygen species (ROS) that are induced by chemotherapeutics. Histone deacetylases (HDACs) can promote resistance to rituximab combinatorial chemotherapies (R-CHOP) by upregulating mTOR and Bcl-2 and downregulating CD20. Mutation in the p53 gene causes defects in the DNA damage response and upregulation of multidrug resistance pumps (MDR, Pgp). Mutations in Atm can cause deficiencies in the p53-induced DNA damage response, leading to lack of expression of proapoptotic BH3 proteins (Bim, Puma, Noxa) and blocking of intrinsic apoptosis. Downregulation of CD20 through epigenetic silencing can lead to rituximab resistance. (A color version of this figure is available in the online journal)

tumour cells and inhibit prosurvival signalling from the stroma environment.

With the exception of those patients eligible for allogeneic or autologous stem-cell transplantation, combination chemotherapy offers a potentially curative option for a subset of DLBCL patients.¹⁷² However, responses to current combination chemotherapy regimens (e.g. rituximab with cytoxan, hydroxyrubicin, oncovin and prednisone) vary considerably depending on multiple factors, including disease stage and genetic profile, among others. In particular, patients with the ABC-DLBCL subtype, which is NF κ B-dependent,^{37,390} appear to have a significantly worse prognosis than other subtypes.³⁹¹ Collectively, these considerations have motivated the search for more effective combinatorial treatment strategies in DLBCL that are pathway-targeted to specifically target tumour cells without toxicity to nonmalignant cells.

Multitargeted combinatorial experimental therapies composed of new targets and conventional chemotherapeutics may provide more immediate hope for relapsed patients who have failed current chemotherapies. For example, preclinical studies have documented synergistic

interactions between PIs, such as bortezomib and HDAC inhibitors in diverse malignant cell types.^{311,392,393} Targeting CD40 with dacetuzumab enhanced the antitumor activity of rituximab (CD20) in cell line and xenograft NHL models.³⁹⁴ In MCL, a sequence-dependent synergistic effect was observed with PIs in combination with cytarabine.³⁹⁵ Tipifarnib and bortezomib combination was well-tolerated and produced clinical responses in refractory acute leukemias.³⁹⁶ Multilevel inhibition of the PI3K/Akt/mTOR and cdc2/cdk1 cell-cycle pathways may be more effective in treating DLBCL patients that present with overactive Akt and cdc2/cdk1.³⁹⁷

Thus, understanding genotype-response relationships in NHL will be important for the effective use of new targeted therapies in the clinic. Responsiveness to multitargeted therapies will be predicted based on molecular markers to predefine patients who will most likely benefit from these targeted therapies. For instance, 'BH3 profiling' can identify those cells that are sensitive to the Bcl-2 antagonist ABT-737.³⁹⁸ Determining the activity of the NF κ B pathway in DLBCL tumour biopsies by GEP can predict responsiveness to the I κ B kinase inhibitor PS1145.¹⁰⁵ Future approaches to

NHL treatment will employ molecular signatures identified through GEP to provide prognostic information and to identify therapeutic targets in patients who relapse or those presenting with high risk disease to guide clinicians in designing a personalized approach to combinatorial molecular therapies.

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