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Proteasome Inhibitors in Cancer Therapy

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Abstract

The ubiquitin proteasome pathway was discovered in the 1980s to be a central component of the cellular protein degradation machinery with essential functions in homeostasis, which include preventing the accumulation of misfolded or deleterious proteins. Cancer cells produce proteins that promote both cell survival and proliferation, and/or inhibit mechanisms of cell death. This notion set the stage for preclinical testing of proteasome inhibitors as a means to shift this fine equilibrium towards cell death. Since the late 1990s, clinical trials have been conducted for a variety of malignancies, leading to regulatory approvals of proteasome inhibitors to treat multiple myeloma and mantle cell lymphoma. First-generation and second-generation proteasome inhibitors can elicit deep initial responses in patients with myeloma, in whom these drugs have dramatically improved outcomes, but relapses are frequent and acquired resistance to treatment eventually emerges. In addition, promising preclinical data obtained with proteasome inhibitors in models of solid tumours have not been confirmed in the clinic, indicating a role for primary resistance. Investigation of the mechanisms of resistance is, therefore, essential to further maximize the utility of this class of drugs in the era of personalized medicine. Herein, we discuss

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Competing interests statement

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By preventing the accumulation of misfolded or damaged proteins, the ubiquitin-proteasome pathway has essential functions in cell homeostasis. Cancer cells produce proteins that promote cell survival and proliferation, and inhibit mechanisms of cell death, and thus, clinical trials have tested the therapeutic effect of proteasome inhibitors on patients with a variety of cancer types, mainly haematological malignancies. Herein, Manasanch and Orlowski discuss the advances and challenges derived from the introduction of proteasome inhibitors in the clinic, including therapeutic resistance.

R.Z.O. has served on advisory boards for Amgen, which developed and markets carfilzomib, and for Takeda Pharmaceuticals, which developed and markets bortezomib and ixazomib, and has received research support from these firms for clinical and laboratory projects. E.E.M. declares no competing interests.

the advances and challenges resulting from the introduction of proteasome inhibitors into the clinic.

Introduction

The ubiquitin proteasome pathway (UPP) is an extensive and complex protein degradation pathway present in all eukaryotic cells^{$1-3$}. The UPP is the most important regulated intracellular protein degradation system, and is involved in processes such as apoptosis, cell survival, cell-cycle progression, DNA repair, and antigen presentation, among others. To ensure appropriate destruction of damaged or misfolded proteins, or of proteins that are no longer needed, the components of this system must act in a highly coordinated manner through different steps that include polyubiquitination, deubiquitination, and degradation of the target protein. To facilitate this coordination, the components of the UPP associate in various physical structures, including the proteasome itself⁴. A single ubiquitin activating enzyme 1 (E1), and multiple ubiquitin-conjugating enzymes (E2) and ubiquitin-protein ligases (E3) mediate initial polyubiquitination of the target. The proteasome regulatory subunits, which include both the 19S particle in the constitutive proteasome and the 11S particle in the immunoproteasome, mediate deubiquitination. Once the target proteins have been deubiquitinated, the proteasome degrades them via the function of the 20S core particle catalytic sites, thereby releasing oligopeptides. The three catalytic sites present in the 20S core particle are named after enzymes that have a similar proteolytic activity, and include sites with chymotrypsin-like $(\beta 5)$, trypsin-like $(\beta 2)$, and post-glutamyl peptide hydrolyzing, or caspase-like (β_1) activities. In some cases, the 20S proteasome core can act alone through ubiquitin-independent degradation pathways. Alternative forms of the proteasome, such as the immunoproteasome and thymoproteasome, are involved in routine proteolytic functions, antigen processing, and T-cell selection⁵. Thus, the total capacity of a cell to digest proteins through the UPP encompasses the contribution of both ubiquitin-dependent and ubiquitin– independent pathways. Nevertheless, the pool of proteins destined for degradation through the UPP is referred to as the load on the proteasome. Further digestion by aminopeptidases and carboxypeptidases then turns the oligopeptides into amino acids that can be reused by the cell^{1–3}. Similarly, deubiquitination yields monomeric ubiquitin as part of a recycling mechanism that maintains a free pool of ubiquitin within the cell and avoids ubiquitin degradation. Sensitivity to proteasome inhibition has been linked to an imbalance between cellular proteasome load and capacity. For example, lower levels of proteasome activity and higher proteasome workload can result in accumulation of polyubiquitinated proteins, which could potentially lead to proteasomal stress and increased sensitivity to proteasome inhibition. Proteins can also be destroyed within the cell through alternative pathways, for example, by aggregation in microtubule-based cellular structures called aggresomes with subsequent degradation via the autophagy pathway⁶. Readers interested in an in-depth summary of the assembly, regulation, and biology of the UPP are referred to a review on this topic⁴ that was published in 2014.

Deregulation of the UPP can result in either enhanced or reduced degradation of key targets that contribute to oncopathogenesis⁷. Notable examples include down-regulation of cellcycle and tumour-suppressor proteins, such as p53, and cyclin-dependent kinase inhibitor 1B

(p27), or up-regulation of oncogenic proteins, including activation of the nuclear factor kappa-B (NF- κ B)^{8–10}. In this Review, we describe the current status of UPP inhibition as a therapeutic strategy in cancer.

Inhibitors of the UPP

Proteasome inhibitors were initially developed as agents with potential benefit in preventing cancer-related cachexia, owing to the role of the UPP in protein turnover. Many preclinical studies then emerged showing that small-molecule proteasome inhibitors could induce apoptosis in cultured cell lines and murine models of cancer, at which point their utility as chemotherapeutics was postulated. One of the early hypotheses driving the study of these agents was that they could inhibit NF-κB signaling by blocking degradation of the NF-κB inhibitor I_{KB}, thereby preventing nuclear translocation of NF- κ B. This rationale led to the development of bortezomib, a first-generation proteasome inhibitor, and later to that of second-generation agents, including carfilzomib, ixazomib, and oprozomib, which were developed, in part, in attempts to improve upon the benefits observed with bortezomib.

First-generation proteasome inhibitors—Inhibitors of the 20S proteolytic core of the proteasome are the most extensively studied proteasome inhibitors to date, and three of these agents (bortezomib, ixazomib and carfilzomib) are currently approved for the treatment of multiple myeloma or mantle-cell lymphoma (MCL). Bortezomib was the first proteasome inhibitor to be brought into clinical use.

Bortezomib is a slowly reversible inhibitor, which binds with the catalytic site of the 26S proteasome, enabling inhibition of the β5/chymotrypsin-like and, to a lesser extent, the β2/ trypsin-like and β 1/post-glutamyl peptide hydrolyzing activities¹¹. This agent is commonly used in the first-line and relapsed and/or refractory settings in patients with multiple myeloma, and in those with MCL^{12} (Table 1). About a decade ago, bortezomib showed impressive clinical activity as a single agent in the treatment of relapsed and/or refractory multiple myeloma initially in a phase I study¹³, and then in phase II clinical trials^{14,15}. These findings supported the accelerated approval of bortezomib by the FDA in 2003 as a salvage treatment, initially for patients with treatment-refractory disease. Importantly, and for the first time, bortezomib prolonged progression-free survival (PFS) in this patient population compared with the previous line of therapy (regardless of the prior treatment used), and some patients were able to achieve their first complete remissions (Table 1). Full regulatory approval occurred in 2005, following the publication of results from a large phase III trial¹⁶ in 669 patients with relapsed multiple myeloma after $1-3$ prior lines of therapy. In comparison with high-dose dexamethasone, which was then a standard of care in this setting, improvements in time to progression (TTP), overall response rate (ORR), and overall survival were demonstrated in the patients who received bortezomib¹⁶ (Table 1).

Once the efficacy of bortezomib was established in patients with relapsed and/or refractory multiple myeloma, attention turned to those with newly diagnosed disease. In 2008, a randomized phase III trial¹⁷ comparing melphalan plus prednisone (MP) alone or with bortezomib (VMP) in newly diagnosed patients considered ineligible for transplantation; increased TTP, PFS and overall survival were observed in the patients who received VMP

combinations, perhaps most notably with immunomodulatory drugs (IMiDs), resulting in active regimens associated with high overall and complete response rates $17,18$. For example, one of the most widely used combination-treatment options for patients with newly diagnosed multiple myeloma comprises bortezomib, lenalidomide and dexamethasone $(RVD)^{18}$ (Table 1). Notably, in 2015, Durie *et al.*¹⁹ reported results of the SWOG S0777 phase III trial, in which the efficacy of an induction regimen consisting of RVD was compared with that of lenalidomide plus dexamethasone. The results of this trial confirmed the superiority of the RVD regimen, which in many patients led to remission of a prolonged duration and improved overall survival¹⁹ (Table 1). The results of other key clinical trials demonstrated the efficacy of bortezomib as part of induction therapy in patients with newly diagnosed multiple myeloma (Table 1), which was further established by a meta-analysis of the results from randomized phase III trials that were available at the time 20 . This metaanalysis revealed that the median PFS with bortezomib-based therapy was 35.9 months compared with 28.6 months without bortezomib ($P < 0.001$), and the overall survival at 3 years was 79.7% compared with 74.7%.

Bortezomib might also be effective as a maintenance therapy, according to data from a phase III trial²¹ in patients with newly diagnosed multiple myeloma, in which bortezomib was used in both the induction and maintenance regimens. Patients were randomly assigned to receive bortezomib, doxorubicin and dexamethasone (PAD), or vincristine, doxorubicin and dexamethasone (VAD), followed by autologous stem-cell transplantation in both groups, and then maintenance with either bortezomib (PAD group) or thalidomide (VAD group). Patients who received PAD–bortezomib showed improved responses and PFS compared with those treated with VAD–thalidomide (Table 1), especially those with high-risk multiple myeloma harbouring chromosome 17p deletions²¹.

Bortezomib has also been successfully combined with other agents to improve clinical outcomes in the relapsed and/or refractory settings. For example, the efficacy of bortezomib plus pegylated doxorubicin was compared with that of bortezomib monotherapy in patients with relapsed multiple myeloma, and the combination regimen prolonged TTP and improved overall survival, and these benefits were statistically significant²² (Table 1). In a study published in 201423, bortezomib and dexamethasone were combined with the oral pandeacetylase inhibitor panobinostat, partly on the basis that the latter agent would inhibit aggresome formation, a potential mechanism of inducible or acquired resistance to proteasome inhibitors²⁴. This phase III trial revealed a median PFS of 12.0 months with the three-drug regimen versus 8.1 months with bortezomib plus dexamethasone²⁵ ($P < 0.0001$; Table 1). On the basis of a subgroup analysis showing improved PFS for the triplet combination²³, the FDA and European Medicines Agency (EMA) approved panobinostat in combination with bortezomib and dexamethasone for the treatment of patients with relapsed and/or refractory myeloma who had received at least two prior lines of therapy (including bortezomib and an IMiD). Panobinostat is now being studied in combination with RVD as a first-line treatment for myeloma²⁶; after four cycles of treatment, the ORR was 93% , including a complete response rate of 44%. Of note, patients with multiple myeloma who have had a previous response to bortezomib can be re-treated with the same agent if they had

a relapse at least 6 months after completion of a prior course of bortezomib treatment²⁶, further demonstrating the therapeutic value of this drug.

Bortezomib has also been successfully combined with the anti-CD38 monoclonal antibody daratumumab. Palumbo et aL^{27} conducted a randomized phase III trial in patients with relapsed and/or refractory myeloma using bortezomib and dexamethasone with or without daratumumab. The 12-month PFS improved from 27% to 60% when daratumumab was added to the combination of bortezomib and dexamethasone, providing evidence of another effective therapeutic strategy for patients with myeloma.

The development of peripheral neuropathy can be a dose-limiting factor in patients receiving bortezomib. Up to 80% of patients with newly diagnosed multiple myeloma treated with bortezomib develop any grade neuropathy¹⁸, and long-term exposure and/or higher doses can increase the risk of neuropathy. Changes in the route of bortezomib administration, from intravenous to subcutaneous, or in the dosing schedule, from biweekly to weekly, seem to reduce the incidence of neuropathy while maintaining efficacy^{28,29}. Indeed, owing to the results of a large randomized study²⁸, the subcutaneous administration of bortezomib was approved in 2012 by both the FDA and EMA, and the intravenous administration of this agent has, to some extent, fallen out of favour among clinicians. Neuropathy might be a result of the off-target effects of bortezomib³⁰, and is, to some extent, a class effect of proteasome inhibitors, but the exact underlying mechanisms are not fully understood. In addition to neuropathy, bortezomib can induce thrombocytopenia, which is cyclical and, to some extent, predictable, with a 60% reduction from baseline during each treatment cycle and recovery between cycles 31 . Other adverse events associated with bortezomib include nausea and diarrhoea, fatigue, and neutropenia. Finally, the use of bortezomib and, indeed, of other proteasome inhibitors, both alone and in combinations, has been associated with an increased risk of herpes zoster virus reactivation³², indicating the need for prophylaxis with antivirals, which is recommended for all patients.

Second-generation proteasome inhibitors—A number of different pharmacophores have been described as having the ability to interact with the N-terminal threonine residues in the catalytic proteasome subunits that are responsible for the nucleophilic attacks involved in the cleavage of peptide bonds. Similarly to boronic acids (which include bortezomib and ixazomib), epoxyketones can also bind to these N-terminal threonines; however, unlike boronates, which bind reversibly, epoxyketones form irreversible bonds that can prolong the duration of proteasome inhibition. The possibility of a long duration of inhibition provided the rationale for phase I studies of carfilzomib (previously known as PR-171), which revealed that this agent is both tolerable and active against relapsed and/or refractory multiple myeloma, even in some patients who had received prior bortezomib therapy^{33,34}. Subsequently, carfilzomib received accelerated approval in 2012 by the FDA as a single agent for the treatment of multiple myeloma in patients who have received at least two prior lines of therapy and with disease that was refractory to the most-recent line of treatment. The approval decision was based on results from a single-arm study in 266 patients³⁴, in whom carfilzomib was given on days 1, 2, 8, 9, 15 and 16 of 28-day cycles at 20 mg/m² during the first cycle, and then at 27 mg/m², starting in cycle two, for up to 12 cycles $(20/27 \text{ schedule})$. An ORR of 23.7% was reported, including one complete response and 13 very good partial

responses (VGPR; the criteria for determining responses have been defined elsewhere 35), with a median duration of response (DOR) of 7.8 months 36 .

A confirmatory phase III trial³⁷ compared standard-dose carfilzomib (20/27 schedule) with best supportive care (in the form of low-dose steroids with optional cyclophosphamide) in patients with treatment-refractory multiple myeloma. Interestingly, this trial did not meet its primary end point of improving overall survival (hazard ratio (HR) 0.98, 95% confidence interval (CI) $0.76-1.2$), owing, in part, to the substantial activity of the control regimen³⁸. A second confirmatory study³⁸ in a cohort of patients with multiple myeloma who had received 1–3 lines of prior treatment compared lenalidomide plus dexamethasone (RD; control) with RD plus carfilzomib (KRD). In this phase III trial, Stewart *et al.*³⁸ randomly assigned 792 patients to receive RD or KRD with carfilzomib at 20 mg/m² on days 1 and 2 of cycle one, and then at 27 mg/m^2 for the remainder of cycle one and beyond. The use of KRD improved PFS compared with that achieved with RD (26.3 months versus 17.6 months; $P = 0.0001$ ³⁹. An interim analysis showed that the 24-month overall survival was 73.3% and 65% for the KRD and RD groups, respectively, and, although the median survival was not reached in either group, a statistically significant benefit favouring KRD was observed ($P = 0.04$). Dose adjustments were made in both groups; however, in the KRD arm, the lenalidomide dose was reduced more frequently than that of carfilzomib (in 43.4% and 11% of patients, respectively). Furthermore, disease progression was the most frequent cause of treatment discontinuation, and discontinuation was less likely with KRD than with RD (39.8% versus 50.1%). Adverse events of any rate were more frequent with KRD, including cardiopulmonary events, such as dyspnoea (2.8% versus 1.8%), cardiac failure (3.8% versus 1.8%), ischaemic heart disease (3.3% versus 2.1%) and hypertension (4.3% versus 1.8%). The frequency of other events, such as peripheral neuropathy, was similar in both groups. Despite this higher rate of certain types of adverse events, patients reported superior health-related quality of life and derived substantial added benefit from KRD, owing to the effectiveness of this treatment, which has been established as a new standard of care for patients with relapsed multiple myeloma.

In 2014, a study tested high-dose carfilzomib, administered as a 30-minute infusion, and given initially at 20 mg/m² on days 1 and 2 of cycle one, and then escalated to 56 mg/m² (20/56 schedule) for the remaining doses, along with dexamethasone. This regimen showed evidence of potentially enhanced activity compared with the standard-dose regimen⁴⁰. This observation supported the design and initiation of a large phase III trial⁴¹, in a cohort of 929 patients with relapsed multiple myeloma after 1–3 prior lines of therapy, comparing highdose carfilzomib plus dexamethasone (KD) with bortezomib and dexamethasone (VD). In this trial, which is one of only a few completed studies comparing two agents with similar mechanisms of action in myeloma, KD was found to be superior to VD (PFS 18.7 versus 9.4 months; HR 0.53, 95% CI 0.44–0.65; $P \le 0.0001$ ⁴². Serious adverse events were more common in the carfilzomib arm (48% versus 36%), although grade ≥2 peripheral neuropathy was considerably more common with bortezomib (32% versus 6%; P<0.0001). Cardiac adverse events of any grade were, however, more common with KD, including hypertension (25% versus 9%), cardiac failure (8% versus 2%) and shortness of breath (28% versus 13%). Acute renal failure (all grades) was also more common with carfilzomib plus dexamethasone (8% versus 4%). Despite a higher number of adverse events in the carfilzomib group,

treatment discontinuation and treatment-related deaths were comparable in both groups $(5\%)^{41}$. Beyond the 20/56 dosing schedule, interest has emerged in administering carfilzomib at an even higher dose given weekly instead of twice weekly. A phase I study⁴² has identified 70 mg/m² carfilzomib (or 20/70 dosing) as the maximum-tolerated dose when given with dexamethasone, with updated efficacy data demonstrating a 72% ORR in patients who had received $1-3$ prior lines of therapy⁴³. Of note, a phase III trial comparing once weekly with twice weekly administration of carfilzomib plus dexamethasone in patients with relapsed and/or refractory multiple myeloma is currently underway (NCT02412878)⁴⁴.

In the setting of newly diagnosed disease, data from two early phase uncontrolled studies^{43,45} have shown that KRD is well-tolerated and effective^{45,46}. Similar to other treatment studies⁴⁷, the depth of response of patients with multiple myeloma to treatment improved with continued therapy. KRD also was also well tolerated in patients deemed ineligible for transplantation⁴⁸. Notably, the National Clinical Trials Network (National Cancer Institute, USA) is performing a study comparing KRD and RVD in patients with newly diagnosed multiple myeloma $(NT01863550)^{49}$ that is expected to shed further light on the comparative efficacy and toxicity of these powerful combination regimens. Carfilzomib has also been evaluated in combination with melphalan and prednisone (CMP) as induction therapy in patients with newly diagnosed multiple myeloma who are deemed ineligible for transplantation⁵⁰. The results of this phase I/II study established a maximumtolerated dose of 20 mg/m² on days 1 and 2 of the first cycle, followed by carfilzomib up to 36 mg/m² on days 8, 9, 22, 23, 29 and 30 of a 42-day cycle, and on days 1, 2, 8, 9, 22, 23, 29 and 30 every 42 days for the remaining cycles, along with 9 mg/m² melphalan and 60 mg/m^2 prednisone on days $1-4^{50}$. In this study, dose-limiting toxicities included deep vein thrombosis, febrile neutropenia, fever and hypotension, while adverse events of any grade, as observed in at least 25% of patients included anaemia, fatigue, neutropenia, infections, nausea, elevated levels of liver enzymes and peripheral neuropathy. An ORR of 90% was noted, which included VGPR and complete response rates of 58% and 12%, respectively. These encouraging data led to a phase III trial comparing CMP with VMP, but a press release indicated that no statistically significant difference was observed between the two arms, and formal presentation of the data is pending⁵¹. Several clinical trials of proteasome inhibitors in patients with multiple myeloma that might be relevant for the field are also underway (Table 2).

Carfilzomib seems to have a distinctly different adverse-event profile compared to that of bortezomib. Whereas the rates of peripheral neuropathy are lower with carfilzomib, a few patients have developed cardiovascular complications, including hypertension and heart failure with decreased left ventricular ejection fraction⁴⁶. Endothelial dysfunction has been proposed to occur after carfilzomib administration through inhibition of endothelial nitric oxide synthase activity⁵². An echocardiography assessment is recommended for all patients before starting carfilzomib treatment, though utility of this evaluation in predicting those at risk for cardiac events has not been proven, and additional studies are needed in this area. Close monitoring for shortness of breath, lower-extremity oedema or paroxysmal nocturnal dyspnoea is also warranted. Furthermore, carfilzomib can infrequently cause renal impairment, which is even rarer with bortezomib. These differences highlight the need for additional studies of the apparently distinct downstream effects of these two drugs⁵³.

Other novel proteasome inhibitors—The efficacy of other proteasome inhibitors has been evaluated in clinical trials, including the orally bioavailable reversible peptide boronate ixazomib, the irreversible epoxyketone oprozomib, the intravenous β-lactone marizomib, and the boronate delanzomib (Tables 2 and 3). Among these oral proteasome inhibitors, ixazomib is most advanced in clinical development^{54–56}, which started with several phase I studies in patients with relapsed and/or refractory myeloma, in whom treatment-associated toxicities were mostly related to gastrointestinal adverse events or skin rash. The overall rate of neuropathy was 20%, but because the response rates were under 20%, development was moved forward in combination regimens, especially with RD^{55} ; among 64 evaluable patients with newly diagnosed disease, 58% had a VGPR or better after 12 cycles of treatment with this regimen54, and this supported a randomized phase III study of ixazomib plus RD compared with RD56. Treatment with ixazomib plus RD improved PFS (20.6 months versus 14.7 months with RD) in patients with relapsed or refractory myeloma after 1–3 prior lines of therapy⁵⁷. These results supported the regulatory approval of ixazomib by the FDA in 2015. Additional studies of this agent in several settings, including as induction and maintenance therapy, are underway. Another oral proteasome inhibitor, oprozomib, is being evaluated in phase I/II clinical trials as a single agent^{58,59}, or in combination with other d_{rugs} ^{57,60}, with encouraging early data, but later-phase trials have not yet been initiated. Finally, marizomib, which might target the proteasome more broadly, as it seems to inhibit all three major proteolytic activities of the proteasome⁶¹, is also being studied, and has shown early signs of activity in combination regimens⁶².

Lymphoma and myeloma-related disorders

Bortezomib has also been approved by the FDA and EMA for the treatment of MCL, initially in the relapsed and/or refractory setting for patients who have received at least one prior line of therapy. MCL is a heterogeneous B-cell non-Hodgkin lymphoma that can have an aggressive course and is regarded as incurable. In phase II clinical trials in patients with relapsed or refractory MCL, bortezomib showed signs of effectiveness over previous standard therapies, with a response rate of up to 50%, including a complete response rate of 4–8%63–68. The most common high-grade adverse events described in these studies included fatigue, peripheral neuropathy and cytopenias $63-68$. In 2006, the FDA granted approval of bortezomib for patients with relapsed and/or refractory MCL, based on the results of a multicentre phase II study in 155 patients⁶⁶. In this trial, the ORR and median DOR observed in patients who received bortezomib were 31% and 6.3 months, respectively⁶⁶. In 2015, an open-label phase III study¹² was conducted in 487 patients with previously untreated MCL who were ineligible for a bone marrow transplant and were randomly allocated to receive R-CHOP (rituximab, cyclophosphamide, doxorubicin, vincristine and prednisone) or VR-CAP (bortezomib, rituximab, cyclophosphamide, doxorubicin and prednisone). An improved median PFS (24.7 months versus 14.4 months; $P \le 0.001$) and four-year overall survival (64.4% versus 53.9%; $P = 0.17$) were observed in patients who received VR-CAP¹². The results of this study led to the approval of bortezomib in 2014 for patients with previously untreated MCL. Bortezomib might also benefit patients with MCL as a maintenance therapy, as suggested by the results of a phase II trial⁶⁸, in which R-CHOP was administered as induction therapy, followed by bortezomib as maintenance therapy. This treatment was well tolerated, and the reported toxicities were mainly haematological and

grade 3 or higher peripheral neuropathy (in 5% of patients)⁶⁹. With this regimen, the 5-year overall survival and 2-year PFS were 66% and 62%, respectively, indicating a more favourable response than that observed in previous studies in patients with MCL treated only with R-CHOP^{68,70}. Proteasome inhibitors have also been used for the treatment of MCL in other trials (Table 4).

Bortezomib has been shown to be effective for the treatment of Waldenström's macroglobulinaemia, another type of non-Hodgkin lymphoma. The use of bortezomib is not approved for this indication, but this agent is often used in clinical practice in the first-line and relapsed and/or refractory settings. Investigators conducting three phase II studies $69,71,72$ testing rituximab and bortezomib combinations in patients with newly diagnosed Waldenström's macroglobulinaemia reported response rates of 66–85%, with responses occurring in the first 2–3 months of treatment^{71–73}. A randomized phase III trial⁷⁴ evaluating the addition of bortezomib to a dexamethasone, rituximab and cyclophosphamide regimen is currently ongoing, and results from this study should be reported in the next few years, and will hopefully help to clarify the role of bortezomib in the first-line setting (Table 5). Bortezomib can aggravate pre-existing neuropathies, and therefore, the substitution of this agent with carfilzomib to potentially spare the onset of neuropathy has been tested in a trial for patients with Waldenström's macroglobulinaemia. In this study⁷³, 28 newly diagnosed patients received carfilzomib together with rituximab plus dexamethasone, with an observed ORR of 87%, and only one patient developed neuropathy⁷⁵. Early phase trials with carfilzomib are planned in the setting of relapsed Waldenström's macroglobulinaemia, as well as with ixazomib in the first-line setting (Table 5).

Light-chain (AL) amyloidosis is a plasma-cell dyscrasia that can be associated with multiple myeloma or Waldenström's macroglobulinaemia, and is caused by the abnormal deposition of amyloidogenic monoclonal light chains secreted by neoplastic clonal B cells or plasma cells. AL amyloidosis can be treated effectively with proteasome inhibitors⁷⁶, and a combination of bortezomib, cyclophosphamide and dexamethasone is currently a widely accepted initial standard of care for the treatment of this condition, in part, owing to a report by Mikhael *et al.*⁷⁶ In their study⁷⁶, 17 patients with AL amyloidosis received cyclophosphamide, bortezomib and dexamethasone before stem-cell transplantation, resulting in a haematological response rate of 94%, including a complete response rate of 71%, and a median DOR of 22 months. In a larger retrospective collaborative European study investigating first-line cyclophosphamide, bortezomib and dexamethasone in 230 patients with AL amyloidosis $77,78$, a 60% haematological response rate (including a 23% complete response rate) was observed. Importantly, preliminary results of a phase III trial⁷⁸ evaluating the effect of bortezomib in patients newly diagnosed with AL amyloidosis who were not eligible for autologous transplantation showed higher response rates with the combination of bortezomib, melphalan and dexamethasone compared with melphalan plus dexamethasone (ORR 76% versus 58%, $P = 0.17$; and VGPR 65% versus 35%, $P = 0.036$)⁷⁹. In addition, the oral proteasome inhibitor ixazomib is being evaluated in a study currently registering patients with relapsed and/or refractory AL amyloidosis (NCT01659658)⁸⁰, results of which are expected to be reported in the next few years. Other clinical trials testing proteasome inhibitors in patients with AL amyloidosis and Waldenström's macroglobulinaemia are currently ongoing (Table 5).

Other malignancies

The effect of proteasome inhibitors, especially bortezomib, has been studied in clinical trials involving patients with other haematological malignancies, including acute myeloid leukaemia^{79,81,82}, myelodysplastic syndrome⁸¹ and acute lymphoblastic leukaemia⁸³, but the responses observed in these settings did not merit further exploration $81-84$. Similarly, despite highly encouraging preclinical data, clinical studies in patients with solid tumours failed to demonstrate any efficacy of this agent⁸⁵. A mechanism proposed to account for this resistance involves the pharmacokinetic and pharmacodynamic profile of bortezomib, with impaired distribution to solid tumours and increased availability in the blood and/or bone marrow. Some authors have suggested that the administration of bortezomib doses higher than those approved for the treatment of myeloma $(1.3 \text{ mg/m}^2 \text{ per dose})$ might help to overcome this problem. This theory, however, is not widely accepted, and the use of doses of bortezomib at >1.3 mg/m² might be limited by the toxic effects of this agent⁸⁶. Nevertheless, the use of novel proteasome inhibitors, such as carfilzomib or ixazomib, might enable higher and better-tolerated treatment doses to be administered to patients with solid tumours (NCT00531284, NCT01949545)^{87,88}.

Plasma-cell sensitivity

Cells depend on the correct functioning of the UPP for survival, and must balance proteasome load and capacity to maintain homeostasis (Figure 1a). Plasma cells, which produce high quantities of immunoglobulins, are among the most sensitive cell types to the deregulation of protein-degradation systems. For example, bortezomib can be used to prevent acute antibody-mediated rejection of solid organ transplants by abrogating the function of nonmalignant plasma cells 89 . The use of bortezomib is also under investigation for the treatment of antibody-mediated autoimmune diseases, and in experimental model systems, including systemic lupus erythematosus⁷⁴. Interestingly, in a preclinical model of the latter disease, both short-lived and long-lived nonmalignant plasma cells were sensitive to proteasome inhibition^{90–93}. In these models, plasma-cell death occurs, at least partially, through the activation of programmed cell death when the unfolded protein response (UPR), which normally helps to protect plasma cells from apoptosis, is overwhelmed by a large load of ubiquitin–protein conjugates $88-92$. The important role of UPR balance is also supported by prior observations of decreased proteasomal capacity⁹³ — despite increased immunoglobulin secretion — which leads to apoptosis triggered by an unfavourable proteasome load–capacity ratio⁹⁴. The UPR is a cellular stress response that is activated as a result of the accumulation of unfolded or misfolded proteins in the lumen of the endoplasmic reticulum. The main function of the UPR, initially, is to restore cellular homeostasis, which is accomplished by reducing protein synthesis and increasing the production of molecular chaperones to assist protein folding. Temporarily, the UPR enables cell survival in an adverse environment by balancing proteasome load and capacity. If proteotoxic stress persists, however, through mechanisms such as prolonged proteasome inhibition — which reduces proteasome capacity while increasing proteasome load (Figure 1b) — the main role of the UPR is then to enable the activation of cell-cycle arrest and apoptotic processes^{95,96}.

Malignant plasma cells are thought to be even more exquisitely sensitive to proteasome inhibition than non-malignant plasma cells. This selectivity might be explained, in part, by the constitutive activation of NF- κ B described in myeloma cells⁹⁷. NF- κ B mediates survival and resistance to chemotherapeutic agents and radiotherapy by inducing the expression of cytokines, such as IL-6, anti-apoptotic factors and adhesion molecules. Usually, NF-κB is bound to inhibitory proteins (I κ Bs) that tether NF- κ B in the cytoplasm, thus blocking its activity as a nuclear transcription factor; when I κ Bs are degraded through the UPP, NF- κ B is released to activate transcription of its target genes in the nucleus. Importantly, blockade of the function of I κ Bs with an inhibitor of I κ B kinase resulted in only a 20–50% decrease in cell proliferation⁹⁸. This result suggests that mechanisms independent of NF- κ B function also contribute to the increased sensitivity of malignant plasma cells to proteasome inhibition. For example, malignant plasma cells are under considerably more stress to produce immunoglobulins than normal plasma cells. This increased protein production is positively correlated with proteasome sensitivity, such that an increase in the proteasomal load-versus-capacity ratio increases sensitivity to proteasome inhibition, whereas a decrease in protein synthesis renders plasma cells more resistant⁹⁹ (Figure 1a). Decreased levels of proteasome activity in myeloma cells have also been shown to result in the accumulation of polyubiquitinated proteins at the expense of a free ubiquitin pool, a mechanism that results in induction of apoptosis¹⁰⁰. Interestingly, the absolute number of immunoproteasomes in multiple-myeloma cell lines has also been positively correlated with increased resistance to treatment with bortezomib⁹⁹, presumably because such proteasomes add to proteasome capacity. Myeloma cells might also be more sensitive to proteasome inhibition through the accumulation of defective ribosomal products, which trigger the activation of pro-apoptotic factors, such as C/EBP homologous protein (CHOP)-10, which is induced in response to stress and leads to UPR activation¹⁰¹. Myeloma cells have been reported to constitutively express the endoplasmic reticulum chaperones glucose-regulated protein (GRP)-78 and GRP-94, the functions of which are to allow for increased immunoglobulin production and assembly as a way of protecting from endoplasmic reticulum stress and activation of proapoptotic factors, such as CHOP- $10^{102,103}$.

Resistance to proteasome inhibitors

Several preclinical studies have been published that examined mechanisms of resistance to proteasome inhibitors, most of which have focused on bortezomib. In initial studies, investigators reported that cell lines with resistance to bortezomib harboured mutations in the highly conserved binding pocket targeted by such drugs within the proteasome subunit β 5^{104,105}. The authors of these studies hypothesized that these substitutions affect the reversible binding of bortezomib, and suggested that screening for mutations in the gene that encodes this protein, $PSMB5$, should be considered¹⁰⁶. When bortezomib-resistant patient samples were analyzed, however, no $PSMB5$ mutations were identified¹⁰⁷⁻¹⁰⁹. This finding is consistent with early studies showing that mutations in genes encoding proteasome subunits tend to result in a lethal phenotype in yeast¹¹⁰. The overexpression of proteasome subunit β5 and other subunits, such as β2 and β1, has also been detected in cell lines derived from Burkitt lymphoma, myeloid leukaemia, plasmacytoid lymphoma, and myeloma, and has been reported to act as possible mechanisms of resistance to bortezomib^{111–113}. Studies in myeloma cell lines, however, suggest that the induction of these proteins is modest and

might contribute only minimally to resistance^{111,112}. Moreover, free β 5 subunits are catalytically inactive by themselves and cannot typically bind inhibitors unless they are assembled into functional proteasomes⁶.

Transcriptional blockade of proteasome-mediated protein degradation¹¹³ leads to induction of heat shock proteins (HSPs) and related chaperones¹¹⁴, which function to maintain protein folding and, therefore, might contribute to drug resistance¹¹⁵. Indeed, the results of many preclinical studies indicate that inhibition of various HSPs, especially HSP90, can enhance the efficacy of proteasome inhibitors¹¹⁶. Results from early phase trials combining HSP90 inhibitors with proteasome inhibitors have led to the identification of safe dose ranges for both drugs; however, randomized studies evaluating the possible superiority of these combinations over other standards have not been reported to date. Proteasome inhibition can also force cells to rely on other pathways for either sequestration or proteolysis of toxic proteins; one such pathway might be, as mentioned earlier, the aggresome–autophagy pathway. Supporting evidence for this pathway as a contributor to drug resistance was provided by a phase II study of panobinostat, an inhibitor of aggresome formation, in combination with bortezomib and dexamethasone in patients with multiple myeloma who had relapsed and/or refractory disease after bortezomib treatment¹¹⁷. Among 55 patients, 34.5% achieved a partial response or better, and another 18% had a reduction in disease burden of \sim 25–50%. Of note, many novel agents, such as daratumumab¹¹⁸, have been shown to be effective in a proportion of patients with multiple myeloma harbouring resistance to proteasome inhibitors, but whether these data are sufficient to validate molecular mechanisms of resistance remains unclear. This lack of validation is partly caused by clinical resistance not being uniformly defined: patients who are resistant to an agent or regimen at one particular time point might recover sensitivity to the same agent(s) at a later point, given the 'clonal tides' hypothesis of myeloma biology¹¹⁹. Moreover, the ideal trial design to prove the ability of one agent to resensitize disease to another agent, for example, bortezomib, would involve enrolment only of patients with progressive myeloma after receiving a bortezomib-containing regimen as their most recent line of therapy. These patients would then be randomly assigned to receive the novel agent or regimen either without or with bortezomib, with the aim of determining whether the cohort receiving the bortezomib-containing combination would have a higher response rate and/or DOR; such studies have not been performed.

Activation of a number of alternative mechanisms has been implicated in the proteasomeinhibitor-resistant phenotype. One preclinical study using bortezomib-resistant myeloma cell lines addressed the induction of the IGF-1/IGF-1R pathway. In these cell lines, blockade of IGF-1 downstream effectors re-sensitized cell lines to bortezomib. Furthermore, in the presence of bortezomib, treatment with the IGF-1R inhibitor OSI-906 induced higher rates of myeloma cell death than bortezomib alone, both *in vitro* and *in vivo*¹¹³. A downstream target of IGF-1/IGF-1R is AKT (protein kinase B), which has been shown to be activated by proteasome inhibitors in preclinical studies in models of myeloma¹²⁰. These data are relevant in light of early phase clinical trial data published in 2015 suggesting that the inhibition of AKT might overcome resistance to bortezomib in clinical settings¹²¹.

In another interesting line of investigation, Stessman *et al.*¹²² used a mouse myeloma model to identify gene-expression signatures associated with resistance or sensitivity to bortezomib. Resistance-related gene signatures were enriched for expression of nuclear factor (erythroid-derived 2)-like 2 (*NFE2L2*), which is activated as part of an antioxidantresponse pathway¹²². Interestingly, high baseline expression of antioxidant-related pathway genes has been associated with resistance to treatment with bortezomib in patients with leukaemic MCL^{123} . Thus, cancer cells that have an elevated antioxidant capacity before treatment might be resistant to bortezomib. The downstream NFE2L2 gene target POMP encodes the proteasome maturation protein proteassemblin, a chaperone responsible for the assembly of active proteasome particles from inactive precursor subunits. In 2015, Li and collaborators¹⁰⁸ found that *POMP* is a mediator of the bortezomib-resistant phenotype, providing a potential novel target for chemosensitization¹²⁴.

In 2013, using RNA-interference screens, Leung-Hagesteijn and colleagues¹²⁵ identified that the expression of serine/threonine-protein kinase/endoribonuclease (IRE1) and its downstream transcription factor, effector X-box-binding protein 1 (XBP-1), are required for bortezomib sensitivity. XBP-1 is also a transcription factor involved in plasma-cell differentiation and immunoglobulin production¹²⁶; these researchers found that, prior to treatment, the myeloma tumour contained subpopulations with different expression levels of IRE1 and XBP-1, which were associated with different sensitivities to bortezomib. Cells with low IRE1 and XBP-1 levels were less-differentiated plasma cells with lower levels of immunoglobulin synthesis, lower proteasome load and lower endoplasmic reticulum stress compared with other subpopulations, and with an inherent resistance to bortezomib (Table 6). In another study¹¹¹, MCL-derived cells resistant to bortezomib were also found to have plasmacytic differentiation with decreased immunoglobulin production¹²⁷. These findings suggest that some myeloma cell subpopulations are inherently resistant to proteasome inhibitors, and could lead to identification of biomarkers that might predict sensitivity to bortezomib. These findings, however, would also suggest that all patients harbouring resistance to proteasome inhibitors should have non-secretory myeloma, but only a small minority of patients have this disease phenotype.

Finally, the authors of a study published in 2016^{127} reported that the expression levels of tight junction protein 1 (ZO-1) are strongly and directly associated with high sensitivity to bortezomib in both myeloma and MCL cell line models and primary myeloma cells 128 . Interestingly, the downstream mechanism implicated in sensitivity was activation of EGFR signaling, which enhanced the levels of proteasome subunit synthesis in a signal transducer and activator of transcription 3 (STAT3)-dependent manner¹²⁷. The use of therapies targeting EGFR, such as erlotinib, and/or its downstream signaling intermediates could, therefore, be a promising approach that might overcome the activation of this pathway in patients with suppression of ZO‐1 and EGFR activation. These data also further underscore the importance of the ratio of proteasome load to capacity (Figure 1) as a determinant of drug sensitivity, and suggest that the effect of other resistance mechanisms in the load– capacity balance might be discovered in the future. Continued research to investigate other — as yet undescribed — mechanisms of resistance and possible strategies to target them will be necessary to maximize the role of proteasome inhibitors as successful therapies for multiple myeloma.

Conclusions

The UPP is a major mechanism of protein turnover in eukaryotic cells, and deregulation of this pathway contributes to the pathobiology of a myriad of malignancies. Therapeutic targeting of the UPP through the use of inhibitors of the 20S proteasome core proteolytic activities has constituted an important advance in the treatment of patients with haematological malignancies, such as MCL and especially multiple myeloma. Indeed, the ability of many patients to achieve complete remissions, long PFS and overall survival durations, and even reach a status of no detectable minimal residual disease after being treated with these agents is a clear triumph of translational medicine. Moreover, the availability of novel, chemically distinct drugs with an irreversible mode of action and/or an oral formulation, indicates that the benefits of proteasome inhibitors could be further extended in the treatment of myeloma. Challenges remain, however, as both primary (or innate) and secondary (or acquired) resistance mechanisms increasingly compromise the effectiveness of proteasome-inhibitor therapy. The identity of these mechanisms remained elusive for some time, but studies carried out in the past 10 years have begun to unravel many of the pathways involved, suggesting the feasibility of a biomarker-driven approach that will enable the identification of patients most likely to benefit from proteasome inhibitor-based therapies. Future approaches also need to examine the effectiveness of novel combination regimens as strategies to achieve chemosensitization and overcome resistance. The optimization of combination regimens might help to broaden the applicability of this class of drugs to other haematological malignancies and possibly also to solid tumours, for which the efficacy of proteasome inhibitors has so far been unimpressive, despite a strong preclinical rationale. A greater understanding of the mechanisms by which toxicities manifest (in particular, peripheral neuropathy and cardiotoxicity) could help to improve the safety profile of these agents — for example, via the development of specific and active immunoproteasome inhibitors¹²⁹.

Beyond the proteasome, the UPP has multiple other potential targets that are suitable for pharmacological intervention. For example, new compounds targeting deubiquitinases and other upstream regulatory components of the protein-turnover machinery might show antitumour activity alone, and/or synergistic cytotoxic efficacy in combinations with proteasome inhibitors. In this regard, the neural precursor cell expressed developmentally downregulated 8 (NEDD8)-activating enzyme inhibitor pevonedistat^{130,131}, and the E3 ubiquitinprotein ligase MDM2 inhibitor $RG7112^{132}$ have demonstrated clinical activity in patients with acute myeloid leukaemia. Also, the anti-tumour activity of proteolysis-targeting chimeric molecules $(PROTACs)^{133,134}$ that induce proteasome-mediated degradation of specific protein targets is being evaluated preclinically, and hopefully these agents will soon be incorporated into clinical trials. The general mode of action of PROTACs is based, in part, on the use of a phthalimide moiety conjugated with other protein-binding moieties to bring specific targets protein into close proximity with the E3 ligase Cereblon, resulting in target polyubiquitination and subsequent proteasomal degradation 135 . Of note, this mechanism of action builds on that hypothesized to at least partially explain the activity of IMiDs135,136, such as thalidomide, lenalidomide and pomalidomide, one of the major classes of agents used to treat patients with multiple myeloma and other haematological

polyubiquitination of the DNA-binding proteins Ikaros and Aiolos^{138,139}, demonstrating that these drugs also affect the UPP. Thus, proteasome inhibition is just one of several approaches that can already be leverage to alter UPP function in anti-tumour therapeutic approaches; our ability to target the UPP will likely continue expanding in years to come.

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Key Points

- **•** The proteasome is a central component of the protein degradation machinery in eukaryotic cells
- **•** Both transformed and normal cells depend on proteasome function to control the expression of proteins linked to cell survival and proliferation
- **•** Clinical trials using proteasome inhibitors in myeloma, lymphoma and amyloidosis have transformed the treatment of these diseases by establishing new standards of care
- **•** Three proteasome inhibitors have received regulatory approval and are routinely used in clinical settings, including bortezomib, carfilzomib and ixazomib, which have transformed the care of patients with myeloma and MCL
- **•** Primary proteasome inhibitor resistance remains a challenge in patients with solid tumors, and acquired resistance can develop even after initial responses in myeloma and MCL, the mechanisms of which are beginning to be understood
- **•** Clinical evaluation of compounds targeting the upstream regulatory components of the proteasome is underway; in the future, compounds that target proteasome-mediated degradation of specific proteins might also become available

Figure 1.

Balance between proteasomal load and capacity. **a.** Under normal conditions, cells maintain a balance between proteasome load and capacity via modulation of factors such as the protein-synthesis rate, chaperone capacity, deubiquitination activity, and the synthesis and assembly of proteasome subunits. **b.** Multiple factors can enhance or mitigate the load and capacity of the proteasome, thereby disturbing this balance. If compensatory mechanisms cannot be activated, this disturbance leads to proteotoxic stress and to the activation of apoptotic pathways.

Key clinical trials with bortezomib in multiple myeloma

The results of these trials led to the adoption of new standards of care. *Bortezomib standard schedule: 1.3 mg/m² i.v. on days 1, 4, 8 and 11 of 21day cycles. CR, complete response; DaVD, daratumumab, bortezomib, dexamethasone; DCEP, dexamethasone, cyclophosphamide, etoposide, cisplatin; DVT/PE: deep venous thrombosis/pulmonary embolism;; GI, gastrointestinal; HDD, high-dose dexamethasone; ISS, International Staging System; i.v., intravenous; MM, multiple myeloma; MP, melphalan, prednisone; MR, minor response; MTD, maximum tolerated dose; NA, not available; nCR, near-complete response; NDMM, newly diagnosed myeloma; ORR, overall response rate; OS, overall survival; PAD, bortezomib, doxoruicin, dexamethasone; peg-dox, pegylated doxorubicin; PFS, progression-free survival; PR, partial response; RD, lenalidomide, dexamethasone; RRMM, relapsed and/or refractory multiple myeloma; s.c., subcutaneous; TD, thalidomide, dexamethasone; TTP, time to progression; VAD, vincristine, doxorubicin, dexamethasone; VBMCP/VBAD/B, regimen that alternates vincristine, doxorubicin, dexamethasone followed by 2 cycles of bortezomib, melphalan, cyclophosphamide, prednisone and vincristine; VCD, bortezomib, cyclophosphamide, dexamethasone; VCD-mod, modified VCD; VD, bortezomib, dexamethasone; VGPR, very good partial response; VMP, bortezomib, melphalan, prednisone; VRCD, bortezomib, lenalidomide, cyclophosphamide, dexamethasone; VRD, bortezomib, lenalidomide, dexamethasone; VTD, bortezomib, thalidomide, dexamethasone.

Selected ongoing clinical trials with proteasome inhibitors in multiple myeloma

aSCT, autologous stem cell transplantation; CMP, carfilzomib, melphalan, prednisone; CRD, carfilzomib, lenalidomide, dexamethasone; IRD, ixazomib, lenalidomide, dexamethasone; i.v., intravenous; NDMM, newly diagnosed multiple myeloma; ORR, overall response rate; OS, overall survival; PFS, progression-free survival; p.o, by mouth; RD, lenalidomide, dexamethasone; RRMM, relapsed and/or refractory myeloma; s.c., subcutaneous; VMP, bortezomib, melphalan, prednisone; VRD, bortezomib, lenalidomide, dexamethasone.

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Table 3

Selected inhibitors of the 20S proteasome Selected inhibitors of the 20S proteasome

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overall survival; PR, partial response; RD, lenalidomide, dexamethasone; RRMM, relapsed and/or refractory multiple myeloma; sCR, stringent complete response; VGPR, very good partial response; WM, overall survival; PR, partial response; RD, lenalidomide, dexamethasone; RRMM, relapsed and/or refractory multiple myeloma; sCR, stringent complete response; VGPR, very good partial response; WM, International Myeloma Working Group; IRD, ixazomib, lenalidomide, dexamethasone; NDMM, newly diagnosed multiple myeloma; NSCLC, non-small cell lung cancer; ORR, overall response rate; OS, International Myeloma Working Group; IRD, ixazomib, lenalidomide, dexamethasone; NDMM, newly diagnosed multiple myeloma; NSCLC, non-small cell lung cancer; ORR, overall response rate; OS, AML, acute myeloid leukaemia; ASCT, autologous stem-cell transplantation; CBR, clinical benefit rate; CR, complete response; EBMT, European Group for Blood and Marrow Transplant; INWG, AML, acute myeloid leukaemia; ASCT, autologous stem-cell transplantation; CBR, clinical benefit rate; CR, complete response; EBMT, European Group for Blood and Marrow Transplant; IMWG, Waldenström's macroglobulinaemia. Waldenström's macroglobulinaemia.

Selected clinical trials with proteasome inhibitors in mantle cell lymphoma

CR: complete response; DOR, duration of response; ORR, overall response rate; OS, overall survival; PFS, progression-free survival; R-CHOP, rituximab, cyclophosphamide, doxorubicin, vincristine and prednisone; TTP, time to progression; VR-CAP: bortezomib, rituximab, cyclophosphamide, doxorubicin and prednisone; VR-CHOP: bortezomib, rituximab, cyclophosphamide, doxorubicin, vincristine and prednisone.

Ongoing clinical trials with proteasome inhibitors in myeloma-related cell dyscrasias

AL amyloidosis, light-chain amyloidosis; DRC, dexamethasone, rituximab and cyclophosphamide; GVHD, graft-versus-host disease; MD, dexamethasone, melphalan; NA, not available; OS, overall survival; PFS, progression-free survival; VGPR, very good partial response; VMD, bortezomib, dexamethasone, melphalan; WM, Waldenström's macroglobulinaemia.

Mechanisms of acquired resistance to proteasome inhibition

