Antitumoral Activity of Lenalidomide in *In Vitro* and *In Vivo* Models of Mantle Cell Lymphoma Involves the Destabilization of Cyclin D1/p27KIP1 Complexes

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Abstract

**Purpose:** Clinical responses to the immunomodulatory drug lenalidomide have been observed in patients with relapsed/refractory mantle cell lymphoma (MCL), although its mechanism of action remains partially unknown. We investigated whether the expression and subcellular localization of cyclin D1, a major cell-cycle regulator overexpressed in MCL, and the cyclin-dependent kinase inhibitor p27KIP1, could identify MCL cases sensitive to lenalidomide, and whether the compound could modulate cyclin D1/p27KIP1 complexes in MCL cells.

**Experimental Design:** MCL primary samples and cell lines were analyzed for subcellular levels of cyclin D1/p27KIP1 complexes by Western blot, immunohistochemistry, immunoprecipitation, and flow cytometry. Activity of lenalidomide *in vitro* and its effect on cyclin D1/p27KIP1 complexes were evaluated by real-time PCR, immunoprecipitation, immunofluorescence, and Western blot. *In vivo* validation was carried out in a mouse xenograft model of human MCL.

**Results:** We found cyclin D1 and p27KIP1 to be coordinately expressed in all the MCL samples tested. Immunoprecipitation analyses and siRNA assays suggested a direct role of cyclin D1 in the regulation of p27KIP1 levels. The nuclear accumulation of both proteins correlated with MCL cell tumorigenicity *in vivo*, and sensitivity to lenalidomide activity *in vitro* and *in vivo*. Lenalidomide mechanism of action relied on cyclin D1 downregulation and disruption of cyclin D1/p27KIP1 complexes, followed by cytosolic accumulation of p27KIP1, cell proliferation arrest, apoptosis, and angiogenesis inhibition.

**Conclusions:** These results highlight a mechanism of action of lenalidomide in MCL cases with increased tumorigenicity *in vivo*, which is mediated by the dissociation of cyclin D1/p27KIP1 complexes, and subsequent proliferation blockade and apoptosis induction. *Clin Cancer Res; 20*(2); 393–403. ©2013 AACR.

Introduction

Mantle cell lymphoma (MCL) is an aggressive lymphoid neoplasm that accounts for 5% to 10% of all B-cell non-Hodgkin lymphomas. It is genetically characterized by the chromosomal translocation t(11;14)(q13;q32), resulting in the overexpression of cyclin D1. Moreover, high levels of chromosomal instability because of the disruption of the DNA damage response pathway associated with the abnormal activation of cell survival mechanisms may confer an aggressive clinical course to the disease (1). Standard chemotherapy approaches are frequently used, but long-term remissions are rare. After failure of first- or second-line treatments, various single agents are used despite limited response rates (2). Thus, there is still a strong unmet medical need for new treatment options in MCL.

Promising results were achieved in a subset of relapsed MCL patients with a selective cyclin-dependent kinase (CDK) 4/6 inhibitor. However, this strategy seems to be insufficient for long-term disease control (3). In this line, preclinical studies have proposed that CDK-independent functions of cyclin D1 may account for its oncogenic and antiapoptotic properties (4), suggesting that other(s) partner(s) of cyclin D1 could represent attractive therapeutic targets. Among these partners, the CDK inhibitor p27KIP1 is strongly expressed in the highly proliferative and aggressive blastoid MCL variants while is only present in a minority of the good prognosis and low proliferative MCL tumors (5–7). It was thus proposed that mantle cell lymphomagenesis may result, at least in part, from the

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Translational Relevance
Mantle cell lymphoma (MCL) is an aggressive hematological neoplasm that lacks effective therapy. MCL cells express high level of cyclin D1, a major cell-cycle regulator recently shown to be involved in MCL resistance to chemotherapeutic-induced cell death. However, the pharmacological targeting of cyclin D1/cyclin-dependent kinase (CDK) complexes has shown modest activity in the clinical settings. Here, we find a tight correlation between contents of cyclin D1 and the CDK inhibitor p27KIP1, underlying the sequestration of this latest in cyclin D1/CDK4 complexes, and protection from degradation. We show this phenomenon to be associated with increased tumorigenicity of MCL cells in vitro, and describe the possibility to counteract this process by using the thalidomide derivative, lenalidomide. Lenalidomide efficiently disrupts cyclin D1/p27KIP1 complexes, thus reducing tumor growth and angiogenesis and inducing apoptosis in a MCL xenotransplant model. This study thus provides evidences of lenalidomide efficacy in aggressive, cyclin D1/p27KIP1-driven MCL tumors.

ability of the overexpressed cyclin D1 to buffer changes of p27KIP1 levels, thereby rendering ineffective the p27KIP1-mediated inhibition of cellular growth (8). Therefore, the role of p27KIP1 in the pathogenesis of MCL remains controversial.

Although no drug has been shown so far to specifically modulate p27KIP1 expression/activity in MCL, the immunomodulatory agent lenalidomide has been shown to regulate p27KIP1 levels in multiple myeloma cell lines and patient cells (9). This structural analogue of thalidomide approved by the U.S. Food and Drug Administration for the treatment of multiple myeloma, myelodysplastic syndromes, and relapsed/refractory MCL is also currently under active investigation with promising results for the treatment of chronic lymphocytic leukemia and non-Hodgkin lymphomas including MCL, in combination with steroids or rituximab/bendamustine (10). Lenalidomide treatment leads to enhanced proliferative and functional capacity of T lymphocytes, activation of effector responses, and suppression of inflammation (11). Although lenalidomide shows superior safety and efficacy relative to thalidomide, its mechanism of action remains partially unknown.

We reported previously that the overexpression of cyclin D1 in pro-B leukemic cells does not induce p27KIP1 relocalization from the nucleus to the cytoplasm but rather induces its sequestration of in trimeric complexes with cyclin D1 and CDK4, thereby regulating its stability (12). Here, we investigated whether the CDK inhibitor exerted similar functions in MCL cells, and the impact of cyclin D1/p27KIP1 complex formation on MCL cell growth and response to lenalidomide in both in vitro and in vivo settings.

Patients, Materials, and Methods
Isolation and culture of primary cells
Cells from 13 previously untreated MCL patients, diagnosed according to the World Health Organization classification criteria (13), were used. Informed consent was obtained from each patient in accordance with the guidelines of the Ethical Committee of the Hospital Clínic in Barcelona, Spain, the CHU Côte de Nacre, Caen, France, and the Declaration of Helsinki. The clinical characteristics of patients are listed in Table 1. Mononuclear cells from peripheral blood samples (PBMC) were isolated by Ficoll/hypaque sedimentation (GE Healthcare), and conserved within the Biobank of our institutions (Hematopathology collection from IDIBAPS Biobank and the tumor library of Basse-Normandie, CHU Caen). Cells were either used directly or cryopreserved in liquid nitrogen in the presence of 10% dimethyl sulfoxide, 60% FBS, and 30% RPMI 1640. All samples contained more than 80% of CD19+/CD5+ malignant lymphocytes, as assessed by flow cytometry.

Cell lines
Six previously described human MCL cell lines (Z-138, ZBR, Jeko-1, JBR, Rec-1, and JVM-2; ref. 14) were used in this study. Cell lines were grown in RPMI 1640 or Dulbecco’s Modified Eagle’s Medium, supplemented with 10% to 20% heat-inactivated FBS, 2 mmol/L glutamine, 50 μg/mL penicillin-streptomycin (Life Technologies) and maintained in a humidified incubator at 37°C with 5% carbon dioxide. All cultures were routinely tested for Mycoplasma infection by PCR and the identity of all cell lines was verified by using AmpFISTR identifier kit (Life Technologies).

Detection of p27KIP1 and cyclin D1 proteins in MCL primary samples by flow cytometry
Primary MCL cells (10⁶) were washed in phosphate-buffered saline (PBS) and permeabilized with Perm & Stab reagent (Beckman Coulter). Cells were labeled with anti-cyclin D1 (M-20) or anti-p27KIP1 (C-19; Santa Cruz Biotechnology) antibodies (Abs) for 30 minutes, washed in PBS, and then labeled with Alexa Fluor 647-conjugated goat anti-rabbit immunoglobulin G (IgG; Life Technologies) before being washed and fixed in PBS/PFA 0.5% solution. As a negative control, cells were labeled only with the secondary antibody. Cellular fluorescence of at least 10⁴ events was analyzed with a Gallios cytometer and data with the Kaluza software (Beckman Coulter).

Apoptosis detection by annexin V labeling
Cells were treated with 1 μmol/L lenalidomide (kindly provided by Celgene) for 72 hours, and the percentage of apoptotic cells was quantified by staining with annexin V-fluorescein isothiocyanate (FITC) and propidium iodide (Bender Medsystems) as described (15). A total of 10⁴ stained cells per sample were acquired and analyzed in an Attune acoustic focusing cytometer using Attune software (Life Technologies).
Immunohistochemical analysis of MCL cell lines

MCL cell cultures (5 x 10⁷ cells per line) were washed once in PBS and resuspended in 200 μL of a mix (v/v) of human thrombin (Sigma) and freshly isolated human plasma. Once solidified, cell pellets were formalin-fixed before paraffin embedding on silane-coated slides in a fully automated immunostainer (Bond Max; Leica Microsystems). Immunohistochemical studies were performed on consecutive tissue sections as previously described (14) using anti-phospho(p)-histone H3 (Epitomics), anti-cyclin D1 (EP12), or anti-p27KIP1 (sx53g8; Dako) primary Abs. Preparations were evaluated with an Olympus DP70 microscope by means of a 40×/0.75 NA objective and DPManager software v2.1.1 (Olympus).

Immunofluorescence

Cyclin D1 and p27KIP1 expression was determined by fluorescence microscopy in Rec-1 cells untreated or treated with 1 μmol/L lenalidomide. Cells (5 x 10⁶) were fixed on poly-L-lysine-coated glass coverslips with 4% paraformaldehyde, permeabilized with a solution containing 0.1% saponin and 10% FBS, and labeled with anti-cyclin D1 (DCS-6; Cell Signaling Technology), anti-p27KIP1 (C-19; Santa Cruz Biotechnology), or anti-p27KIP1-phospho(p) Thr198 (R&D Systems) Abs, followed by appropriate anti-mouse-tetramethylrhodamine isothiocyanate (TRITC) or anti-rabbit-FITC (Sigma) secondary Abs. Coverslips were mounted on glass slides with DAPI-containing Fluoroshield mounting medium (Sigma) and visualized on a Nikon H5505 microscope by means of a 40×/0.75 NA objective and DPManager software v2.1.1 (Olympus).

Immunoprecipitation and Western blotting

Whole protein extracts were obtained by cell lysis in Triton buffer (20 mmol/L Tris-HCl pH 7.6, 150 mmol/L NaCl, 1 mmol/L EDTA, 1% Triton X-100) supplemented with protease and phosphatase inhibitors (10 mg/mL leupeptin, 10 mg/mL aprotinin, 1 mmol/L phenylmethylsulfonyl fluoride, 5 mmol/L NaF, and 2 mmol/L Na₃VO₄). For cyclin D1 and p27KIP1 immunoprecipitation, 3 x 10⁷ cells were resuspended in immunoprecipitation buffer (10 mmol/L Tris-HCl, 150 mmol/L NaCl, 5 mmol/L EDTA, 20% glycerol, and protease/phosphatase inhibitors as above) and incubated for 15 minutes on ice. Cells were centrifuged for 15 minutes at 16,000 × g and the supernatants were recovered. Then, 500 μg of proteins were incubated overnight at 4°C with 2 μg cyclin D1 (M-20) or p27KIP1 (C-19; Santa Cruz Biotechnology) Abs. Protein A-agarose beads (50 μL; Roche) were then added and the mixture was incubated for 1 hour at 4°C. Beads were washed 3 times in immunoprecipitation buffer, resuspended in 20 μL of Laemmli buffer before SDS-PAGE. Cytosolic and nuclear extracts were prepared from 5 x 10⁶ cells with the BioVision nuclear/cytosol fractionation kit as recommended by the supplier. Fifty micrograms of proteins were loaded onto 12% to 15% SDS-PAGE and transferred to an Immobilon-P membrane (Millipore). Membranes were probed with Abs against p27KIP1 (C-19; Santa Cruz Biotechnology), cyclin D1 (DSC-6) and active caspase-3 (5A1E; Cell Signaling Technology), and p27KIP1-phospho(p) Thr198 (R&D Systems) Abs, followed by appropriate anti-mouse or anti-rabbit Abs. Membranes were incubated with horseradish peroxidase–labeled anti-mouse or anti-rabbit Abs. Chemiluminescence detection was done by using ECL system (Pierce) in a mini-LAS4000 (Fujifilm).

Table 1. Characteristics of MCL patients

<table>
<thead>
<tr>
<th>Patient no.</th>
<th>Age/gender&lt;sup&gt;a&lt;/sup&gt;</th>
<th>Histologic variant</th>
<th>Cell source&lt;sup&gt;b&lt;/sup&gt;</th>
<th>% Tumoral cells&lt;sup&gt;c&lt;/sup&gt;</th>
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<td>Classical</td>
<td>LN</td>
<td>91</td>
</tr>
</tbody>
</table>

<sup>a</sup>M, male; F: female.
<sup>b</sup>Source of the cells used in the in vitro analysis; PB, peripheral blood; LN, lymph node.
<sup>c</sup>% of tumor cells quantified by flow cytometry.
or FluorSimager (Bio-Rad) device and densitometry analyses were performed with Image Gauge (Fujifilm) or QuantityOne software (Bio-Rad), respectively.

**Determination of protein half-life**

MCL cells were cultured in the presence of 50 ng/mL cycloheximide (CHX; Sigma) for 0 to 180 minutes and then harvested. Whole cell extracts were analyzed by SDS-PAGE as previously. The density of each band was measured with FluorSimager and QuantityOne software (Bio-Rad). P27KIP1 or cyclin D1 half-life was deduced from the semi-log curve: time/f(p27KIP1 or cyclin D1/β-actin or β-tubulin ratio).

**RNA interference assay**

Jeko-1 cells (10^5) were electroporated (250 V, 950 μF; Gene Pulser II; Bio-Rad) with 750 nmol/L control (sc-37007; Santa Cruz Biotechnology) or cyclin D1 siRNAs [r(UIGA CCC CGC ACG AUU UCA U)d(TT); r(AUG AAA UCG UGC GGG GUU A)d(TT); Qiagen] in RPMI 1640 medium without FBS, cultured 48 hours in complete medium and harvested thereafter. Whole cell lysates were obtained and analyzed by immunoblotting with anti-cyclin D1, anti-p27KIP1, and anti-β-tubulin Abs as before. Densitometry analyses were performed as before.

**Real-time PCR**

Total RNA was extracted using TRIZOL (Life Technologies) following manufacturer’s instructions. One microgram of RNA was retrotranscribed to cDNA with M-MLV reverse transcriptase (Invitrogen) and random hexamer primers (Roche). Cyclin D1 and p27KIP1 mRNA expression was analyzed in duplicate by quantitative real-time PCR on the Step one system (Applied Biosystems) by using predesigned Assay-on-Demand probes (Applied Biosystems). The relative expression of each gene was quantified by the comparative cycle threshold (Ct) method (ΔCt) using β-actin as endogenous control. Expressions levels are given using control untreated cells as a calibrator.

**Xenograft mouse model and tumor phenotyping**

With the use of a protocol approved by the animal testing ethical committee of the University of Barcelona, CB17-severe combined immunodeficient (SCID) mice (Charles River) were inoculated subcutaneously into their lower dorsum with the indicated MCL cell line (10^5 cells per mice) in Matrigel (1:1; Becton Dickinson). Twenty-three days postinoculation, animals were killed according to institutional guidelines, and tumor xenografts were extirpated. For the lenalidomide protocol, mice-bearing JBR tumors were randomly assigned into cohorts of 4 mice each at day 8, when tumors were palpable. Then, animals received a daily intraperitoneal injection of 10 mg/kg lenalidomide or an equal volume of vehicle for 3 weeks. The shortest (s) and longest (l) diameters of the tumor were measured with external calipers and tumor volume (in mm^3) was calculated with the use of the following standard formula: s x l x 0.5. Tumor samples were snap-frozen in OCT medium (Sakura Tissue Tek) or formalin fixed and included in paraffin. Tissue sections were stained for p-histone H3, cyclin D1, and p27KIP1 as above, or using antiplatelet endothelial cell adhesion molecule-1 (PECAM-1, M20; Santa Cruz Biotechnology) or anti-caspase-3 cleaved (5A1E; Cell Signaling Technology) primary Abs, followed by evaluation with an Olympus DP70 microscope. Total protein extracts from cryopreserved tumor samples were obtained as previously described (14) and analyzed by SDS-PAGE as above for p27KIP1-pThr198 and activated caspase-3 levels.

**Statistical analysis**

Presented data are the means ± SD or SEM of 3 independent experiments. All statistical analyses were done by using GraphPad Prism 4.0 software (GraphPad Software). Comparison between 2 groups of samples was evaluated by nonparametric Mann–Whitney test to determine how response is affected by 2 factors. Pearson test was used to assess statistical significance of correlation. Results were considered statistically significant when P value < 0.05.

**Results**

P27KIP1 and cyclin D1 are simultaneously expressed and interact in MCL cells

We assessed the protein levels of p27KIP1 and cyclin D1 by Western blot in a set of 6 MCL samples, including a blastoid case. As shown in Fig. 1A, although both cyclin D1 and p27KIP1 were present at variable levels in all the patients analyzed, the blastoid case (Pt #3) harbored higher levels of the 2 proteins, when compared with the conventional cases. The nuclear accumulation of the 2 proteins was detectable by immunohistochemistry in tumor specimens from both conventional and blastoid cases, but at increased levels in cells from the blastoid MCL patient (25% vs. 9% cyclin D1-positive nuclei and 94% vs. 34% p27KIP1-positive nuclei between Pt#3 and Pt#1, respectively; Fig. 1B and Supplementary Fig. S1A). We developed an immunolabeling protocol for accurate detection and quantification of these proteins by flow cytometry and observed a significant correlation (r = 0.774, **P** = 0.009) between intracellular p27KIP1 and cyclin D1 protein contents in an extended series of 10 MCL primary cases (Fig. 1C; Supplementary Fig. S2A). In addition, the calculation of the ratio (r) between the mean fluorescence intensity of cyclin D1- and p27KIP1-positive cells and isotypic control-stained cells allowed observing differences between patients with apparent similar levels of both proteins by Western blot. This could be observed between the representative patients #4 and #6 (Fig. 1D compared with Fig. 1A). Independently of the level of each protein, p27KIP1 protein was present in cyclin D1/Cdk4 complexes in 3 representative cases (Pts #4-6; Fig. 1E), in accordance with previous studies (8). Altogether, these results confirm the existence of a physical interaction of cyclin D1 and p27KIP1 that may underlie the coexpression of both proteins in MCL primary samples, independently of the MCL subtype.
High levels of cyclin D1 and p27\textsuperscript{KIP1} are associated with increased tumorigenicity of MCL in vivo

Previous studies have shown that increased nuclear levels of both cyclin D1 and p27\textsuperscript{KIP1} are encountered mainly in the blastoid MCL cell lines albeit with no direct relation with the proliferation rates (8). We assessed the expression and subcellular localization of these 2 proteins by immunohistochemistry in a set of 6 MCL cell lines, including 2 cell lines with induced drug resistance to bortezomib (JBR and ZBR; ref. 14). As shown in Fig. 2A, all cell lines expressed both proteins in the nucleus and the cytoplasm. The nuclear contents of cyclin D1, p27\textsuperscript{KIP1}, as well as the mitotic-associated antigen phospho-histone H3 revealed 2 main groups of tumors. The first group includes Rec-1, JBR, and ZBR cells, where the 3 proteins were highly expressed, mainly in the nucleus. In these cells, cyclin D1 and p27\textsuperscript{KIP1} were detected in 95% and 76% of the nuclei, respectively, when compared with the second group composed by Jeko-1, JVM-2, and Z-138 showing an average of 55% cyclin D1- and 41% p27\textsuperscript{KIP1}-positive nuclei, respectively (Fig. 2A and Supplementary Fig. S1B). The interaction between cyclin D1 and p27\textsuperscript{KIP1} was similar between the
2 groups of cell lines, as shown in the representative Jeko-1 and JBR cell lines (Fig. 2B). To assess the possible implication in vivo of increased cyclin D1/p27^KIP1 complexes, this set of cell lines was subcutaneously inoculated in immunosuppressed mice and tumor burden was evaluated after 23 days. As shown in Fig. 2C, a significant increase in tumor volume was observed in mice inoculated with the subgroup of cells with higher cyclin D1/p27^KIP1 content. Representative tumor sections from Jeko-1 and JBR cells were studied by immunohistochemistry and demonstrated a remarkable nuclear accumulation of cyclin D1 and p27^KIP1 in JBR tumors together with an increased mitotic index, as illustrated in Fig. 2D. Interestingly, this was associated with a higher tumor vascularization as shown by increased labeling ofPECAM-1 (also known asCD31), in accordance with the previously reported role of cyclin D1 in tumor angiogenesis (16).

Altogether, these data suggest that, by contrast with solid tumors (17, 18), the overexpression of cyclin D1 in MCL cells is not associated with the cytoplasmic relocalization of p27^KIP1, and that cases with higher contents in both proteins are more susceptible to generate fast growing tumors in vivo.

**p27^KIP1** is stabilized upon its binding to cyclin D1. p27^KIP1 is an unstable protein, which is rapidly degraded by the proteasome pathway after its dissociation from...
cycin/CDK complexes (19). As reported previously in another B-cell model (12), we hypothesized that p27KIP1 could be stabilized by its binding to cycin D1 in MCL cells. To explore this hypothesis, Jeko-1 cells were transfected with either nonevailable, scramble siRNA, or cycin D1-specific siRNA, and levels of both proteins were assessed 48-hour posttransfection. As shown in Fig. 3A, a 35% decrease of cycin D1 level resulted in a remarkable down-regulation of p27KIP1 level closed to 60%. In line with this, in the 4 representative cell lines Jeko-1, Rec-1, JBR, and Z-138, cycin D1 half-life was always shorter than p27KIP1 half-life, suggesting that the degradation of p27KIP1 occurred after the degradation of cycin D1 (Fig. 3B and C and Supplementary Fig. S2B). This was confirmed in a B-cell lymphoma cell line transduced with a TAT-cyclin D1 fusion protein, where we found that the degradation of p27KIP1 occurred after the degradation of cycin D1 (Supplementary Fig. S2C). Altogether, these data argued in favor of a direct role of cycin D1 in p27KIP1 protection from proteasomal degradation resulting in p27KIP1 stabilization.

Lenalidomide disrupts cycin D1/p27KIP1 complexes in vitro

The inhibition of β-catenin/cycin D1 signaling has been recently involved in the mechanism of action of the immunomoduladory drug lenalidomide in multiple myeloma cells (20). To gain insights into the role of cycin D1/p27KIP1 interaction in MCL cell proliferation and tumor growth, we assessed the capacity of lenalidomide to downregulate cycin D1 in MCL. Rec-1 cells were treated for 72 hours with 1 μmol/L lenalidomide and cycin D1 complexes were analyzed for their content in p27KIP1 and CDK4. As shown in Fig. 4A, although the drug induced a 16% increase in annexin V-positive apoptotic cells when compared with control condition, it also provoked a substantial decrease of cycin D1-bound p27KIP1. No alteration in CDK4 interaction with cycin D1 was noticed. This effect did not result from a transcriptional modulation of CCND1 and CDKN1B genes, as no significant modification of their respective transcripts could be observed by quantitative real time-PCR upon lenalidomide treatment (Fig. 4B). More interestingly, the analyses of cycin D1 and p27KIP1 subcellular localization by dual immunofluorescence showed that, although both proteins mainly colocalized in the nuclei of Rec-1 cells in control condition, cell exposure to lenalidomide led to a decreased cycin D1 expression, as well as a reduced p27KIP1 nuclear amount, leading to a perinuclear cytosolic redistribution of the protein (Fig. 4C, left). Accordingly, lenalidomide-treated cells became positive for the cytosolic, Thr198-phosphorylated form of p27KIP1 (Fig. 4C). Western blots performed with nuclear and cytosolic extracts from control and lenalidomide-treated Rec-1 cells confirmed this remarkable increase in cytosolic p27KIP1, pThr198 levels after lenalidomide treatment (Fig. 4D). Of note, this cytosolic relocalization of the CDK inhibitor, together with the induction of caspase-dependent apoptosis, could represent a specific hallmark of the activity of the drug in vitro, as illustrated by the screening of proliferation and cell death markers using an antibody array and by the detection of distinct apoptotic features by multispectral imaging flow cytometry (Supplementary Fig. 3A and B). Altogether, these results suggest that, in in vitro settings, lenalidomide is able to overcome the nuclear sequestration of p27KIP1 by cycin D1, leading to cytosolic relocalization of the CDK inhibitor and consequent induction of MCL cell death.

Antitumoral activity of lenalidomide in vivo involves cycin D1/p27KIP1 inhibition

In addition to its known direct proapoptotic activity toward MCL cells (21, 22), several studies appointed for an important antiangiogenesis activity of lenalidomide in multiple cancer models (23). As MCL tumors with high
contents of cyclin D1 and p27KIP1 also presented a high level of vascularization, we next determined whether lenalidomide could target in vivo cyclin D1/p27KIP1 complexes, as well as tumor angiogenesis and progression. CB17-SCID mice were inoculated with JBR cells to generate a cyclin D1high-p27high-MCL xenograft animal model. Within 1 week of inoculation, animals developed palpable tumors that increased rapidly over the next 2 weeks (Fig. 5A). On day 8, when the tumor size reached 5 mm in diameter, mice were randomized into lenalidomide-treated (10 mg/kg) and control (vehicle) groups, receiving the corresponding administration diary, and tumor volume was calculated 23 days postinoculation. As shown in Fig. 5A, lenalidomide therapy achieved a significant MCL tumor regression (*, P < 0.05), when compared with vehicle groups. At this moment, tumor size was reaching about 10% of body weight in control mice, with no evidence of tumor-related toxicity and no differences in mean body weight between vehicle and lenalidomide groups (data not shown). Tumors isolated from control and drug-treated MCL-bearing mice revealed a 40% reduction in tumor burden in the lenalidomide-receiving group (Fig. 5B). As exemplified in Fig. 5B and C, a remarkable decrease in the mitotic index, together with the activation of caspase-3 and the tightening of blood vessels, was observed in tumors from lenalidomide-receiving mice. Lenalidomide treatment induced a substantial decrease of cyclin D1 and p27KIP1, which was associated with the phosphorylation of the CDK inhibitor at threonine 198 (Fig. 5B and C). Taken together, these data confirm the in vitro observation that lenalidomide is able to impede the growth of MCL tumors with high cyclin D1 and p27KIP1 contents, its antitumor effect being related to the cytosolic redistribution p27KIP1, and subsequent apoptosis induction.

Discussion

Current treatment strategies for MCL rely on poly-immunochemotherapy (24) that provides high overall response rates, although the responses are not durable and sequential therapies are thus necessary. In this context, preclinical and clinical studies have proved that MCL is sensitive to a range of novel agents that may become useful adjuvants to standard regimens. Among them, the second-generation immunomodulatory compound lenalidomide has recently demonstrated single-agent efficacy in relapsed and refractory MCL patients (25). Mechanistically, lenalidomide has been
found in preclinical studies to enhance NK- and T-cell activities against tumor cells, to alter the balance of pro- and anti-inflammatory cytokines, to regulate tumor–stroma interaction, to inhibit angiogenesis, and albeit to a lesser degree, to induce cell-cycle arrest and apoptosis (23). However, it is presently unclear which of these mechanisms are responsible for its clinical activity in responding MCL patients. In this study, we show that lenalidomide antitumor activity in in vitro and in vivo preclinical models of MCL involves both a tumoricidal role against malignant B cells and an antiangiogenic activity in MCL cultures and xenografts in agreement with previous results obtained in MCL and multiple myeloma models (21, 22, 26).

Of special interest, we demonstrate herein that the drug is able to target the interaction between cyclin D1 and its inhibitor p27KIP1. According to our results, this interaction may physiologically underlie the parallelism between p27KIP1 and cyclin D1 levels, as well as in the elevated levels of both proteins in aggressive MCL subtypes. We report here that p27KIP1 is detected in all MCL samples with significantly higher levels in blastoid MCL and cell lines analyzed. Conversely, previous studies have reported an overall inverse correlation between these 2 proteins in most neoplastic models and a low frequency of p27KIP1 expression in MCL (5–7). In these studies, the methods used for p27KIP1 detection did not distinguish tumor cells from residual normal cells and their sensitivity was remarkably weak. The presence of the CDK inhibitor in all our primary cases and its correlation with cyclin D1 expression were confirmed by a more selective and sensitive cytofluorimetric approach in tumor cell-enriched primary samples.

Our data reveal that increased mitotic index in MCL cell lines is associated with increased tumorigenic potential in vivo. This also suggests that, although p27KIP1 alone is not recognized as a proliferation marker in gene expression studies, elevated contents of both cyclin D1 and p27KIP1 may be used as a surrogate for the identification of aggressive MCL tumors (27–29).

Although p27KIP1 is an instable protein, which is rapidly degraded after its dissociation from cyclin D1/CDK complexes by the proteasome pathway (19), we and others (8) have demonstrated by co-immunoprecipitation experiments that p27KIP1 and cyclin D1 are bound in MCL cell lines in basal conditions, independently of their expression levels. The calculated half-life of cyclin D1 and p27KIP1 in all MCL cell lines showed that they were similar among the cell lines analyzed, although cyclin D1 half-life was always shorter than p27KIP1 half-life. By means of a validated model of transduction of TAT-cyclin D1 fusion protein (30), we found that the presence de novo of cyclin D1 in mature B-cell was accompanied by the upregulation of p27KIP1 and that the degradation of p27KIP1 followed that of cyclin D1. Finally, we noticed that p27KIP1 half-life was shortened in the cells in which cyclin D1 was transiently downregulated. Altogether, these data strongly suggest that, in MCL cells, p27KIP1 degradation could not occur as long as...
it is sequestered by cyclin D1. Our results further explains, at least in part, the coexistence of both proteins at high levels in aggressive MCL, associated with elevated mitotic index, high tumorigenicity in vivo, and with reported drug resistance. As we show here, lenalidomide is effective in these aggressive cases and high cyclin D1 and p27KIP1 expression may become a useful surrogate to determine the sensitivity in the clinical settings, although more studies are required.

In contrast to solid tumors, where nuclear cyclin D1 overexpression induces the relocation of p27KIP1 in the cytoplasmic compartment and increases the proliferation of the malignant cells (17, 18), our data indicate that both cytoplasmic compartment and increases the proliferation of possible role in the tumoricidal activity of lenalidomide in solic p27KIP1 has been involved in the control of microtubule stability (35), providing a biological rationale to evaluate new lenalidomide-based combination strategies with microtubule-destabilizing agents. However, further studies are required to completely unravel the functions of nuclear and cytosolic p27KIP1 in MCL pathogenesis and its possible role in the tumoricidal activity of lenalidomide in this model.

References

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Antitumoral Activity of Lenalidomide in In Vitro and In Vivo Models of Mantle Cell Lymphoma Involves the Destabilization of Cyclin D1/p27kip1 Complexes

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