Clinical Pharmacokinetics, Metabolism, and Drug-Drug Interaction of Carfilzomib

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ABSTRACT

Carfilzomib, an irreversible proteasome inhibitor, has a favorable safety profile and significant antitumor activity in patients with relapsed and refractory multiple myeloma (MM). Here we summarize the clinical pharmacokinetics (PK), metabolism, and drug-drug interaction (DDI) profile of carfilzomib. The PK of carfilzomib, infused over 2–10 minutes, was evaluated in patients with solid tumors or MM. Metabolites of carfilzomib were characterized in patient plasma and urine samples. In vitro drug metabolism and DDI studies were conducted in human liver microsomes and hepatocytes. A clinical DDI study was conducted in patients with solid tumors to evaluate the effect of carfilzomib on CYP3A activity. Plasma concentrations of carfilzomib declined rapidly and in a biphasic manner after intravenous administration. The systemic half-life was short and the systemic clearance rate was higher than hepatic blood flow. Carfilzomib was cleared largely extrahepatically via peptidase cleavage and epoxide hydrolysis. Cytochrome P450 450–mediated metabolism played a minor role, suggesting that coadministration of P450 inhibitors or inducers is unlikely to change its PK profile. Carfilzomib showed direct and time-dependent inhibition of CYP3A in human liver microsome preparations and exposure to carfilzomib resulted in reductions in CYP3A and 1A2 gene expression in cultured human hepatocytes. However, administration of carfilzomib did not affect the PK of midazolam in patients with solid tumors, and there were no safety signals indicative of potential drug interactions. We conclude that the rapid systemic clearance and short half-life of carfilzomib limit clinically significant DDI.

Introduction

The proteasome is a multicatalytic protease complex that plays a critical role in mediating the regulated degradation of intracellular proteins. The dipeptide boronate bortezomib (Velcade; Millennium Pharmaceuticals, Inc., Cambridge, MA) is a reversible proteasome inhibitor first approved in 2003 for the treatment of multiple myeloma (MM) and mantle cell lymphoma (Bross et al., 2004) and has validated the proteasome as a therapeutic target in B-cell neoplasms. As a result, several next-generation agents have entered clinical trials (Bennett and Kirk, 2008; Dick and Fleming, 2010). The tetrapeptide epoxycetone carfilzomib is the first irreversible proteasome inhibitor to have been approved by the US Food and Drug Administration (FDA) for the treatment of relapsed and refractory MM. It differs from bortezomib both in the duration of proteasome inhibition and in its selectivity for the unique class of seven proteases that encompass the proteasome active sites (Demo et al., 2007; Arastu-Kapur et al., 2011). In several phase 2 studies, single-agent carfilzomib has demonstrated significant antitumor activity and a favorable safety profile (Martin et al., 2010; Siegel et al., 2012; Vij et al., 2012). Furthermore, preliminary data suggest that the combination of carfilzomib with lenalidomide and low-dose dexamethasone, with each drug administered at full doses and for an extended duration, was effective and well tolerated in patients with MM (Niesvizvyd et al., 2009). Preclinical studies in rats and monkeys have shown that carfilzomib is rapidly and extensively distributed and potently inhibits proteasome activity in a variety of tissues after i.v. administration (Yang et al., 2011). Carfilzomib has a systemic clearance (CL) greater than hepatic blood flow and a terminal half-life ($t_{1/2}$) shorter than 30 minutes. The rapid elimination

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of carfilzomib is mediated primarily by metabolism via peptidase cleavage and epoxyde hydrolysis (Yang et al., 2011), making carfilzomib a unique small molecule therapeutic agent.

Here we describe the pharmacokinetic (PK) and metabolic profiles of carfilzomib in patients with either solid tumors or MM. The major elimination pathways of carfilzomib were characterized in vitro using human hepatocytes and ex vivo using human plasma and urine samples. In vitro studies were performed to assess the effects of carfilzomib on the activity of cytochrome P450 enzymes. A clinical drug-drug interaction (DDI) study is presented to evaluate the effect of carfilzomib on the PK of midazolam.

Materials and Methods

All clinical trials were conducted according to Good Clinical Practice standards. The protocol, informed consent, and other relevant study documentation were approved by the appropriate institutional review board at each participating site. All participants provided written informed consent in accordance with federal and institutional guidelines. Analyzes of human plasma and urine samples, unless specified otherwise, were done using liquid chromatography–tandem mass spectrometry (LC–MS/MS) methods fully validated according to US FDA guidance in compliance with Good Laboratory Practice. Quality control samples covering concentrations across the calibration range were included in each analytical run to ensure accuracy, precision, and reproducibility. The percentages of deviation from nominal values (accuracy) for all quality control samples were ≤ ±15% (≤ ±20% at lower limit of quantification) and the percentages of the coefficient of variation (precision) were ≤ ±15% (≤ ±20% at lower limit of quantification). All samples were analyzed within the established stability period for sample collection and storage.

Pharmacokinetic Studies. Plasma samples for PK analysis of carfilzomib were taken from patients participating in an open-label, phase 1b/2, multicenter study with relapsed solid tumors (PX-171-007; Clinical trial reg. no. NCT00531284). Carfilzomib was administered to three patients intravenously within the established stability period for sample collection and storage. An analog (d10-carfilzomib) was used as the internal standard for quantification and analyzed using a nonvalidated LC–MS/MS method. Carfilzomib was then extracted by acetonitrile protein precipitation and dialysis device (Thermo Fisher Scientific Inc., Rockford, IL). At the end of drug administration and 5 minutes after drug administration on days 1 and 16 of cycle 1 before carfilzomib dosing, at the end of drug administration, and 5 minutes on days 1, 2, 8, 9, 15, and 16 of a 28-day cycle. Patients received 4 mg of oral i.v. dexamethasone before each carfilzomib dose for the first cycle. Plasma samples were collected on days 1 and 16 of cycle 1 before carfilzomib dosing, at the end of drug administration, and at 5, 15, and 30 minutes, and 1, 2, and 4 hours after the end of administration. Samples were processed by solid phase extraction using Oasis HLB 10-mg cartridges (Waters Corporation, Milford, MA) followed by LC–MS/MS analysis to measure the plasma concentration of carfilzomib. A deuterated analog (d10-carfilzomib) was used as the internal standard for quantification with a calibration range of 0.100–200 ng/ml.

PK parameter calculations, using the actual elapsed time relative to the start of infusion, including maximum plasma concentration (Cmax), area under the plasma concentration-time curve from time 0 to the time of last quantifiable concentration (AUClast), area under the plasma concentration-time curve extrapolated to infinity (AUC∞), t1/2, CL, and volume of distribution at steady state (Vss), were carried out using noncompartmental methods (constant i.v. infusion model 202) in WinNonlin Enterprise software (version 5.2; Pharsight, Mountain View, CA), and statistical analyses were performed using SAS software (version 9.2; SAS Institute Inc., Cary, NC).

Plasma Protein Binding. Plasma protein binding of carfilzomib was determined using plasma samples collected in a phase 2, open-label, multicenter study in MM patients with varying degrees of renal dysfunction (PX-171-005; Clinical trial reg. no. NCT00721734) (Niesvizky et al., 2011). In that study, patients received 15 mg/m² i.v. carfilzomib over 2–10 minutes on days 1, 2, 8, 9, 15, and 16 of a 28-day cycle. If patients tolerated the first cycle of treatment, the dose was escalated to 20 mg/m² in cycle 2. Plasma samples were collected at the end of drug administration and 5 minutes after drug administration on days 1 and 15 of cycle 1 and day 15 of cycle 2. Plasma samples were dialyzed at 37°C against sodium phosphate buffer (pH 7.4) for 6 hours using a rapid equilibrium dialysis device (Thermo Fisher Scientific Inc., Rockford, IL). At the end of dialysis, aliquots of plasma samples were mixed with an equal volume of phosphate buffer, and aliquots of dialysates were mixed with an equal volume of blank plasma. Carfilzomib was then extracted by acetonitrile protein precipitation and analyzed using a nonvalidated LC–MS/MS method.

Metabolism. Plasma and urine samples collected in a separate phase 1 clinical trial (PX-171-002; NCT00150462) (Alsina et al., 2012) were used to characterize the metabolic profile of carfilzomib. In this trial, patients with relapsed and/or refractory hematologic malignancies received carfilzomib intravenously at 20 or 27 mg/m² following the dosing schedule described for PX-171-007. Plasma samples were collected predose and at 5, 15, and 30 minutes and 1, 2, 4, and 4 hours after administration, whereas urine samples were collected from 0 to 4 hours after administration on cycle 1 day 1. Equal volumes of plasma or urine samples from two to four patients at each dose level and time point were pooled and analyzed by LC–MS/MS for metabolite profiling based on molecular mass and fragmentation patterns (XenoBiotic Laboratories, Plainsboro, NJ) as previously described (Yang et al., 2011). Structures of major metabolites, M14 (morpholino-hPhe), M15 (morpholino-hPhe-Leu), and M16 (morpholino-hPhe-Leu-Phe-Leu-diol), were further confirmed by authentic standards. The PK and excretion of M14, M15, and M16 were then determined in human plasma and urine samples collected in the PX-171-005 study. For PK, plasma samples were collected before dosing, at the end of the infusion, at 5, 15, and 30 minutes and 1, 1.5, 2, 4, 6, and 24 hours postdosing on day 1 of cycle 1. Samples were processed by protein precipitation and analyzed using a LC–MS/MS method with a calibration range of 0.300–300 ng/ml for carfilzomib and 0.500–500 ng/ml for metabolites using deuterated analogs as the internal standards. For excretion, urine samples were collected from 0 to 5 hours and from 5 to 24 hours postinjection on day 1 of cycle 1. Acetonitrile (25% of the sample volume) was added to the bulk urine samples to minimize potential binding of carfilzomib to the collection container. The treated samples were then aliquoted and analyzed over a concentration range of 1.000–2000 ng/ml for carfilzomib and M15, and 10.0–5000 ng/ml for M14.

Pooled human hepatocytes (XenoTech LLC, Lenexa, KS) suspended in Waymouth Medium (Sigma-Aldrich, St. Louis, MO) were incubated with 1 µM carfilzomib at 37°C in an atmosphere of 5% CO2 at a final viable cell density of approximately 0.5 × 10⁶ cells/ml in the presence and absence of known chemical inhibitors for each P450 isofrom. Incubations with specific P450 substrates were also conducted as positive controls. At 0, 15, 30, 60, and 120 minutes, the reactions were quenched by adding 200 µl of acetonitrile containing appropriate internal standards. Concentrations of carfilzomib and major metabolites were determined using a nonvalidated LC–MS/MS method after protein precipitation.

In Vitro P450 Inhibition. Human liver microsomes (HLMs) (XenoTech LLC) pooled from 16 donors of mixed gender were incubated at 37°C in duplicate with varying concentrations of carfilzomib (0.01–10 µM) to determine the inhibitory activity against six major human P450 isofroms (1A2, 2C8, 2C9, 2C19, 2D6, and 3A). The inhibitory potentials of M14, M15, and M16 on human CYP3A4 were assessed at concentrations of 0.04–30 µM. Substrates for the individual P450 isofroms were phenacetin (1A2; Km = 39 µM), amiodarone (2C8; Km = 6.4 µM), diclofenac (2C9; Km = 5.9 µM), S-mephenytoin (2C19; Km = 36 µM), dextromethorphan (2D6; Km = 7.8 µM), testosterone (3A; Km = 100 µM), and midazolam (3A; Km = 3.8 µM). The microsomal protein concentration was 0.1 mg/ml except for incubations with midazolam, where a protein concentration of 0.05 mg/ml was used. After 5 minutes, the reactions were quenched by protein precipitation with acetonitrile containing appropriate internal standards, and analyzed using validated LC–MS/MS methods (Rodrigues, 2008).

For IC₅₀ measurements, determination of NADPH dependence and resistance to dilution, the concentrations of probe substrates were prepared to be approximately equal to their Km values. For Km measurements, the concentrations of midazolam were approximately equal to 0.3 × Km, 3 × Km, 6 × Km, and 10 × Km in the absence of carfilzomib or at carfilzomib concentrations ranging from 0.5 to 10 µM.

To determine the inactivation potency of carfilzomib on CYP3A4, carfilzomib was preincubated in duplicate at 0, 0.5, 1, 3, 5, and 8 µM with pooled HLMs (2.5 mg/ml for testosterone and 1.25 mg/ml for midazolam) and a NADPH-generating mixture (1 mM NADP, 5 mM glucose-6-phosphate, and 1 U/ml glucose-6-phosphate dehydrogenase) for 0, 5, 10, 20, and 30 minutes. After preincubation, 16-µl aliquots of the mixtures were diluted 25-fold with 50 mM potassium phosphate buffer containing 3 mM MgCl₂ and 1 mM EDTA (pH 7.4) and incubated with testosterone (200 µM) or midazolam (40 µM) and NADPH-generating mixture for 5 minutes to measure the residual enzymatic activity.
activity. $K_t$ (a carfilzomib concentration that caused half the maximal rate of inactivation) and $k_{max}$ (maximal rate of enzyme inactivation) were determined.

**In Vitro P450 Induction.** Human hepatocytes from three donors (BD Biosciences, Woburn, MA) were seeded at a density of approximately 2.0 x 10^5 viable cells/cm^2 in 24-well collagen I-coated plates and maintained in Williams’ Medium E (Sigma-Aldrich Co. LLC) for 2 days before treatment with solvent control (0.08% dimethyl sulfoxide), carfilzomib (0.1, 0.5, and 2.5 µM), rifampin (20 µM, an inducer of CYP3A), or β-naphthoflavone (20 µM, an inducer of CYP1A2) for an additional 3 days with daily medium and compound changes. After this, the medium was aspirated and replaced with fresh serum-free hepatocyte assay medium. Cells were incubated in triplicate with 200 µl of testosterone (200 µM) or phenacetin (100 µM), specific substrates for CYP3A and CYP1A2, respectively, for 30 and 60 minutes. The rates of 6β-hydroxytestosterone and acetaminophenol formation were measured by LC-MS/MS (Perloff et al., 2009). To test the potential inhibitory effects of carfilzomib on P450 catalytic activity, cells exposed to the positive control were treated with fresh medium containing 2.5 µM carfilzomib for 30 minutes and washed once with drug-free medium before incubation with probe substrates for CYP1A2 and CYP3A activity measurement. Cellular toxicity assays were carried out using 3-[4,5-dimethyl-2-thiazolyl]-2,5-diphenyl-2H-tetrazolium bromide (MTT; Promega Corporation, Madison, WI), and expression of CYP3A and CYP1A2 mRNA was determined by quantitative polymerase chain reaction (qPCR).

**Clinical Drug Interaction Study.** Patients ($n = 18$) with solid tumors received a single 2-mg oral dose of midazolam on day –7 followed by i.v. administration of carfilzomib at 27 mg/m^2 over 2–10 minutes on days 1, 2, 8, 9, 15, and 16 of a single 28-day cycle. Patients also received a 2-mg oral dose of midazolam immediately after carfilzomib on days 1 and 16. Plasma samples were collected at predose, at 5, 10, and 30 minutes, and at 1, 2, 3, 4, 6, 8, 12, and 24 hours after the midazolam dose on days –7, 1, and 16. On day 1, an additional plasma sample was collected at the end of carfilzomib dose. Midazolam concentrations in plasma were determined using automated liquid-liquid extraction with methyl tert-butyl ether followed by LC-MS/MS analysis across a calibration range of 0.100–100 ng/ml using d4-midazolam as the internal standard. The PK profile of carfilzomib was determined as described above, using samples obtained on day 1.

PK analyses were performed via noncompartmental methods using WinNonlin 5.2 software (Pharsight Corporation) to determine the midazolam pharmacokinetic parameters: time to $C_{max}$ ($T_{max}$), $C_{max}$, AUC from time 0 to 12 hours (AUCO–12), $AUC_{last}$, $AUC_{inf}$, and $t_{1/2}$. $AUC_{last}$, instead of $AUC_{last}$ determined on day 16 was used to compare with that on day 1 because plasma samples were not collected at 24 hours postdose on day 16. Descriptive statistics for the plasma concentrations versus time as well as all PK parameters were calculated for each treatment (midazolam alone (day –7) and cotreatment with carfilzomib (days 1 and 16)). Using the geometric linear model procedure in SAS software (version 9.2; SAS Institute Inc.), analysis of variance was performed on the ln-transformed AUCdata for day –7 and day 1 only. AUCdata for day –7 and day 16 only, $C_{max}$, and $C_{max}$ data at the α level of 0.05. Geometric mean ratios of midazolam with and without carfilzomib treatment (i.e., day 1 versus day –7, and day 16 versus day –7) with 90% confidence intervals (90% CIs) were calculated. Based on the analysis of ln-transformed data, the point estimates and 90% CIs for the least-squares mean difference between treatments ([day 1] – [day –7]) were exponentiated to obtain point estimates and 90% geometric CIs for the ratio ([day 1]/[day –7]) on the original scale.

As defined in the protocol, no clinically significant change in midazolam exposure was to be concluded if the 90% geometric CI of the ratio ([day 1]/[day –7] and [day 16]/[day –16]) of least-squares means from the analysis of variance of the ln-transformed AUClast ([day 1]/[day –7] only), AUCO–12 ([day 16]/[day –16] only), $AUC_{last}$, and $C_{max}$ were entirely within the standard equivalence range of 80–125%. Interactions were described as strong, moderate, or weak if AUC alterations were $>5$-fold, 2- to 5-fold, or 1.25- to 2-fold, respectively.

**Results**

**Pharmacokinetics and Metabolism of Carfilzomib.** After i.v. administration of a dose of 20 mg/m^2 to patients with solid tumors, carfilzomib concentrations declined rapidly with time in a biphasic manner, and the majority of the drug was eliminated from the plasma compartment within 30 minutes (Fig. 1; Table 1). Plasma CL was 146 ± 22 and 136 ± 53 l/h on days 1 and 16, respectively, exceeding hepatic blood flow (Kwon, 2001). Similar to results from an earlier in vitro rat blood partitioning experiment (Yang et al., 2011), preliminary data showed that carfilzomib had a low blood to plasma ratio in human blood (data not shown), indicating that the blood clearance is higher than the plasma clearance. These results suggest a significant contribution of extrahepatic mechanisms to carfilzomib elimination. No accumulation of carfilzomib was detected between doses, and exposure to carfilzomib was not changed upon repeat dosing. Carfilzomib was extensively protein bound in the plasma; plasma protein binding was 97.6–98.2%, independent of carfilzomib concentration across 21.6–7841 ng/ml and was not affected by the status of renal function (data not shown).

Pooled plasma and urine samples derived from a phase 1 trial (Alsina et al., 2012) were used to determine the metabolic fate of carfilzomib after administration. A total of 15 metabolites were identified in human plasma and urine samples (Supplemental Table 1). The major metabolites (M14, M15, and M16) were derived from peptide cleavage and epoxide hydrolysis of carfilzomib and their MS/MS spectra are shown in Fig. 2. P450-mediated metabolites detected only at very low levels. This correlated with the in vitro study in which the rate of carfilzomib metabolism in human hepatocytes was unaffected by the addition of inhibitors of the major P450 enzymes (Supplemental Table 2). Fourteen of the metabolites detected in human plasma and urine were also detected in animal studies, with only M6, a sulfated tyrosine detected at low levels in human urine samples, not observed in animal samples (Yang et al., 2011). M14, M15, and M16 were detectable in plasma immediately after carfilzomib administration (Fig. 3). In patients with normal renal function

**TABLE 1**

<table>
<thead>
<tr>
<th>Pharmacokinetic Parameter</th>
<th>Cycle 1 Day 1</th>
<th>Cycle 1 Day 16</th>
</tr>
</thead>
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<tr>
<td>$C_{max}$ (ng/ml)</td>
<td>2760 ± 520</td>
<td>3707 ± 1953</td>
</tr>
<tr>
<td>$AUC_{last}$ (h*ng/ml)</td>
<td>238 ± 36</td>
<td>301 ± 180</td>
</tr>
<tr>
<td>$AUC_{inf}$ (h*ng/ml)</td>
<td>238 ± 36</td>
<td>301 ± 180</td>
</tr>
<tr>
<td>$t_{1/2}$ (h)</td>
<td>1.0 ± 0.6</td>
<td>1.1 ± 0.1</td>
</tr>
<tr>
<td>CL (l/h)</td>
<td>146 ± 22</td>
<td>136 ± 53</td>
</tr>
</tbody>
</table>

Data are presented as mean ± S.D. (n = 3).

*Fig. 1. Pharmacokinetics of carfilzomib in patients with solid tumors. Plasma concentration-time profiles of carfilzomib after dosing at 20 mg/m^2 on days 1 and 16 (n = 3) of cycle 1. The concentrations are presented as mean concentrations ± S.D. CI, cycle 1 day 1; CID16, cycle 1 day 16.*
Fig. 2. MS/MS spectra of carfilzomib and its major metabolites (M14, M15, and M16). (A) Carfilzomib. (B) M14. (C) M15. (D) M16. All x-axes are m/z, and all y-axes are relative intensity.
The epoxyketone pharmacophore of carfilzomib has been shown to interact with human P450s. Carfilzomib’s potential to alter the exposure of coadministered medications was assessed in vitro. In the P450 inhibition study using HLMs, the IC_{50} values for CYP1A2, 2C8, 2C9, 2C19, and 2D6 were >10 \mu M (7194 ng/ml), the maximum concentration tested. This was greater than the mean C_{max} values from the clinical studies described above. In contrast, carfilzomib acted as a direct inhibitor of CYP3A (Fig. 4A). The effects of carfilzomib were more pronounced when midazolam (IC_{50}: 1.7 \mu M) was used as the CYP3A substrate relative to testosterone (>10 \mu M) and the inhibition was competitive. The inhibitory effect of carfilzomib on human CYP3A was time-dependent. When carfilzomib was preincubated with HLMs for 30 minutes, the IC_{50} value decreased from 1.7 to 0.49 \mu M when using midazolam as the substrate, and from >10 to 0.97 \mu M when testosterone was used as the substrate. This time-dependent inhibition required NADPH as a cofactor and was resistant to dilution. This suggests that carfilzomib is an irreversible or quasi-irreversible inhibitor of CYP3A (Supplemental Fig. 1) and the time-dependent inhibition is not due to direct reaction of the epoxyketone with CYP3A. The K_{i} was determined to be 11 \mu M and the k_{inact} was 0.10 min^{-1} using both substrates.

Based on the in vitro inhibition results and the data on the exposure of carfilzomib in patients, we estimated the ratio of intrinsic clearance values (R values) of a CYP3A probe substrate in the absence and presence of carfilzomib using a basic model (US Food and Drug Administration, 2012). The R1 value for direct inhibition was approximately 4.5–5.7 using a total maximum plasma concentration of 5.9–8.0 \mu M (unpublished data; Supplemental Fig. 2) with a carfilzomib dose of 27 mg/m^2. The calculated R2 value for time-dependent inhibition ranged from 84 to 540 using the maximum carfilzomib plasma concentration (above), the values of k_{inact} and K_{i} measured in this study, and the reported K_{m} values for CYP3A4 (Yang et al., 2008).

Neither of the major circulating metabolites, M14 and M15, showed either direct or time-dependent inhibition of CYP3A at concentrations up to 30 \mu M, whereas M16 showed time-dependent inhibition of CYP3A as the IC_{50} value decreased from >30 to 1.8 \mu M in the absence or presence of a 30-minute preincubation (data not shown). The effect of carfilzomib on the activity and expression of CYP1A2 and 3A was evaluated by treating cultured primary human hepatocytes with varying concentrations of carfilzomib. CYP3A activity was decreased in a concentration-dependent manner after 3 days of treatment (Fig. 4B). At a carfilzomib concentration of 2.5 \mu M, CYP3A4 activity decreased by 45–96%, and CYP1A2 activity dropped to below the limit of quantification in two of three hepatocyte cultures. Exposure to Rifampin (20 \mu M) or \beta-naphthoflavone (20 \mu M), known inducers of CYP3A and CYP1A2, resulted in 14- to 50-fold or 9- to 47-fold induction of enzyme activity, respectively. In addition, cell viability was unaffected by the exposure to carfilzomib (data not shown), demonstrating that the cell cultures were suitable for assessment of P450 induction.

Exposure to carfilzomib resulted in a concentration-dependent decrease in gene expression relative to solvent controls, with >95% decrease for CYP3A (three donors) and an approximately 40% decrease for CYP1A2 (one donor) at 2.5 \mu M (Fig. 4C). In contrast, exposure of cells to known P450 inducers resulted in increases in gene expression proportionate to the changes in enzymatic activity. Because carfilzomib demonstrated an inhibitory effect on midazolam metabolism in HLMs and reduced CYP3A activity and expression in human hepatocytes, a drug interaction study in patients with solid tumors was conducted to determine whether carfilzomib administration would alter the exposure of a CYP3A substrate in a physiologic setting. Of 18 patients enrolled, 17 received at least 1 dose of carfilzomib, and 12 patients completed a full cycle of administration. Fig. 4D depicts the mean plasma concentration versus time profiles for midazolam in samples taken before carfilzomib administration and on days 1 and 16 of cycle 1 of carfilzomib dosing. Table 2 lists the PK parameters of midazolam. The 90% geometric CI of the ratios of midazolam exposure before carfilzomib dosing (day –7) and after a single dose of carfilzomib (day 1) fell within the equivalence range of 80–125% (Supplemental Table 5), indicating that there was no clinically significant effect of carfilzomib on the PK of midazolam. Similarly, repeat dosing of carfilzomib failed to demonstrate a major impact on midazolam exposure. Administration of carfilzomib to these patients resulted in systemic clearance similar to those described above (Supplemental Fig. 2). In addition, no safety signals suggesting an overexposure to midazolam arose during the cycle of coadministration of the two compounds, providing further supporting evidence for a lack of a drug interaction (Supplemental Table 6).

### Discussion

Carfilzomib is a potent, irreversible inhibitor of the chymotrypsin-like activity of the proteasome that displays rapid tissue distribution, high systemic clearance, and a short half-life in animal models.

![Fig. 3. Rapid metabolism of carfilzomib in patients with multiple myeloma. Plasma samples from patients receiving a single dose of 15 mg/m^2 carfilzomib were analyzed for quantification of levels of three metabolites (M14, M15, and M16). Data are presented as mean concentrations ± S.D. Inset shows metabolite concentration in the first 30 minutes after end of infusion.](image-url)
In patients with MM, significant antitumor activity and a favorable safety profile have been reported (Martin et al., 2010; Siegel et al., 2012). However, the presence of a reactive pharmacophore makes an assessment of the PK, metabolism, and drug interactions of carfilzomib essential to understanding the practical clinical use of this promising new agent. The data presented here extend earlier preclinical findings and show that carfilzomib’s characteristic PK profile results in a lack of drug interactions in patients.

Fig. 4. In vitro and in vivo effects of carfilzomib on P450 enzyme activity. (A) Human liver microsomes were incubated in duplicate with varying concentrations of carfilzomib (0.01–10 μM) without preincubation (open circle) or with a 30-minute preincubation (open triangle) before the addition of testosterone (left panel) or midazolam (right panel). Formation of the metabolites of the substrates was measured after 5 minutes, and data are presented as mean extent of substrate metabolism relative to 0.5% acetonitrile controls. (B) Human hepatocytes from three donors were treated with 0.08% DMSO, 0.1, 1, and 2.5 μM carfilzomib, 20 μM rifampin, or 20 μM β-naphthoflavone for 3 days followed by 60-minute incubation with phenacetin as a substrate for CYP1A2. Data are presented as the mean activity (±S.D.) relative to DMSO-treated samples from triplicate measurements for each donor. (C) qPCR was used to analyze mRNA expression of CYP3A in the cells treated as in (B). mRNA expression of CYP1A2 was tested using hepatocytes from an additional donor treated as in B. Data are presented as the mean expression (±S.D.) relative to DMSO-treated samples from triplicate measurements for each donor. (D) Midazolam plasma concentration-time profiles in patients with solid tumors were measured on day −7 (before carfilzomib administration) and on days 1 and 16 (after carfilzomib administration at 27 mg/m²). Data are presented as mean concentrations ± S.D. DMSO, dimethyl sulfoxide.
In animals, after single doses of up to 48 mg/m², carfilzomib displayed rapid clearance from plasma and a nearly instantaneous formation of metabolites (Yang et al., 2011). Consistent with these observations, carfilzomib displays high systemic clearance and a short half-life in patients with solid tumors. A similar PK profile was also observed in patients with hematologic malignancies (O’Connor et al., 2009; Alsina et al., 2012) and MM having varying degrees of renal dysfunction (Niesvizky et al., 2011). The rapid clearance of carfilzomib is primarily mediated by metabolism instead of renal excretion. On the other hand, potent proteasome inhibition (>80%) persists in blood after the drug is cleared systemically (O’Connor et al., 2009) due to the irreversible mechanism of target inhibition. Recovery of proteasome activity is independent of the duration of exposure to carfilzomib and is due to the rate of new proteasome synthesis (Meiners et al., 2003; Demo et al., 2007). These pharmacokinetic and pharmacodynamic properties are distinct from those of reversible inhibitors, in which sustained drug exposure at or above the therapeutic concentration is necessary to achieve the desired duration of action (Singh et al., 2011). Therefore, the rapid elimination can minimize systemic exposure to carfilzomib and reduce potential off-target toxicities without affecting efficacy. This may partially account for the favorable safety profile of carfilzomib (Singhal et al., 2011).

The major metabolites (M14, M15, and M16) are inactive as proteasome inhibitors and are formed immediately after the administration of carfilzomib via peptidase cleavage and epoxide hydrolysis. The generation of these metabolites is likely to occur largely via extrahepatic mechanisms as supported by preclinical studies using tissue homogenates of lung, heart, and kidney (Yang et al., 2011). In addition, there were very low levels of oxidative metabolites detected in plasma and urine samples, and the presence of P450 inhibitors did not affect the rate of carfilzomib metabolism in human hepatocytes, further suggesting that P450 enzymes play only a minor role in the clearance of carfilzomib. Although an approximately 7-fold increase in the exposure of M14 in patients receiving chronic dialysis was noted relative to those patients with normal renal function, the lack of a reactive pharmacophore and the absence of an inhibitory effect on P450 enzymes suggest that this increase in exposure is not likely to be clinically relevant. The results from these metabolic studies suggest that carfilzomib can be coadministered with P450 inhibitors or inducers without altering its PK profile. In contrast, potent CYP3A inhibitors and inducers are known to have significant effects on the exposure of borombiz in patients (Venkatakrishnan et al., 2009; Hellmann et al., 2011); consequently, coadministration is not recommended.

Assessment of potential P450 inhibition is important in mitigating potential adverse drug effect to coadministered medications. This is particularly true for drugs such as carfilzomib with an electrophilic functional group. In HLMs, carfilzomib induced direct and time-dependent inhibition of the metabolism of CYP3A substrates but had minimal effects on the other P450 isoforms. This inhibitory effect was minimal in cultured hepatocytes with elevated CYP3A activity when testosterone was used as the substrate. In a separate experiment, carfilzomib inhibited midazolam metabolism by 30–40% in hepatocytes, with no apparent trend toward time-dependent inhibition (data not shown). The apparent discrepancy in time-dependent inhibition observed in HLMs and hepatocytes may be explained by the differences in the metabolism of carfilzomib in these two in vitro testing systems. The most abundant metabolite in human hepatocytes was the diol of carfilzomib (M16). On the other hand, P450-mediated pathways, which are far less relevant in vivo, predominate in liver microsome incubations (data not shown).

In cultured human hepatocytes, carfilzomib decreased the activities of CYP3A and 1A2 due to reductions in the expression of mRNA over a 3-day treatment. The ability of proteasome inhibitors to reduce P450 expression in vitro has been described previously (Zangar et al., 2003, 2008; Anwar-Mohamed et al., 2008; Acharya et al., 2009), but the mechanism of this effect remains unclear.

On the basis of the in vitro inhibition results and the data on the exposure of carfilzomib in patients, we estimated the ratio of intrinsic clearance values (R values) of a CYP3A probe substrate in the absence and presence of carfilzomib using a basic model (US Food and Drug Administration, 2012). The results suggest potential DDIs in patients. In addition, carfilzomib also decreased CYP3A mRNA expression in cultured human hepatocytes. The clinical drug interaction study was therefore designed to assess both the effect of single- and repeat-dose administration of carfilzomib on CYP3A in solid tumor patients. The results of this study indicated that carfilzomib does not significantly alter the PK of midazolam after either single- or repeat-dose administration. Because midazolam is a highly sensitive CYP3A substrate (US Food and Drug Administration, 2012), it is reasonable to conclude that carfilzomib would not be expected to interact with other CYP3A substrates in vivo. Taken together, the results of the present study suggest that carfilzomib can be administered with other medications that are substrates of P450 enzymes without altering their exposure.

The lack of clinically significant drug interactions of carfilzomib with CYP3A may be attributed to the pharmacokinetic properties of carfilzomib. First, the drug is rapidly metabolized after i.v. administration with a short systemic half-life. The mean plasma concentration at 5 minutes postinfusion was approximately 20% of the mean Cmax and was further reduced to <1% by 30 minutes. Although the true intracellular hepatic concentration of carfilzomib is unknown, the exposure of P450 enzymes to intact carfilzomib is likely to be of a short duration. Furthermore, the major circulating metabolites, M14 and M15, are not inhibitors of CYP3A. Second, the NADPH-dependent oxidative metabolic pathway(s) responsible for time-dependent inhibition of CYP3A by carfilzomib and M16 in HLMs were not significant in vivo. This is supported by the lack of time-dependent inhibition in hepatocyte cultures. Finally, carfilzomib is highly bound to plasma proteins, further limiting the potential exposure of P450 enzymes to the free drug. Indeed, the level of proteasome inhibition in liver after i.v. administration of carfilzomib to rats was less than that seen in blood and other organs (Demo et al., 2007). Therefore, carfilzomib is unlikely to result in decreased mRNA expression of P450 isoforms in vivo as was seen in cultured hepatocytes.

In summary, carfilzomib displays high systemic clearance, a short half-life, and rapid metabolism largely via extrahepatic peptidase cleavage and epoxide hydrolysis. P450-mediated metabolism does not play an important role in the elimination of carfilzomib; therefore,

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**Table 2**

Pharmacokinetic parameters of midazolam in solid tumor patients alone (day −7) or in coadministration (days 1 and 16) with 27 mg/m² carfilzomib

<table>
<thead>
<tr>
<th>Pharmacokinetic Parameter</th>
<th>Day −7 (n = 17)</th>
<th>Day 1 (n = 17)</th>
<th>Day 16 (n = 12)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cmax (ng/ml)</td>
<td>16.3 ± 7.6</td>
<td>15.7 ± 6.2</td>
<td>16.0 ± 7.7</td>
</tr>
<tr>
<td>AUCinf (hr·ng/ml)</td>
<td>49.8 ± 30.9</td>
<td>47.3 ± 26.4</td>
<td>48.4 ± 23.0</td>
</tr>
<tr>
<td>AUC0–12 (hr·ng/ml)</td>
<td>42.5 ± 23.2</td>
<td>40.3 ± 19.1</td>
<td>48.4 ± 23.0</td>
</tr>
<tr>
<td>AUC12 (hr·ng/ml)</td>
<td>54.3 ± 36.0</td>
<td>51.5 ± 30.3</td>
<td>59.9 ± 32.5</td>
</tr>
<tr>
<td>Tmax (h)</td>
<td>0.5 ± 0.2</td>
<td>0.7 ± 0.3</td>
<td>0.8 ± 0.7</td>
</tr>
<tr>
<td>t1/2 (h)</td>
<td>6.6 ± 2.2</td>
<td>6.3 ± 1.9</td>
<td>5.5 ± 1.5</td>
</tr>
</tbody>
</table>

n = 11 on day 16 for AUC12 and t1/2.

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coadministration of carfilzomib with drugs that are potent P450 inhibitors or inducers is unlikely to alter its PK profile. Although exposure to carfilzomib resulted in modest inhibition of CYP3A activity in vitro in HLMs and caused a decrease in P450 gene expression in human hepatocytes, clinically significant drug interaction was not noted in a study specifically designed to determine the effect of carfilzomib on CYP3A activity. Carfilzomib is a proteasome inhibitor with a distinct pharmacokinetic profile relative to bortezomib that may allow greater opportunity for general use in combination with other medications with less cause for concern regarding DDI.

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