Proteasome Inhibitors Bortezomib and Carfilzomib Stimulate the Transport Activity of Human Organic Anion Transporter 1

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ABSTRACT

Organic anion transporter 1 (OAT1), expressed at the basolateral membrane of renal proximal tubule epithelial cells, mediates the renal excretion of many clinically important drugs. Previous study in our laboratory demonstrated that ubiquitin conjugation to OAT1 leads to OAT1 internalization from the cell surface and subsequent degradation. The current study showed that the ubiquitinated OAT1 accumulated in the presence of the proteasomal inhibitors MG132 and ALLN rather than the lysosomal inhibitors leupeptin and pepstatin A, suggesting that ubiquitinated OAT1 degrades through proteasomes. Anticancer drugs bortezomib and carfilzomib target the ubiquitin-proteasome pathway. We therefore investigate the roles of bortezomib and carfilzomib in reversing the ubiquitination-induced downregulation of OAT1 expression and transport activity. We showed that bortezomib and carfilzomib extremely increased the ubiquitinated OAT1, which correlated well with an enhanced OAT1-mediated transport of p-aminohippuric acid and an enhanced OAT1 surface expression. The augmented OAT1 expression and transport activity after the treatment with bortezomib and carfilzomib resulted from a reduced rate of OAT1 degradation. Consistent with this, we found decreased 20S proteasomal activity in cells that were exposed to bortezomib and carfilzomib. In conclusion, this study identified the pathway in which ubiquitinated OAT1 degrades and unveiled a novel role of anticancer drugs bortezomib and carfilzomib in their regulation of OAT1 expression and transport activity.

SIGNIFICANCE STATEMENT

Bortezomib and carfilzomib are two Food and Drug Administration–approved anticancer drugs, and proteasome is the drug target. In this study, we unveiled a new role of bortezomib and carfilzomib in enhancing OAT1 expression and transport activity by preventing the degradation of ubiquitinated OAT1 in proteasomes. This finding provides a new strategy in regulating OAT1 function that can be used to accelerate the clearance of drugs, metabolites, or toxins and reverse the decreased expression under disease conditions.

Introduction

Many clinically important drugs, including antiviral therapeutics (e.g., adefovir, acyclovir), antitumor drugs (e.g., methotrexate), antibiotics (e.g., cephaloridine, penicillin G), antihypertensives (e.g., captopril, quinapril), and anti-inflammatories (e.g., salicylate, indomethacin), are eliminated from the kidney through organic anion transporter 1 (OAT1) (You, 2004; Burckhardt, 2012; Liang et al., 2015). OAT1, expressed at the basolateral membrane of the renal proximal tubules, actively transports drugs from blood into tubule cells, followed by the efflux of these drugs to urine by other transporters in the apical membrane (You, 2002; Nigam, 2015; Xu et al., 2016a). The function of OAT1 is the rate-limiting factor in the renal clearance of drugs from the body, affecting drug concentration in the plasma and various tissues, thereby influencing drug therapeutic efficacy and the toxicity.

The transport activity of OAT1 critically relied on its expression level at basolateral membranes of kidney proximal tubule cells, which may be altered under certain pathologic and pharmacological conditions (Burckhardt, 2012; Wang and Sweet, 2013). For example, OAT1 expression in basolateral membranes was increased in the early phase of acute extrahepatic cholestasis or chronic administration of furosemide (Kim et al., 2003; Brandoni et al., 2006b), whereas the expression was decreased after 3 days of obstructive cholestasis, bilateral ureteral obstruction, chronic or acute renal failure, or administration of 1α,25-dihydroxyvitamin D3 (the biologically active form of vitamin D) (Monica Torres et al., 2005; Villar et al., 2005; Brandoni et al., 2006a; Kwon et al., 2007, 2008; Miao et al., 2013).

Our laboratory previously demonstrated that OAT1 constitutively internalizes from and recycles back to cell surface, and ubiquitin (an 8-kDa polypeptide) conjugation was a precedent step in initiating OAT1 internalization to early endosomes (Zhang et al., 2008, 2013). Once in the endosomes, OAT1 is deubiquitinated and recycles back to cell surface or undergoes proteolytic degradation. We further demonstrated...
that activation of protein kinase C inhibits OAT1 transport activity and reduces the amount of OAT1 at the cell surface by enhancing OAT1 ubiquitination, resulting in accelerated OAT1 internalization from cell surface to intracellular early endosomes and subsequent proteolytic degradation (Zhang et al., 2008, 2013; Xu et al., 2017). Ubiquitination is an important post-translational mechanism of OAT1 regulation (Xu et al., 2016a; Xu and You, 2017).

The proteasomes and the lysosomes are two major systems through which cells degrade proteins (Clague and Urbe, 2010). The two proteolytic systems can be differentiated by the sensitivity to corresponding inhibitors. Degradation of polypeptides through the proteasomes can be prevented by proteasomal inhibitors, such as MG132, whereas lysosomal proteolysis can be hindered by lysosomal inhibitors, such as leupeptin (Kisselev and Goldberg, 2001; Goldberg and Rock, 2002; Lee et al., 2011; Yang et al., 2013). Since ubiquitination leads to OAT internalization and degradation, the alteration of proteasome or lysosome activity can potentially affect the transporter function. In the present study, we investigated the proteolytic system in which the ubiquitinated OAT1 is degraded and explored the strategies of reversing ubiquitination-dependent OAT1 degradation and its influence on OAT1 expression and transport activity.

### Materials and Methods

**Materials.** Human embryonic kidney 293 (HEK293) cells were purchased from American Type Culture Collection (Manassas, VA). 3H-labeled p-aminohippuric acid (PAH) was purchased from PerkinElmer (Waltham, MA). Sulfosuccinimidyl-2-(biotinamido)ethyl-1,3-dithiopropionate (Sulfo-NHS-SS-biotin), streptavidin-agarose resin, and protein G-agarose were purchased from Thermo Scientific (Rockford, IL). Mouse anti-Myc antibody (9E10) was purchased from Roche (Indianapolis, IN). Mouse anti–E-Cadherin antibody was purchased from Abcam (Cambridge, MA). Mouse anti-ubiquitin antibody, mouse anti-glyceraldehyde-3-phosphate dehydrogenase (GAPDH) antibody, and normal mouse IgG were purchased from Santa Cruz Biotechnology (Dallas, TX). Lactate dehydrogenase (LDH) cytotoxicity assay kit and 20S proteasome assay kit were purchased from Cayman Chemical (Ann Arbor, MI). Bortezomib and carfilzomib were purchased from Cell Signaling (Danvers, MA). MG132, ALLN, leupeptin, pepstatin A, and other reagents were purchased from Sigma-Aldrich (St. Louis, MO).

**Cell Culture.** Parental HEK293 cells were cultured in Dulbecco’s modified Eagle’s medium (DMEM) (Corning, Tewksbury, MA) supplemented with 10% FBS (Gibco, Grand Island, NY) at 37°C in 5% CO₂. HEK293 cells stably expressing human OAT1 (hOAT1) were generated in our laboratory (Xu et al., 2016b). hOAT1 cells were maintained in DMEM medium supplemented with 0.2 mg/ml of G418 (Gibco) and 10% FBS (Gibco, Grand Island, NY) at 37°C in 5% CO₂.

**Transport Measurement.** The transport activity was measured using the method published in our laboratory (Zhang et al., 2013). hOAT1 cells were incubated with 1 ml of freshly made sulfo-NHS-SS-biotin (0.5 mg/ml in PBS/CM) in two successive 20-minute incubations on ice with very gentle shaking. After biotinylation, each dish was briefly rinsed with 3 ml of PBS/CM containing 100 mM NaCl and then incubated with the same solution for 20 minutes on ice to ensure complete quenching of the unreacted sulfo-NHS-SS-biotin. The cells were then lysed on ice for 50 minutes in 400 μl of lysis buffer (10 mM Tris-HCl, pH 7.5, 150 mM NaCl, 1 mM EDTA, 0.1% SDS, 1% Triton X-100) with 1% proteinase inhibitor cocktail. The cell lysates were cleared by centrifugation at 16,000g at 4°C. Streptavidin-agarose resin (40 μl) was then added to the supernatant to isolate cell membrane proteins. hOAT1 was detected in the pool of surface proteins by SDS-PAGE and immunoblotting using anti-Myc antibody 9E10.

**Cell Surface Biotinylation.** The cell surface expression level of hOAT1 was examined using the method published in our laboratory (Zhang et al., 2013). hOAT1 cells were incubated with 1 ml of freshly made sulfo-NHS-SS-biotin (0.5 mg/ml in PBS/CM) in two successive 20-minute incubations on ice with very gentle shaking. After biotinylation, each dish was briefly rinsed with 3 ml of PBS/CM containing 100 mM NaCl and then incubated with the same solution for 20 minutes on ice to ensure complete quenching of the unreacted sulfo-NHS-SS-biotin. The cells were then lysed on ice for 50 minutes in 400 μl of lysis buffer (10 mM Tris-HCl, pH 7.5, 150 mM NaCl, 1 mM EDTA, 0.1% SDS, 1% Triton X-100) with 1% proteinase inhibitor cocktail. The cell lysates were cleared by centrifugation at 16,000g at 4°C. Streptavidin-agarose resin (40 μl) was then added to the supernatant to isolate cell membrane proteins. hOAT1 was detected in the pool of surface proteins by SDS-PAGE and immunoblotting using anti-Myc antibody 9E10.

**Immunoprecipitation.** The ubiquitination of hOAT1 was detected using the immunoprecipitation method published in our laboratory (Zhang et al., 2013). hOAT1 cells were lysed with lysis buffer (50 mM Tris-HCl, pH 8.0, 150 mM NaCl, 1% Triton X-100, 10% glycerol, 5 mM EDTA, and 1 mM NaF) with 1% proteinase inhibitor cocktail and 20 mM N-ethylmaleimide. Cell lysates were preclarified with protein G-agarose to reduce nonspecific binding at 4°C for 2 hours. Anti-Myc antibody was incubated with 30 μl of protein G-agarose at 4°C for 2 hours. The preclarified protein sample was then mixed with antibody-bound protein G-agarose and underwent end-over-end rotating at 4°C overnight. Proteins bound to the protein G-agarose were eluted with urea buffer containing β-mercaptoethanol and analyzed by immunoblotting with indicated antibodies.

**Degradation Assay.** The degradation of hOAT1 was assayed using the method published in our laboratory (Wang et al., 2016). hOAT1 cells were first biotinylated, and then the labeled cells were incubated in DMEM with or without bortezomib and carfilzomib at 37°C. Treated cells were collected at 0, 4, 8, and 12 hours and lysed in lysis buffer with 1% protease inhibitor cocktail. The cell lysates were cleared by centrifugation at 16,000g at 4°C. Streptavidin-agarose resin (40 μl) was then added to the supernatant to isolate cell membrane proteins. Samples were loaded on 7.5% SDS-PAGE gels and analyzed by immunoblotting with anti-Myc antibody.

**Electrophoresis and Immunoblotting.** Electrophoresis and immunoblotting were performed using the method published in our laboratory (Zhang et al., 2008). Protein samples were resolved on 7.5% SDS-PAGE gels and electroblotted onto polyvinylidene difluoride membranes. The blots were blocked for 1 hour with 5% nonfat dry milk in PBS-0.05% Tween 20, washed, and incubated overnight at 4°C with appropriate primary antibodies, followed by horseradish peroxidase–conjugated secondary antibodies. The signals were detected by SuperSignal West Dura Extended Duration Substrate kit (Thermo Scientific). Nonsaturating immunoreactive protein bands were quantified by scanning densitometry with the FluorChem 8000 imaging system (Alpha Innotech Corp., San Leandro, CA).

**Data Analysis.** Each experiment was repeated a minimum of three times. The statistical analysis was derived from multiple experiments. Among multiple treatments, a one-way ANOVA or two-way ANOVA.
Effects of Protease Inhibitors on the Accumulation of Ubiquitinated OAT1. To determine the intracellular degradation system for ubiquitinated OAT1, we treated OAT1-expressing cells with proteasome inhibitors MG132 or ALLN and lysosome inhibitors leupeptin or pepstatin A for 2 hours. The treated cells were lysed, and OAT1 was pulled down by anti-Myc antibody (epitope Myc was tagged to OAT1 to facilitate immunodetection) or with mouse IgG (as negative control), followed by immunoblotting (IB) with anti-ubiquitin antibody (anti-Ub) to detect ubiquitinated OAT1. Our results (Fig. 1, top panel) revealed that although incubation of the cells with the lysosomal inhibitors leupeptin and pepstatin A was without any effect, incubation with proteasomal inhibitors MG132 and ALLN both led to a substantial accumulation of ubiquitinated OAT1, suggesting that ubiquitinated OAT1 degrades through proteasomes rather than lysosomes. The change of ubiquitinated OAT1 did not result from the difference of OAT1 immunoprecipitated because the amount of OAT1 pulled down was similar among all samples (Fig. 1, bottom panel).

Effects of Proteasomal Inhibitors Bortezomib and Carfilzomib on the Accumulation of Ubiquitinated OAT1. Bortezomib and carfilzomib are Food and Drug Administration–approved anticancer drugs acting as selective proteasome inhibitors. We therefore examined the effects of bortezomib and carfilzomib on the accumulation of ubiquitinated OAT1. OAT1-expressing cells were treated with bortezomib or carfilzomib for 12 hours. The treated cells were lysed, and OAT1 was pulled down by anti-Myc antibody, followed by immunoblotting (IB) with anti-Ub to detect ubiquitinated OAT1. Our results (Fig. 2, top panel) revealed that incubation of the cells with bortezomib or carfilzomib led to a substantial accumulation of ubiquitinated OAT1. The change of ubiquitinated OAT1 did not result from the difference of OAT1 immunoprecipitated because the amount of OAT1 pulled down was similar among all samples (Fig. 2, bottom panel; the full blot is included in Supplemental Fig. 1).

Effects of Bortezomib or Carfilzomib on OAT1-Mediated Uptake of \(^{3}H\)p-Aminohippuric Acid. As OAT1 is a multi-substrate transporter, we examined whether bortezomib and carfilzomib are inhibitors for OAT1 by carrying out a \(cis\)-inhibition experiment (Fig. 3). We measured a 3-minute uptake of \(^{3}H\)PAH (20 \(\mu\)M) into OAT1-expressing cells with 20 \(\mu\)M probenecid, 3 \(\mu\)M bortezomib, or carfilzomib being present in the same solution as PAH. Probenecid is a well-known competitive inhibitor for OAT (Vallon et al., 2012; Wang et al., 2014; Nigam et al., 2015). Under such conditions, probenecid inhibited OAT1-mediated transport of \(^{3}H\)PAH by 41% [95% confidence interval (CI): 36%–46%], whereas bortezomib and carfilzomib were without any effect, suggesting that bortezomib and carfilzomib are not inhibitors for OAT1. Therefore, bortezomib and carfilzomib do not regulate OAT1 through its ability to interfere with the transporter.

Results

Effects of Bortezomib and Carfilzomib on OAT1-Mediated Uptake of p-Aminohippuric Acid. OAT1-expressing cells were treated with bortezomib and carfilzomib for 12 hours, and then cytotoxicity and OAT1-mediated uptake of PAH were measured. Both bortezomib and carfilzomib induced stimulation of PAH uptake at 25–100 nM for bortezomib (Fig. 4A) and 0.1–1 \(\mu\)M for carfilzomib (Fig. 4B) without cytotoxicity at corresponding concentration (Fig. 5). The transport activity of OAT1 was increased by 11% (95% CI: −7% to 30%) and 49% (95% CI: 31%–67%), respectively, at 5 and 25 nM bortezomib. In contrast, 12 hours of treatment with lysosome inhibitors leupeptin and pepstatin A did not affect the uptake of PAH (Fig. 4C). Further study showed that, like MG132, bortezomib and carfilzomib inhibited the 20S proteasome activity after 2 hours of treatment (Fig. 6A). For bortezomib at 1, 5, and 25 nM with treatment for 12 hours, the proteasome activity was inhibited by 8% (95% CI: 5%–12%), 29% (95% CI: 26%–33%), and 87% (95% CI: 84%–91%), respectively, which
showed a concentration-dependent inhibition of proteasome activity at 1–25 nM bortezomib (Fig. 6B).

Effect of Bortezomib and Carfilzomib on OAT1 Expression. OAT1-expressing cells were treated with bortezomib or carfilzomib, and OAT1 expression both at the cell surface and in the total cell lysates was examined. We showed that treatment with bortezomib or carfilzomib led to an increase of OAT1 expression at the cell surface (Fig. 7A, top panel, and Fig. 7B) and in total cell lysate (Fig. 7C, top panel, Fig. 7D). Such a change in OAT1 expression was not due to the general perturbation of cellular proteins, as the expression of cell surface membrane protein marker E-Cadherin (Fig. 7A, bottom panel) and cellular protein marker GAPDH (Fig. 7C, bottom panel) was not affected under these conditions.

Effect of Bortezomib and Carfilzomib on OAT1 Stability. The stability of cell surface OAT1 was subsequently assessed based on a biotinylation approach. OAT1-expressing cells were biotinylated with membrane-impermeable biotinylation reagent sulfo-NHS-SS-biotin. Labeled cells were treated with or without bortezomib or carfilzomib for 12 hours. Treated cells were then lysed, and cell surface proteins were isolated using streptavidin-agarose resin, followed by immunoblotting with anti-Myc antibody. Our results (Fig. 8) showed that the rate of OAT1 degradation decreased substantially after 8 and 12 hours of treatment with bortezomib (Fig. 8, A and B) or carfilzomib (Fig. 8, C and D) as compared with that of control. These results indicate that bortezomib and carfilzomib substantially increase OAT1 stability.

Discussion

The transport activity of OAT1 is critically dependent on its expression level at the cell surface. We previously demonstrated that post-translational modification of OAT1 by ubiquitination leads to OAT1 internalization from the cell surface and subsequent degradation in proteolytic systems (Zhang et al., 2008, 2013; Xu et al., 2017). In the current study, we identified the proteolytic system in which the ubiquitinated OAT1 is degraded and revealed a new strategy of reversing ubiquitination-dependent OAT1 degradation.

HEK293 cells, a heterologous cell system, was used in our current studies, as they have been widely used for research in the regulation of the cloned organic anion transporters and other renal transporters (Rodiger et al., 2010; Xue et al., 2011; Zeng et al., 2012; El-Sheikh et al., 2013). The fact that these cells do not express endogenous OATs is particularly advantageous because expression of OAT1 in these cells will permit us to analyze the transport properties of OAT1 without being disturbed by other organic anion transporters. Our studies in HEK293 cells will pave the path for the upcoming work...
focusing on validating whether the same mechanisms exist in primary epithelia.

Our current study unveiled a key role for proteasomes in the regulation of OAT1 expression and transport activity. Treatment of OAT1-expressing cells with proteasomal inhibitors MG132 and ALLN led to an accumulation of ubiquitinated OAT1, whereas treatment of cells with lysosomal inhibitors leupeptin and pepstatin A were without any effect (Fig. 1). The degradation of cell surface OAT1 through proteasomes contrasted with most of the plasma membrane proteins, for which the canonical degradation pathway is through lysosomes (Piper and Luzio, 2007; Varghese et al., 2008). This finding opens the door for new strategies in modulating OAT1 function through controlling proteasomal activity.

Proteasomal inhibition has been developed for antitumor activities. The proteasomal inhibitors used in our current studies, bortezomib and carfilzomib, are two Food and Drug Administration–approved antitumor drugs with the ability to inhibit proteasomes. Bortezomib administration caused a decrease of 20S proteasome activity in the white blood cells, liver, colon, muscle, and prostate (Adams et al., 1999; Bross et al., 2004). Inhibition of the 20S proteasome activity after carfilzomib administration was observed in blood, adrenal, heart, lung, spleen, bone marrow, and kidney (Nooka et al., 2013). Both drugs have also been shown to affect kidney function. Bortezomib can attenuate renal impairment in patients with multiple myeloma, renal fibrosis, and lupus nephritis (Hainz et al., 2012; Ward et al., 2012; Zeniya et al., 2017; Zhang et al., 2017; Cohen et al., 2015; Dimopoulos et al., 2016). Carfilzomib inhibited the chymotrypsin-like activity of the 20S proteasome in the kidney by 50%–60% in rats (https://www.accessdata.fda.gov/drugsatfda_docs/nda/2012/202714Orig1s000PharmR.pdf). Recent studies showed that bortezomib can affect the activities of copper transporter 1, ATP-binding cassette transporter A1 and ATP-binding cassette transporter G1, metal transporter Zrt/IRT-like protein 14, and organic anion transporting polypeptide 1B3 (Jandial et al., 2009; Ogura et al., 2011; Zhao et al., 2014; Alam et al., 2017). However, the potential of these antitumor drugs to modulate OAT1 activity has not been explored. By inhibiting the proteasomal activity, these drugs gained a new role in the regulation of OAT1 activity.

We showed that treatment of OAT1-expressing cells with bortezomib and carfilzomib led to a substantial accumulation of the ubiquitinated OAT1 (Fig. 2), which correlated well with an enhanced OAT1 transport activity and an enhanced OAT1 expression at the cell surface (Figs. 4 and 7). The molecular weight of ubiquitinated OAT1 was more than 180 kDa, ~100 kDa larger than unubiquitinated OAT1 (~80 kDa). Since ubiquitin is an 8-kDa polypeptide, OAT1 may be poly- or multiubiquitinated (Figs. 1 and 2).

The increase of surface OAT1 can be attributed to reduced internalization, increased recycling, or decreased degradation. As internalization and recycling are rapid processes, the alteration of internalization or recycling may be the mechanisms in acute regulation of OAT1 during the short term (<30 minutes), whereas the alteration of degradation may be the mechanism in chronic regulation of OAT1 during the long term (several hours) (Zhang et al., 2008, 2012, 2013; Xu et al., 2017; Wang et al., 2019). Bortezomib and carfilzomib enhanced the surface expression and transport activity of OAT1 with 12 hours of treatment and did not stimulate the transport activity in short-term treatment, suggesting that reduced internalization or increased recycling were not involved in OAT1 regulation. Further exploring the underlying mechanism, we found that the degradation rate of OAT1 was decelerated after treatment with bortezomib and carfilzomib (Fig. 8). The drug target of bortezomib and carfilzomib is 20S proteasome, which is the target of bortezomib and carfilzomib. The 20S proteasome is a multiprotein complex that catalyzes the intramolecular cleavage of a polypeptide chain into peptides of up to 100 amino acids in length (https://www.accessdata.fda.gov/drugsatfda_docs/nda/2012/202714Orig1s000PharmR.pdf). The 20S proteasome is composed of two types of subunits: 14 α-subunits and 7 β-subunits. The α-subunits form the inner core of the proteasome, while the β-subunits form the outer ring. The catalytic activity of the proteasome is mediated by the β5 subunit, which is responsible for the cleavage of peptide bonds. Bortezomib and carfilzomib inhibit the activity of the β5 subunit, leading to the degradation of proteins that are not normally degraded by the proteasome. This leads to the accumulation of ubiquitinated proteins and the inhibition of cell proliferation. The accumulation of ubiquitinated proteins may also lead to the activation of the unfolded protein response, which can lead to cell death.
proteasome. Our results showed that bortezomib and carfilzomib inhibited 20S proteasome activity (Fig. 6A), and there was a correlation between the degree of proteasomal inhibition and increase of OAT1 transporter function at 5 and 25 nM bortezomib (Fig. 4A; Fig. 6B). Therefore, bortezomib- and carfilzomib-stimulated OAT1 expression and transport activity was mainly due to proteasome inhibition and the subsequent deceleration rate of OAT1 degradation.

After intravenous administration of the first 1.3-mg/m² dose to multiple myeloma patients, the mean maximum plasma concentration (Cmax) of bortezomib was 291 nM (112 ng/ml) (Reece et al., 2011). For carfilzomib, the mean Cmax values after a 2- to 10-minute intravenous infusion of a 27-mg/m² dose or a 30-minute infusion of a 5–6 m₉/m² dose were 5.9 (4232 ng/ml) and 2.9 mM (2079 ng/ml), respectively (https://www.accessdata.fda.gov/drugsatfda_docs/label/2018/202714s019lbl.pdf). The concentration of bortezomib (5–100 nM) and carfilzomib (0.1–1 µM) we selected in the cell model has a clinical relevance. Besides, the influence of other proteasome inhibitors, such as ixazomib (approved), marizomib, oprozomib, and delanzomib (in clinical trials), on the kidney OAT1 should be given attention. In this study, we reported the cellular mechanisms, and an in vivo study is currently underway in our laboratory to validate the roles of bortezomib or carfilzomib in OAT1 ubiquitination, expression, and renal clearance of drugs.

Fig. 7. Effect of bortezomib and carfilzomib on OAT1 expression. (A) Top panel: OAT1-expressing HEK293 cells were treated with bortezomib (25 nM) or carfilzomib (0.5 µM) for 12 hours. Cell surface biotinylation was performed. Biotinylated (cell surface) proteins were separated with using streptavidin-agarose resin and analyzed by IB with an anti-Myc antibody. Bottom panel: the same blot from the top panel was reprobed with an anti-E-Cadherin antibody. E-Cadherin is an integral membrane protein marker. (B) Densitometry plot of results from (A), top panel, as well as from other experiments. Values are means ± S.D. (n = 3). *P < 0.05. (C) Top panel: OAT1-expressing HEK293 cells were treated with bortezomib (25 nM) or carfilzomib (0.5 µM) for 12 hours. Cells were then lysed, followed by IB with anti-Myc antibody. Bottom panel: the same blot from the top panel was reprobed with an anti-GAPDH antibody. GAPDH is an internal protein marker. (D) Densitometry plot of results from (C), top panel, as well as from other experiments. Values are means ± S.D. (n = 3). *P < 0.05.

Fig. 8. Effect of bortezomib or carfilzomib on OAT1 stability. (A) OAT1-expressing HEK293 cells were biotinylated with membrane-impermeable biotinylation reagent sulfo-NHS-SS-biotin. Labeled cells were then treated with bortezomib (25 nM) at 37°C for 4, 8, and 12 hours, respectively. Treated cells were lysed, and cell surface proteins were isolated using streptavidin-agarose resin, followed by IB with anti-Myc antibody. (B) Densitometry plot of results from (A) as well as from other experiments. Values are means ± S.D. (n = 3). *P < 0.05. (C) OAT1-expressing HEK293 cells were biotinylated with membrane-impermeable biotinylation reagent sulfo-NHS-SS-biotin. Labeled cells were then treated with carfilzomib (0.5 µM) at 37°C for 4, 8, 12 hours, respectively. Treated cells were lysed, and cell surface proteins were isolated using streptavidin-agarose resin, followed by IB with anti-Myc antibody. (D) Densitometry plot of results from (C) as well as from other experiments. Values are means ± S.D. (n = 3). *P < 0.05; ns, not statistically significant.
Like proteasomes, several deubiquitinases may also regulate the OAT function. These deubiquitinases are associated with the 19S regulatory particles of proteasome (D’Arcy et al., 2015). Recently, it has been revealed that inhibition of proteasome-associated deubiquitinase activity is an alternative strategy to 20S proteasome inhibitors for cancer treatment (Chen et al., 2017; Mofers et al., 2017). Therefore, it is interesting to explore whether proteasome-associated deubiquitinase is a novel target for OAT1 regulation.

Our studies showing that proteasome inhibitors, e.g., bortezomib and carfilzomib, can stimulate the transport activity of OAT1 has physiologic implications. When drugs are overdose or endogenous/exogenous metabolites, uremia/environmental toxins are increased in blood, and we can use this method to accelerate their clearance to avoid systemic toxicity and maintain the body’s homeostasis. It can also be used to reverse the decreased expression under disease conditions.

In conclusion, our study demonstrated for the first time that ubiquitinated cell surface OAT1 degrades through proteasome instead of lysosome, and anticancer drugs bortezomib and carfilzomib have a novel role in regulating OAT1 expression and transport activity, indicating their potential influence on the OAT1-mediated renal excretion of drugs during cancer and comorbidity therapies.

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Authorship Contributions

Participated in research design: Fan, You.
Conducted experiments: Fan.
Performed data analysis: Fan, You.
Wrote or contributed to the writing of the manuscript: Fan, You.

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