Vinylboronic Acids as Efficient Bioorthogonal Reactants for Tetrazine Labeling in Living Cells

Selma Eising, Nicole G. A. van der Linden, Fleur Kleippenning, and Kimberly M. Bonger*

Department of Biomolecular Chemistry, Institute for Molecules and Materials, Radboud University, Heyendaalseweg 135, 6525 AJ Nijmegen, The Netherlands

Supporting Information

ABSTRACT: Bioorthogonal chemistry can be used for the selective modification of biomolecules without interfering with any other functionality present in the cell. The tetrazine ligation is very suitable as a bioorthogonal reaction because of its selectivity and high reaction rates with several alkenes and alkynes. Recently, we described vinylboronic acids (VBAs) as novel hydrophilic bioorthogonal moieties that react efficiently with dipyridyl-γ-tetrazines and used them for protein modification in cell lysate. It is not clear, however, whether VBAs are suitable for labeling experiments in living cells because of the possible coordination with, for example, vicinal carbohydrate diols. Here, we evaluated VBAs as bioorthogonal reactants for labeling of proteins in living cells using an irreversible inhibitor of the proteasome and compared the reactivity to that of an inhibitor containing norbornene, a widely used reactant for the tetrazine ligation. No large differences were observed between the VBA and norbornene probes in a two-step labeling approach with a cell-penetrable fluorescent tetrazine, indicating that the VBA gives little or no side reactions with diols and can be used efficiently for protein labeling in living cells.

In the last years, the development of reactions that are unaffected by any of the molecular functionalities in a biological system has emerged as a major field of research in chemical biology.1−4 These bioorthogonal reactions are used for tagging biomolecules with a high reaction rate by a two-step approach in vitro and in vivo, without the need to attach these tags directly onto the biomolecule. The reactants should be nontoxic to the cellular environment and should not influence the function of the labeled biomolecule of interest; therefore, a small hydrophilic reactant is often preferred. One of the most popular bioorthogonal reactions is the inverse electron-demand Diels−Alder (iEDDA) reaction between electron-poor tetrazines,5−8 and electron-rich or strained alkenes or alkynes, e.g., trans-cyclooctene,9,10 norbornene,11 or cyclopropene.12,13 Recently, we reported a new nonstrained bioorthogonal reactant, vinylboronic acid (VBA), which reacts, depending on its substituents, with second-order rate constants (k2) up to 27 M−1 s−1 with 3,6-dipyridyl-γ-tetrazines. These VBAs are 1 order of magnitude faster than the commonly used tetrazine reactant norbornene (Figure 1A).14 We further showed that the VBA moiety is biocompatible with cellular components, stable in cell lysate, and applicable for protein modification.

Over the past years, boronic acids have been used in living cells for various applications.15 The concept that phenylboronic acid moieties can form reversible complexes with 1,2- and 1,3-cis-diols in aqueous environments has been exploited in the development of chemosensors for carbohydrates (Figure 1C).16 The rate of this condensation reaction is dependent on the pKs of the phenylboronic acid, where electron-withdrawing substituents on the phenyl ring lower the pKs and thereby favor binding to the diols.17,18 Despite the potential condensation reaction with vicinal diols present in and on the cell, many boronic acid-containing compounds have been successfully used inside living cells such as protease inhibitors,19 sensors for reactive oxygen species,20 and reactants in bioconjugation reactions.21 It is not clear, however, if or to what extent the carbohydrate-rich cellular environment interferes with the cellular uptake and distribution of these boronic-acid containing compounds or with molecules containing our bioorthogonal VBA moiety.

To investigate the uptake and bioorthogonality of the VBA moiety in living cells, we chose a two-step labeling strategy of the proteasome using a VBA-modified irreversible inhibitor, followed by visualization using a dipyridyl-γ-tetrazine functionalized with a fluorophore (Figure 1B). The proteasome is a large multisubunit proteolytic complex that is mainly responsible for the degradation of proteins into small peptides by the ubiquitin-proteasome pathway.24−26 The proteolytic core contains seven distinct α and β subunits, whereas the β1, β2, and β5 subunit are responsible for the proteolytic activities of the proteasome. These proteolytic subunits act as N-terminal threonine proteases, where the nucleophilic hydroxyl attacks the peptide carbonyl causing cleavage of the peptide bond. Recent progression in the development of inhibitors of the proteasome or of only one of the proteolytic subunits is extensively reviewed.27−29 The two-step labeling strategy of the proteolytic proteasome subunits using irreversible inhibitors
followed by a bioorthogonal reaction with a fluorescent molecule has been previously performed using the copper-catalyzed alkyne–azide cycloaddition,\textsuperscript{30,31} strain-promoted alkyne–azide cycloaddition,\textsuperscript{32} the Staudinger ligation,\textsuperscript{30,33–36} and the tetrAzine ligation\textsuperscript{30} and thereby serves as a well-established model system for our studies.

The (6-aminohexanoyl)\textsubscript{3}-(leucinyl)\textsubscript{3}-vinyl-(methyl)-sulfone (Ahx\textsubscript{3}L3VS) moiety is found to give strong inhibition of the proteasome, without being selective for any of the three catalytic subunits.\textsuperscript{37} The three leucines are recognized by the proteasome and the vinylsulfone moiety reacts covalently and irreversibly with the γ-hydroxyl of the N-terminal threonine of the catalytic proteasome subunits. The long linker of the scaffold is built up by aminohexanoic acids that are beneficial for efficient binding to the proteasome\textsuperscript{37} and were thought to be an advantage for the two-step labeling of the proteasome as the bioorthogonal moiety could be placed far away from the active site. Here, we describe the synthesis and application of proteasome inhibitor VBA-Ahx\textsubscript{3}L3VS\textsubscript{7}, containing a protected vinylboronic acid moiety that hydrolyzes quickly in aqueous solution to the free boronic acid.\textsuperscript{14} We compared this compound to Nor-Ahx\textsubscript{3}L3VS\textsubscript{8}, which contains the commonly used bioorthogonal norbornene moiety.

The proteasome inhibitors were synthesized using modified literature procedures as depicted in Scheme 1 (SI — experimental section). In short, Boc-Leu-OH\textsubscript{1} was first reduced to its corresponding aldehyde\textsubscript{3} via Weinreb amide\textsubscript{2}. A stabilized Wittig reaction gave trans-VS\textsubscript{4} containing a small amount of cis-VS that was removed using column chromatography. Next, a double round of Boc-deprotection and coupling of Boc-Leu-OH yielded Boc-L3VS\textsubscript{5}. Finally, Boc-

**Scheme 1. Synthesis of Proteasome Inhibitors 7—9**

\textsuperscript{a}(i) N,O-dimethyl hydroxylamine, NMM, EDC, CH\textsubscript{2}Cl\textsubscript{2}, 5 h, 95%. (ii) LiAlH\textsubscript{4}, Et\textsubscript{2}O, 0 °C, 15 min, 81%. (iii) Diethyl(methylsulfonylmethyl)-phosphonate, NaH, THF, 0 °C, 1 h, 35%. (iv) (a) 4 M HCl in dioxane, CH\textsubscript{2}Cl\textsubscript{2}, 2 h, (b) Boc-Leu-OH, EDC, HOBt, Et\textsubscript{3}N, CH\textsubscript{2}Cl\textsubscript{2}, o/n, 94%. (v) Same as iv, yielding \textsuperscript{5} in 98%. (vi) (a) 4 M HCl in dioxane, CH\textsubscript{2}Cl\textsubscript{2}, 2 h, (b) Fmoc-Ahx\textsubscript{3}-OH, EDC, HOBt, Et\textsubscript{N}, CH\textsubscript{2}Cl\textsubscript{2}, o/n, 54%. (vii) (a) piperidine, DMF, 15 min. (b) VBA-NHS\textsubscript{12}, DIPEA, DMF, 1 h, yielding \textsuperscript{7} in 73%. (viii) same as vii, only (b) with norbornene-NHS, yielding endo/exo-8 in 94%. (ix) (a) DBU, DMF, 7 min, (b) BODIPY-FL NHS ester, HOBt, DIPEA, DMF, 1.5 h, yielding \textsuperscript{9} in 44%. (a) Ethyl chloroacetate, K\textsubscript{2}CO\textsubscript{3}, DMF, 16 h, 98%. (a) Trimethylsilylacetylene, Cul, PdCl\textsubscript{2}(PPh\textsubscript{3})\textsubscript{2}, DIPEA, toluene, 30 °C, 2 h, 88%. (a) Pinacolborane, Ru(CO)(CH(PPh\textsubscript{3})\textsubscript{2}, toluene, 50 °C, 16 h, 74%.
deprotection and then coupling of Fmoc-Ahx₃OH, yielded Fmoc-protected Ahx₃L₁₃VS 6.

Next, we prepared the NHS ester of VBA and norbornene to ensure efficient coupling to scaffold 6, after deprotection of the Fmoc. For VBA-NHS 12, we used the alkoxy-substituted phenylvinylboronic acid, as we previously found that this electron rich VBA gave the highest reaction rate with dipryridyl-s-tetrazine. First, etherification of 4-iodophenol using ethyl chloroacetate followed by a Sonagashira coupling yielded TMS-protected alkyne 10 in excellent yield. Deprotection of the TMS group and coupling of the acid with N-hydroxysuccinimide yielded alkyne-NHS 11. Final hydroboration of the alkyne with pinacolborane yielded NHS-boronic ester 12. Norbornene-NHS was prepared in one step from its corresponding alcohol in good yield. The VBA-NHS 12 and the norbornene-NHS were finally coupled to the free amine of Fmoc-deprotected 6, yielding VBA-Ahx₃L₁₃VS 7 and Nor-Ahx₃L₁₃VS 8 in good yields. In addition, the fluorescent BODIPY-Ahx₃L₁₃VS 9 was prepared by direct coupling of the commercially available BODIPY-FL NHS ester to deprotected 6.

Having VBA-Ahx₃L₁₃VS 7 and Nor-Ahx₃L₁₃VS 8 in hand, we initially evaluated the selectivity and potency of the inhibitors in cell lysate (Figure 2A,B). First, we established that a concentration of 0.3 μM of BODIPY-Ahx₃L₁₃VS 9 was essential for visualization of all proteasome subunits in cell lysate (Figure S1). Then, compounds 7 or 8 were incubated for 1 h at various concentrations in the protein lysate, after which BODIPY 9 was added to label all residual unbound proteasomal subunits (Figure 2B). Using this setup, we observed that low micromolar concentrations in the protein lysate, after which BODIPY 9 was added to label all residual unbound proteasomal subunits (Figure 2B). Using this setup, we observed that low micromolar concentrations of inhibitor 7 and 8 were essential for full inhibition of all subunits. In addition, we observed a slight selectivity of VBA 7 for β5 compared to the other subunits, whereas norbornene 8 was more selective for β2 as well as β5.

We continued to evaluate the inhibition of the proteasome with the Ahx₃L₁₃VS probes 7 and 8 in living cells. Here, performing a similar competition experiment as above, a 100X higher concentration of both 7 and 8 was essential to inhibit the proteasome subunits completely. Despite the moderate cell permeability of the probes this indicates that, similarly to the norbornene handle, the VBA moiety did not hamper membrane permeability of the inhibitor (Figure 2C). Elevated concentrations for complete proteasome inhibition and the observed reduced labeling of the β1 subunit in living cells was also observed with BODIPY 9 (Figure S2) and reported previously using a different Ahx₃L₃VS probe. Aside, significant cell death was visible when norbornene 8 was used at concentrations >100 μM, while VBA 7 did not show any toxicity up to 1 mM concentration.

Next, we investigated whether we could visualize the proteasome subunits with a two-step labeling strategy using VBA 7 or norbornene 8 followed by the tetrazine ligation with dipryridyl-s-tetrazine 13, containing a BODIPY-FL fluorophore, in cell lysate as well as in living cells (Figure 3A). After inhibition of the subunits using VBA 7 and norbornene 8 in cell lysate at concentrations that showed full subunit inhibition as established above (3 μM), about 3 μM of tetrazine 13 was necessary to give a complete reaction (Figure S3). In living cells, after inhibition of the proteasome with 300 μM VBA 7 and 100 μM norbornene 8, a comparable concentration of 10 μM tetrazine 13 was necessary to visualize the subunits (Figure 3B and C). To our delight, similar labeling intensities of the proteasome subunits were observed using the probes VBA 7 and norbornene 8 in lysate and in living cells, as evidenced by SDS-PAGE gel.

In addition, we evaluated the stability of the VBA and norbornene handles in living cells and the efficiency of the tetrazine ligation by monitoring the protein labeling over the course of time. After inhibition of the proteasome with VBA 7 and norbornene 8 (300 μM and 100 μM, respectively), the cells were lysed and the subsequent tetrazine ligation was performed with tetrazine 13 for various amounts of time. Complete labeling of the subunits was observed within 2–5 min, indicating that both functionalities were intact and the reaction was very efficient (Figure S4).

Finally, we used the same two-step labeling protocol to visualize the proteasome in living HeLa cells by confocal microscopy (Figure 3B and D). Again, similar intensities were observed using VBA 7 or norbornene 8 followed by addition of 3 μM of tetrazine-BODIPY 13, indicating successful labeling of the proteasome. For comparison, the labeling pattern of BODIPY 9 was measured, which was similar to that observed for 7 and 8, indicating that the VBA, norbornene, and BODIPY labels did not significantly influence the cellular distribution of the inhibitors (Figure S5). Performing the ligation with a higher concentration of tetrazine 13 using the same microscopy settings resulted in higher labeling intensities; however, in this...
In summary, we evaluated the use of the vinylboronic acid functionality for bioorthogonal labeling with tetrazines in living cells. The synthesized proteasome inhibitor containing a vinylboronic acid was successfully used for the two-step labeling of the proteasome in cell lysate and in living cells without showing diminished labeling efficiency with a dipyridyl-s-tetrazine compared to the proteasome inhibitor functionalized with a norbornene moiety. We have to emphasize that the potential condensation of the VBAs to vicinal diols would not be visible on SDS-PAGE gel or on confocal microscopy, as the boronic acid is released after the tetrazine ligation. However, if significant condensation would occur, a higher concentration of VBA-7 would be essential to fully inhibit the proteasome subunits. Our results show that three times more VBA-7 compared to norbornene-8 was needed for complete inhibition of all subunits in vitro as well as in living cells, indicating that the vinylboronic acid handle does not significantly hamper cellular uptake of the probes into the cell.

The number of bioorthogonal reactions that are suitable for labeling inside living cells is limited, because of the requirement of toxic reagents (e.g., copper(I)-catalyzed alkyn–azide cycloaddition) or possible side reactions of the reactants (e.g., the thiol–ene or thiol–yne side reactions of free intracellular cysteines with strained alkenes or alkynes). We have shown that the tetrazine ligation with vinylboronic acid is little or not affected by possible side reactions that can occur in the cell with biomolecules such as carbohydrates, making the reaction a valuable addition to the bioorthogonal toolbox.

**ASSOCIATED CONTENT**

Supporting Information

The Supporting Information is available free of charge on the ACS Publications website at DOI: 10.1021/acs.bioconjchem.7b00796.

Experimental details for the synthesis and proteasome inhibition in cell lysate and in living cells, full spectroscopic data for all new compounds, and additional figures (PDF)

**AUTHOR INFORMATION**

**Corresponding Author**

*E-mail: k.bonger@science.ru.nl.

**ORCID**

Kimberly M. Bonger: 0000-0001-9498-2620

**Notes**

The authors declare no competing financial interest.

**ACKNOWLEDGMENTS**

This work was financially support from The Netherlands Research Institute for Chemical Biology (NRSCB) and the Institute of Molecules and Materials (IMM) of the Radboud University in Nijmegen. We thank Prof. Dr. F.P.J. Rutjes for useful discussions and proofreading this manuscript.

**REFERENCES**


Communication