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# A Genetically Encoded Cyclobutene Probe for Labelling of Live Cells

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## Abstract

We have identified an aminoacyl-tRNA synthetase/tRNA pair for the efficient and site-specific incorporation of a cyclobutene-containing amino acid into proteins in response to amber nonsense codon. Fast and fluorescent labeling of purified proteins and intact proteins in live cells was demonstrated using the inverse electron demand Diels-Alder reaction with a tetrazine.

The increasing demand for bioorthogonal protein labelling has driven the search for new functional groups that can react with their partner reagents with fast reaction rate, high selectivity, and good biocompatibility.<sup>1–6</sup> The inverse electron demand Diels–Alder (IEDDA) reaction between a tetrazine and a strained alkene has been widely explored for bioorthogonal labelling of biomolecules.<sup>7–19</sup> The second-order rate constants for the rate-limiting [4+2] cycloaddition forming the first step of this reaction span nine orders of magnitude, depending on the nature of the two reactants and reaction conditions.<sup>1, 20–21</sup> The broad application of the tetrazine/alkene cycloaddition in biological systems stems from several unique features: (1) the reaction rate is often increased in the presence of water;<sup>8, 22</sup> (2) rapid cycloaddition does not require a metal catalyst; and (3) nitrogen gas is the only by-product.

Medium-sized strained alkenes, predominantly trans-cyclooctene and norbornene, have been extensively explored as IEDDA substrates.<sup>7–19</sup> In recent years, cyclopropene, a less bulky strained alkene, has also been successfully applied as a robust bioorthogonal probe.<sup>23–27</sup> Curiously, cyclobutenes, a class of small and strained alkenes known to be reactive towards IEDDA reactions,<sup>28–30</sup> have received much less attention, with most efforts involving derivatives of the Reppe anhydride, a bicyclic derivative of cyclooctatetraene.<sup>31</sup> Monocyclic cyclobutenes, such as those discussed here, have surprisingly good thermal stability,<sup>29–30</sup> and, in contrast to cyclopropenes,<sup>25</sup> have good chemical stability even in the absence of additional substituents on the alkene.<sup>29–30</sup> Preliminary work in one of our labs had demonstrated that the rate of IEDDA cycloaddition of a cyclobutene-containing fatty acid

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 $(3,6\text{-di}(\text{pyridin-2-yl})-1,2,4,5\text{-tetrazine}; k = 1.21\pm0.12 \text{ M}^{-1} \text{ s}^{-1})^{30}$  is faster than that observed with the majority of cyclopropenes<sup>24</sup> and comparable to the most reactive cyclopropenes ( $k = 2.78\pm0.37 \text{ M}^{-1} \text{ s}^{-1}$ ).<sup>25</sup> In this article, we report an efficient synthesis of a cyclobutene-containing unnatural amino acid (**CbK**; Scheme 2) that is applied as a chemical reporter for protein labelling in live cells. This amino acid was genetically incorporated into proteins in response to amber nonsense codon. While protein labelling through cysteine or lysine by alkylation or amide bond formation reactions are widely employed,<sup>32–33</sup> the selectivity of this approach is limited due to the possibility of containing more than one such residues in the protein of interest. In contrast, the unnatural amino acid mutagenesis approach allows for site-specific conjugation of proteins with a chemical probe.

Given the limited data reported for IEDDA reaction of cyclobutenes, the planned ligation was initially investigated using a previously reported cyclobutene (**1**, Scheme 1).<sup>29–30</sup> In contrast to the reaction of tetrazines with cyclopropenes or *N*-acylazetines,<sup>22</sup> we observed no skeletal rearrangement, instead isolating an approximately 1:1 mixture of inseparable 1,4-dihydro-1,2-diazene tautomers **2a** and **2b** (see ESI-1, Scheme 2 for mechanism). Measurement of kinetics under pseudo-first order conditions (see ESI) revealed bimolecular rate constants lower than those reported for *trans*-cyclooctene, considerably larger than reported for norbornenes or simple alkenes, and comparable to those recently described for cyclopropenes.<sup>1, 34–35</sup> Due to the presence of the tautomers, the cycloadduct(s) were fully characterized following oxidative aromatization to the 1,2-pyrazine (**3**).

In order to apply the cyclobutene-tetrazine reaction to protein labelling, a lysine-derived unnatural amino acid containing cyclobutene moiety (**CbK**; Scheme 2) was synthesized from 3-(2-cyclobutene-1-yl)propanoic acid (**7**) which was prepared by a variant of a route previously described for cyclobuteneoctanoic acid  $1.^{29}$  Benzyl ether **4**, available from protection of 4-penten-1-ol, underwent [2+2] cycloaddition with dichloroketene; in situ reduction of the intermediate dichloroketone furnished a stable dichlorocyclobutanol (**5**). Conversion to the corresponding methanesulfonate was followed by a dissolving metal reduction, which achieved both introduction of the cyclobutene and deprotection of the benzyl ether. The volatile cyclobutenyl propanol (**6**) was not easily isolated and was instead generally carried on to acid **7**. The corresponding acid chloride reacted with N<sub>α</sub>-protected lysine to furnish modified amino acid CbK.

To site-specifically encode CbK into proteins, a mutant library of *Methanosarcina barkeri* pyrrolysyl-tRNA synthetase (PylRS) was generated. According to the crystal structures of PylRS,<sup>36–38</sup> four amino acid residues involved in recognition of pyrrolysine (Leu270, Tyr271, Leu274, and Cys313) were randomized using site-saturation mutagenesis. In addition, a Tyr349Phe mutation was introduced to all PlyRS mutants by site-directed mutagenesis, since this mutation was previously shown to increase aminoacylation efficiency.<sup>27</sup> After one round of negative and one round of positive selection using the previously reported method,<sup>39</sup> a PylRS mutant able to incorporate CbK into proteins was identified. This mutant (designated as CbKRS) has the following two mutations, Leu274Met and Cys313Ala.

To further determine the efficiency and fidelity of CbK incorporation by the evolved CbKRS mutant, a fluorescence-based assay was conducted using a GFP mutant (sfGFP-N149TAG) that contains an amber nonsense codon at position Asn149.<sup>40</sup> Protein expression was carried out in LB medium supplemented with and without 1 mM CbK. Fluorescence analysis of *E. coli* cultures showed that full-length sfGFP protein was produced only in the presence of CbK (Fig. 2). In a large-scale expression of sfGFP-N149TAG (50 ml cell culture), 35 mg/L of sfGFP-N149CbK was obtained after purification using affinity chromatography (Fig. 5 of ESI-1). Mass spectrometry analyses of the in-gel digested protein fragment (LEYNFNSH-CbK-VYITADK; Fig. 6 of ESI-1) confirmed site specific incorporation of CbK at position 149 of sfGFP (expected, 684.40 Da, z = 3 and 1026.10 Da, z = 2; observed 684.35 Da, z = 3 and 1026.02 Da, z = 2).

With the purified sfGFP-N149CbK in hand, we explored the inverse Diels-Alder reaction between the recombinant sfGFP-N149CbK and a commonly used tetrazine scaffold<sup>40-41</sup> containing a fluorescein conjugate (Fl-Tet; Fig. 1). In a typical reaction, 1 µL of Fl-Tet in DMSO (varied stock concentrations to reach the indicated final concentrations in Fig. 3) was added to 9  $\mu$ L of protein (final concentration, 0.24 mg/mL) in PBS buffer. The reaction mixture was incubated at room temperature with gentle agitation on a platform rocker. The reaction was stopped by the addition of a large excess of 5-norbonene-2-methanol (1  $\mu$ L; 100 mM) in DMSO. The quenched reaction was subsequently mixed with SDS-PAGE loading buffer and heated at 95 °C for 15 minutes to denature the protein. Therefore, only the fluorescein-labelled sfGFP protein was expected to be fluorescent under UV irradiation. We first examined the labelling of the sfGFP-N149CbK mutant with varied concentrations of Fl-Tet in PBS buffer following an 80 min reaction. As shown in Fig. 3A, fluorescence could be detected at a FI-Tet concentration of 10 µM or above. The best result was obtained when 100 µM of Fl-Tet was used (Fig. 3A). Control experiments using wild-type sfGFP (sfGFP-wt) and Fl-Tet, or sfGFP-N149CbK only did not show detectable fluorescence (Fig. 3A). These results demonstrate that the unnatural cyclobutene moiety of CbK is biocompatible and orthogonal to functional groups in natural amino acids. Next, we conducted a time dependence labelling study using 50 µM of Fl-Tet. Significant fluorescence was detected from a 5 min reaction (Fig. 3B), indicating that the reaction is very fast as evidenced by our kinetic study. The fluorescence intensity increased gradually in a time-dependent manner. No fluorescence was observed in control experiments when either sfGFP-wt was used or Fl-Tet was omitted. We also conducted mass spectrometry analysis of the product from the 80 min reaction. Expected masses were observed (Fig. 8 of ESI-1; a hydrolysis of thiourea to urea linkage of the labelling reagent, Fl-Tet, was observed). Taken together, the results demonstrate that the cyclobutene/tetrazine IEDDA bioconjugation reaction can be used to efficiently and selectively label a purified protein.

We have also demonstrated the labeling of an outer membrane protein OmpX in live *E. coli* cells. Plasmid pOmpX-TAG was constructed to encode an OmpX mutant containing a seven amino acid insertion (Ala-Ala-Ala-Ala-Ala-Ala-Ala; X denotes an amber mutation) between the two extracellular residues Ser76 and Ser77.<sup>41</sup> The protein expression was conducted in *E. coli* in the presence of CbKRS, the amber suppressor tRNA (tRNA<sup>Pyl</sup>), and 1 mM of CbK. Cells containing the mutant OmpX protein (OmpX-CbK) were collected, washed three times, and resuspended in PBS buffer. The labeling experiment was initiated with the

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addition of Fl-Tet (2  $\mu$ L; 5 mM) to 100  $\mu$ L of cell suspension to a final concentration of 100  $\mu$ M. The reaction mixture was incubated for 1 hour at room temperature with gentle agitation on a platform rocker. Cells were then collected, washed three times with PBS buffer, and imaged under a microscope. As shown in Fig. 4A, labeling of cells containing the mutant protein resulted in strong fluorescent signals which co-localized nicely with cells. As a control, when *E. coli* cells expressing wild-type OmpX protein in the presence of CbK was used in the labeling experiment under the same conditions, no detectable fluorescence was observed. This confirmed that the observed fluorescence in Fig. 4A resulted from labelled OmpX-CbK protein and not from free CbK. This above data suggested the bioorthogonal reaction between cyclobutene and tetrazine is applicable in live cell labeling. While the present work only demonstrated protein labeling in bacteria, the CbKRS-tRNA<sup>Pyl</sup> pair should support the incorporation of CbK into proteins for labeling experiments in mammalian cells. It is known that the PylRS-derived system can be used to incorporate unnatural amino acids in bacterial, yeast, and mammalian cells.<sup>42-44</sup>

In summary, we have synthesized CbK, a cyclobutene-derived unnatural amino acid, and identified a PylRS mutant (CbKRS) for the site-specific incorporation of CbK into proteins in response to amber nonsense codon in *E. coli*. The bioorthogonal reaction between the strained cyclobutene and a tetrazine achieves efficient protein labeling both in vitro and in vivo. Cyclobutenes offer an excellent structural scaffold in terms of stability and limited size; their addition to the family of reactive IEDDA dienophiles should augment current efforts to expand the chemical toolbox for the study of biological systems.

## **Supplementary Material**

Refer to Web version on PubMed Central for supplementary material.

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## Fig. 1.

Fluorescent protein labelling with a genetically encoded unnatural amino acid containing a cyclobutene moiety.



## Fig. 2.

Genetic incorporation of CbK. (A) Crystal structure of the PyIRS in complex with pyrrolysyl-AMP. The structure is derived from PDB 2ZIM; (B) Fluorescence readings of cells expressing CbKRS and sfGFP-Asn149TAG mutant. The expressions were conducted either in the presence or in the absence of 1.0 mM CbK. Fluorescence intensity was normalized to cell growth.



#### Fig. 3.

In vitro protein labelling of sfGFP variants with cyclobutene-tetrazine reaction. Following labeling reactions, protein samples were denatured by heating, then analyzed by SDS-PAGE. The top panel in each figure shows Coomassie blue stained gel and the bottom panel shows the fluorescent image of the same gel before Coomassie blue treatment. (A) Labeling of sfGFP-N149CbK protein with varied concentrations of Fl-Tet for 80 minutes; (B) Reaction progress of sfGFP-N149CbK protein labeling with 50  $\mu$ M of Fl-Tet. Wild-type sfGFP was included in both experiments as the control. The fluorescence intensities of these images were quantified and presented in Fig. 7 of ESI. The  $k_{obs}$  was estimated as 0.37 M<sup>-1</sup> s<sup>-1</sup>.



## Fig. 4.

Selective labeling of *E. coli* cells expressing OmpX-CbK. (A) OmpX-F28CbK mutant that was expressed in the presence of CbK; (B) Wild-type OmpX that was expressed in the presence of CbK. For all images, the left panel shows fluorescent images of *E. coli*, the middle panel shows bright-field images of the same *E. coli* cells, and the right panel shows composite images of bright-field and fluorescent images. Scale bars, 5 µm.





Model of cyclobutene/tetrazine cycloaddition



## Scheme 2.

Synthesis of unnatural amino acid CbK containing short chain cyclobutene moiety.