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Second generation specific-enzyme-activated rotaxane propeptides[†]

Antony Fernandes, \ddagger^{ab} Aurélien Viterisi, \ddagger^{a} Vincent Aucagne, $*^{c}$ David A. Leigh $*^{a}$ and Sébastien Papot $*^{b}$

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A [2]rotaxane, in which the peptidic axle is protected from degradation by the macrocyclic sheath and terminated with a novel glycosidase-cleavable stopper, is rendered water-soluble by derivatisation with tetra(ethylene glycol) (TetEG) or glucosylated tetra(ethylene glycol) (Glc-TetEG) chains using the CuAAC 'click' reaction. The Glc-TetEG-derivatised rotaxane propeptide is > 50 000 times more soluble in aqueous media than the parent rotaxane. Activation of the water-soluble rotaxane propeptide with a β -galactosidase efficiently releases the parent peptide.

The design of enzyme-responsive rotaxanes is an emerging area of activity with potential biological applications.^{1–5} Biodegradable polyrotaxanes have been studied as selective drug and gene delivery systems¹ and enzymatically-triggered 'nanovalves' have been demonstrated to regulate the release of guest molecules stored in mesoporous silica.² Recently, we prepared a [2]rotaxane propeptide that protects a pentapeptide thread from degradation from general peptidases whilst allowing the release of the free peptide in a controlled fashion through treatment with a specific glycosidase.³ Since many bioactive peptides suffer from in vivo instability and poor bioavailability, this approach offers some promise for peptidebased therapies. However, the first generation rotaxane propeptide exhibited poor aqueous solubility and had no convenient functional group 'handles' through which the rotaxane could be subsequently derivatised to improve its properties. Here we report on a second generation rotaxane propeptide, 1, composed of a galactosyl trigger, a novel self-immolative stopper⁶ and a triglycyl peptide thread encapsulated by a macrocycle⁷ bearing two azide groups (Schemes 1 and 2). The azide groups are suitable for introducing hydrophilic (or other) moieties after rotaxane formation via copper(1)-catalysed azidealkyne 1,3-cycloaddition (CuAAC) 'click' reactions (e.g. 2 and 3).8

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‡ These authors contributed equally to this work.

While the first generation rotaxane propeptide system³ was limited to peptide axles with bulky N-terminal residues,⁹ here we demonstrate that a *bis-meta*-substituted *para*-hydroxybenzyl carbamate stopper can be used as a rotaxane stopper for peptides with an N-terminal amino acid as small as glycine. The proposed release mechanism of propeptides **2** and **3** in the presence of the activating enzyme is shown in Scheme 1. Hydrolysis of the glycosidic bond by β -galactosidase triggers a sequence of reactions that decompose the stopper, and thus the rotaxane architecture, releasing the free peptide **6**.

The synthesis of rotaxane 1 was carried out in seven steps from commercially available 4-hydroxy-3-nitrobenzaldehyde (Scheme 2). Alkylation with allyl bromide (K₂CO₃, MeCN, 96%) afforded ether 11, which underwent a Claisen rearrangement at 160 °C to produce the bis-ortho-substituted phenol 12 in 57% yield. Stereoselective glycosylation of 12 with acetobromo-D-galactose (Ag₂O, MeCN, 79%) gave β-galactoside 13. Reduction of the aldehyde and subsequent treatment with *p*-nitrophenylchloroformate afforded the activated carbonate 15 (96%), which was then coupled with tripeptide 6 to furnish the propeptide thread 16 (85%). Treatment of thread 16 with p-xylylenediamine, 5-azido-isophthaloyl dichloride and Et₃N in CHCl₃ gave the corresponding $glyco[2]rotaxane^{3,10}$ 1 in 63% yield.¹¹ Rotaxane 1 appears to be indefinitely stable in solution, indicating that the second generation self-immolative stopper is sufficiently bulky to avoid dethreading even with an N-terminal glycine residue on the axle.

Comparison of the ¹H NMR spectra of **1** and **16** confirmed the interlocked structure of **1** (Fig. 1). Several of the resonances of the stoppered tripeptide (H₁₄, H₁₆, H₁₈, H₂₀ and H₂₁) are significantly shifted to higher field in the rotaxane as a result of the shielding effect of the aromatic rings of the macrocycle. The large shifts (0.4–0.8 ppm) of glycine protons H₁₄, H₁₆ and H₁₈ indicate that the glycyl residues are located in the cavity of the macrocycle in the predominant co-conformations of **1** in CDCl₃. Higher field shifts of the self-immolative stopper protons H₇, H₈ and H₁₂ also occur while no changes are observed for the carbohydrate protons (H_{1–6}). This suggests that the macrocycle is able to shuttle along the peptide axle up to the self-immolative stopper unit but not onto the carbohydrate residue.

Bis-azido-glyco[2]rotaxane **1** was then functionalised with TetEG and $Glc(Ac)_4$ -TetEG alkynes **17** and **18** using the CuAAC reaction (Scheme 3).¹² The carbohydrate units of rotaxanes **19** and **20** were subsequently deprotected (MeONa, MeOH) to afford propeptides **2** and **3**, respectively (Scheme 3).

^a School of Chemistry, University of Edinburgh, The King's Buildings, West Mains Road, Edinburgh, EH9 3JJ, UK.

E-mail: david.leigh@ed.ac.uk; Web: http://www.catenane.net; Fax: (+44) 131-650-6453

^b Université de Poitiers, UMR-CNRS 6514, Laboratoire de Synthèse et Réactivité des Substances Naturelles, 4 rue Michel Brunet, BP 633, 86022 Poitiers, France.

E-mail: sebastien.papot@univ-poitiers.fr

^c Centre de Biophysique Moléculaire, UPR 4301 CNRS, Rue Charles Sadron, 45071 Orléans, Cedex 2, France. E-mail: aucagne@cnrs-orleans.fr



Scheme 1 β -Galactosidase-triggered release of triglycyl peptide 6 from the functionalised [2]rotaxane propeptides 2 and 3.

To assess the effect of the hydrophilic side chains on the properties of rotaxanes 2 and 3, aqueous solubility measurements were carried out. Propeptide thread 21 and rotaxane 22 were synthesised as references for these experiments (Scheme 4). Rotaxane 22 proved to be almost insoluble in water $(3.8 \times 10^{-7} \text{ mol L}^{-1})$ whilst propeptide thread 21 was modestly soluble $(8.6 \times 10^{-4} \text{ mol L}^{-1})$. Derivatisation of 1 in the form of rotaxane 2 bearing two TetEG substituents gave a 15-fold increase in aqueous solubility $(6.0 \times 10^{-6} \text{ mol L}^{-1})$. Introduction of the Glc-TetEG side chains (rotaxane 3) afforded excellent aqueous solubility of $2.2 \times 10^{-2} \text{ mol L}^{-1}$; $50\,000 \times$ more soluble than the model rotaxane (22) and $\sim 25 \times$ higher than that of the parent thread (21).

In order to confirm that the water soluble rotaxane **3** can operate as a triggered-release propeptide system, enzymatic activation of **3** was carried out with *E. coli* β -galactosidase in phosphate buffer (0.02 M, pH 7.0) at 37 °C and monitored by HPLC (Fig. 2).

Under these conditions, rotaxane 3 was degraded over 10 h, the disappearance of 3 being accompanied by the appearance of peptide 6 and macrocycle 10 in the HPLC trace (Fig. 2b and c). The benzylic alcohol 8, formed by hydrolysis of the quinone



Scheme 2 Synthesis of *bis*-azido-glyco[2]rotaxane 1.



Fig. 1 ¹H NMR spectra (400 MHz, 298 K, CDCl₃) of (a) thread **16** and (b) [2]rotaxane **1**. The assignments and colours of the signals correspond to that shown in Scheme 2. Residual solvent peaks are shown in gray.

methide intermediate 7 (Scheme 1), was also detected in the reaction mixture (Fig. 2b and c). The results are consistent with the enzyme-catalysed disassembly of rotaxane 3 proceeding through the self-immolative mechanism shown in Scheme 1.

In summary, we have demonstrated that the aqueous solubility of a rotaxane propeptide can be greatly improved (>50000×) *via* post-functionalisation of a *bis*-azido-glyco[2]rotaxane using



Scheme 3 CuAAC post-functionalisation of rotaxane 1.



Scheme 4 Propeptide thread 21 and rotaxane 22.



Fig. 2 (a) Superimposed HPLC traces ($\lambda = 220$ nm, reverse phase C-18 column) of individual components **3**, **6**, **8** and **10**. (b) and (c) HPLC traces of the enzymatic hydrolysis of rotaxane propeptide **3** with *E. coli* β -galactosidase in phosphate buffer (0.02 M, pH 7.0) at 37 °C using 1000 U/µmol of substrate after (b) 2 h and (c) 10 h (Scheme 1).

the CuAAC reaction. Both the novel self-immolative stopper and the *bis*-azido rotaxane ring employed in this system may prove useful for accessing a wide range of propeptides decorated for specific biological applications. This work was supported by the Science and Technology Department of the French Embassy in the United Kingdom, the Scottish Executive, the Royal Society of Edinburgh and the Engineering and Physical Sciences Research Council (EPSRC).

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