

Since January 2020 Elsevier has created a COVID-19 resource centre with free information in English and Mandarin on the novel coronavirus COVID-19. The COVID-19 resource centre is hosted on Elsevier Connect, the company's public news and information website.

Elsevier hereby grants permission to make all its COVID-19-related research that is available on the COVID-19 resource centre - including this research content - immediately available in PubMed Central and other publicly funded repositories, such as the WHO COVID database with rights for unrestricted research re-use and analyses in any form or by any means with acknowledgement of the original source. These permissions are granted for free by Elsevier for as long as the COVID-19 resource centre remains active.

Available online at www.sciencedirect.com

Bioorganic & Medicinal Chemistry Letters

Bioorganic & Medicinal Chemistry Letters 17 (2007) 5155–5158

Optimized synthesis of aminooxy-peptides as glycoprobe precursors for surface-based sugar–protein interaction studies

Carmen Jiménez-Castells,^a Beatriz G. de la Torre,^a Ricardo Gutiérrez Gallego^{a,b} and David Andreu^{a,*}

^a Department of Experimental and Health Sciences, Pompeu Fabra University, Barcelona Biomedical Research Park, Dr. Aiguader 88, 08003 Barcelona, Spain
Pharmacology Research Unit, Municipal Institute of Medical Research, Barcelona Biomedical Research Park, ^b

Dr. Aiguader 88, 08003 Barcelona, Spain

Received 12 June 2007; revised 27 June 2007; accepted 28 June 2007 Available online 5 July 2007

Abstract—An improved procedure for solid phase coupling of Boc-aminooxyacetic acid to peptides is described. By avoiding basecontaining activation mixtures which cause over-acylation, it practically suppresses this unwanted side reaction and leads to near quantitative yields of Aoa-peptides, useful as glycoprobe precursors in glycomic studies. - 2007 Elsevier Ltd. All rights reserved.

With the ever-increasing awareness of the importance of protein glycosylation as a key player in inter- and intracellular communication, $1-4$ the need for powerful chemical tools to document sugar–protein cross-talk is rising. One reason for such interest in carbohydrate–protein interactions is their implication in the targeting of enveloped viruses such as HIV, influenza-, and coronavirus,5,6 an understanding of which will facilitate the design of carbohydrate-binding agents capable of neutralizing viral fusion and transmission. Different biophysical techniques have been used to monitor sugar–protein interactions,^{7,8} including NMR, X-ray crystallography, and more recently, surface plasmon resonance (SPR). The latter is fast gaining recognition because of its sensitivity, low sample consumption, and capability for real-time monitoring. In this technique, one of the two interacting entities (protein or sugar) is immobilized onto the surface of a sensor chip, the other one is flown across and the resulting read-out enables both quantitation and kinetic analysis of the interaction

Among the two immobilization approaches possible, the sugar-on-chip option has demonstrable advantages^{9,10} but requires a sugar in highly purified form and attached to the chip surface in a chemically well-defined manner. While the synthesis of complex carbohydrate structures is a fast expanding field, $11-15$ the structural diversity encountered in nature cannot yet be fully met in the laboratory. Thus, some glycans (e.g., bacterial polysaccharide repeating units, elongated mucin-type glycans or complex N-glycans) cannot be efficiently produced for lack of suitable synthetic chemistries or glycosyltransferases/glycosidases, 16 and must be purified from natural sources. As the amount of material available is scarce, the immobilization chemistry to the sensor chip surface must be optimal to avoid losses of precious material. Although a direct aldehyde coupling has been described, 17 its efficiency is questionable.

Recently, we reported a practically universal approach to carbohydrate immobilization on carboxymethyl dextran chips via standard peptide-bond chemistry, subsequent to chemical ligation of the sugar to a tailor-made peptide module.¹⁸ A chemospecific oxime linkage between the reducing end of the first monosaccharide and the peptide is achieved (Scheme 1) through the introduction of an Nterminal aminooxyacetic acid (Aoa) residue in the latter.

Over the last decade, oxime chemistry has been proven as one of the most successful approaches to peptide

Abbreviations: Boc, tert-butyloxycarbonyl; DIEA, N,N-diisopropylethylamine; DIC, N,N-diisopropylcarbodiimide; Fmoc, 9-fluorenylmethoxycarbonyl; HBTU, 2-(1H-benzotriazole-1-yl)-1,1,3,3-tetramethyluronium hexafluorophosphate; TFA, trifluoroacetic acid; TIS, triisopropylsilane. Keywords: Glycoprobes; Surface-based interaction studies; Aminooxypeptide; Coupling reagent.

^{*} Corresponding author. Fax:+34 933160901; e-mail: [david.andreu@](mailto:david.andreu@upf.edu) [upf.edu](mailto:david.andreu@upf.edu)

⁰⁹⁶⁰⁻⁸⁹⁴X/\$ - see front matter © 2007 Elsevier Ltd. All rights reserved. doi:10.1016/j.bmcl.2007.06.090

Scheme 1. Illustration of oxime ligation between an N-terminal Aoa-containing peptide and a carbohydrate ligand. See Ref. 18 for further details.

chemical ligation.^{19,20} Moreover, applications to sugar– peptide conjugation have also been described.^{21,22} Despite the obvious advantages of this chemistry, $2³$ it has as a main drawback that over-acylation of the NH–O nitrogen leads to undesired heterogeneity.²⁴ To resolve this problem, deprotection of Ao a^{25} or use of N-trityl protection²⁶ has been advocated; however, neither of these two approaches utilizes commercially available reagents.

and conventional coupling chemistry. Our study is based on two starting peptide substrates, the hexapeptide GFAKKG-amide¹⁸ (A) and a version N-terminally elongated with an e-amino hexanoic acid (Ahx) spacer, Ahx-GFAKKG-amide²⁷ (B), both acylated with Boc-Aoa-OH²⁸ under different conditions (Fig. 1, Table 1).

In line with previous work, 24 we reasoned that the presence of base at the coupling step would favor over-acylation. Indeed, as shown on panels A(i) and B(i), otherwise efficient HBTU-mediated coupling conditions

In this work, we have explored the feasibility of minimizing Aoa over-acylation using Boc-protected Aoa

Figure 1. HPLC analysis of different conditions for Aoa-GFAKKG-amide [entries A(i–iii)] and Aoa-Ahx-GFAKKG-amide [entries B(i–iii)] synthesis. (i) Boc-Aoa-OH/HBTU/DIEA (3:3:6 equiv), 40 min; (ii) Boc-Aoa-OH/DIC (10:10 equiv), 60 min; (iii) Boc-Aoa-OH/DIC (8:8 equiv), 10 min. Peak assignations: a: target Aoa-peptides; b: starting peptide; c: diacylated peptide; d: triacylated peptide; e: N-terminal guanidine byproduct (uronium capping); f: oligomeric impurities. HPLC conditions: Phenomenex Luna C8 column; elution with linear 0–30% [panels A(1–iii)] and 0–40% [panels B(1–iii)] gradient of acetonitrile (+0.036% TFA) into water (+0.045% TFA) over 15 min; flow rate: 1 mL/min.

Substrate	Entry	Boc-Aoa-OH (equiv)	Coupling agent (equiv)	DIEA (equiv)	Time (min)	Product distribution					
						a	h.	c.	_d	e	
A		$3 + 1.5$	$HBTU (3 + 1.5)$	6	40	45	4		13	9	
A	 11	10	DIC(10)		60	93					
A	\cdots 111	8	DIC(8)		10	97	θ				
B		$3 + 1.5$	$HBTU (3 + 1.5)$	6	40	63					
В	 11	10	DIC(10)		60	80	16				
B	iii		DIC(8)		10	94					

Table 1. Acylation of substrates A and B with Boc-Aoa-OH using different coupling conditions

% Estimated by integration of HPLC peaks at 220 nm.

in this particular case generated a rather complex product mixture which, after TFA cleavage/deprotection,²⁹ was shown by MALDI-TOF mass spectrometric analysis to contain the target Aoa-peptide (peak a, Fig. 1) accompanied by the di- and tri-acylated byproducts (peaks c and d, Fig. 1), plus the product of N-terminal guanidine capping, 30 plus other peaks assumed to be higher-order oligomers.

In contrast, couplings relying on carbodiimide (DIC) activation were considerably cleaner (Fig. 1, panels A(ii, iii) and B(ii, iii)). Thus, substantial improvements in the yield of target Aoa-peptides (45% to 93% and 63% to 80%) for **A** and **B**, respectively, panels A(ii) and B(ii)) were observed when 10 equivalent of both Boc-Aoa-OH and DIC was used for 60 min. Interestingly, a shorter reaction time and a slight reduction in the excess of acylating agent led to even better results, amounting to practically quantitative conversion of both substances into the Aoa-derivatives (Table 1).

In conclusion, carbodiimide-based Boc-Aoa coupling, in conjunction with short reaction times, appears to provide a straightforward, efficient way to the Aoa-functionalized peptides required to prepare well-defined, lectin-capturing glycoprobes, by subsequent chemoselective oxime ligation. Using the optimized procedure described above, the Aoa-peptide (in any of its A or B versions) does not require any HPLC purification (see Supplementary Information pages) before the oxime ligation reaction, thus considerably contributing to an efficient preparation of sugar-functionalized sensor surfaces.

Acknowledgments

This work was supported by funds from the Spanish Ministry of Education and Science (Grant BIO2005- 07592-C02-02 to D.A. and predoctoral fellowship BES-2006-12879 to C.J.C.) and from Generalitat de Catalunya (SGR 00494).

Supplementary data

Supplementary data associated with this article can be found, in the online version, at [doi:10.1016/j.bmcl.](http://dx.doi.org/10.1016/j.bmcl.2007.06.090) [2007.06.090.](http://dx.doi.org/10.1016/j.bmcl.2007.06.090)

References and notes

- 1. Taniguchi, N.; Miyoshi, E.; Gu, J.; Honke, K.; Matsumoto, A. Curr. Opin. Struct. Biol. 2006, 16, 561.
- 2. Mitoma, J.; Bao, X.; Petryanik, B.; Shaerli, P.; Gaughet, J. M.; Yu, S. Y.; Kawashima, H.; Saito, H.; Ohtsubo, K.; Marth, J. D.; Khoo, K. H.; Von Adrian, U. H.; Lowe, J. B.; Fukuda, M. Nat. Immunol. 2007, 8, 409.
- 3. Scanlan, C. N.; Offer, J.; Zitzmann, N.; Dwek, R. A. Nature 2007, 446, 1038.
- 4. Varki, A. Nature 2007, 446, 1046.
- 5. Balzarini, J. Antiviral Res. 2006, 71, 237.
- 6. Balzarini, J. Antiviral Chem. Chemother. 2007, 18, 1.
- 7. Takahashi, K.; Hiki, Y.; Odani, H.; Shimozato, S.; Iwaze, H.; Sugiyama, S.; Usuda, N. Biochem. Biophys. Res. Commun. 2006, 350, 580.
- 8. Hashimoto, H. Cell. Mol. Life Sci. 2006, 63, 2954.
- 9. Haseley, S. R.; Kamerling, J. P.; Vliegenhart, J. F. G. Top. Curr. Chem. 2002, 218, 93.
- 10. Duverger, E.; Frison, N.; Roche, A.; Monsigny, M. Biochimie 2003, 85, 167.
- 11. Hölemann, A.; Seeberger, P. H. Curr. Opin. Biotechnol. 2004, 15, 615.
- 12. Seeberger, P. H.; Werz, D. B. Nature 2007, 446, 1046.
- 13. Werz, D. B.; Seeberger, P. H. Chem. Eur. J. 2005, 11, 3194.
- 14. Hanson, S. R.; Hsu, T. L.; Weerapana, E.; Kishikawa, K.; Simon, G. M.; Cravatt, B. F.; Wong, C. H. J. Am. Chem. Soc. 2007, 129, 7266.
- 15. Bond, M. R.; Kohler, J. J. Curr. Opin. Chem. Biol. 2007, 11, 52.
- 16. Yu, H.; Chokhawala, H. A.; Huang, S.; Cheng, X. Nat. Protoc 2006, 1, 2485.
- 17. Satoh, A.; Matsumoto, I. Anal. Biochem. 1999, 275, 268.
- 18. Vila-Perelló, M.; Gutiérrez Gallego, R.; Andreu, D. ChemBioChem 2005, 6, 1831.
- 19. Canne, L. E.; Ferré-D'Amaré, A. R.; Burley, S. K.; Kent, S. B. H. J. Am. Chem. Soc. 1995, 117, 2998.
- 20. Rose, K. J. Am. Chem. Soc. 1994, 116, 30.
- 21. Zhao, Y.; Kent, S. B. H.; Chait, B. T. Proc. Natl. Acad. Sci. U.S.A. 1997, 94, 1629.
- 22. Peri, F.; Dumy, P.; Mutter, M. Tetrahedron 1998, 54, 12269.
- 23. Peri, F.; Nicotra, F. Chem. Commun. 2004, 6, 623.
- 24. Decostaire, I. P.; Lelièvre, D.; Zhang, H.; Delmas, A. F. Tetrahedron Lett. 2006, 47, 7057.
- 25. Brask, J.; Jensen, K. J. J. Peptide Sci. 2000, 6, 290.
- 26. Wahl, F.; Mutter, M. Tetrahedron Lett. 1996, 3, 6861.
- 27. Both peptides were synthesized by Fmoc-based solid phase synthesis on a Rink MBHA resin $(0.70 \text{ mmol g}^{-1})$ using Fmoc chemistry at 0.1 mmol scale. An aliquot of each peptide–resin was deprotected and cleaved prior to the study, to ensure the sequence was satisfactorily assembled.

In both cases, a highly homogeneous product (>95% by HPLC, m/z 606 and m/z 719, corresponding to the $[M + H]$ ⁺ ion of **A** and **B**, respectively) was obtained.

- 28. From Novabiochem (Läufelfingen, Switzerland).
- 29. Peptide–resin was treated with 95% TFA, 2.5% TIS, 2.5% H2O for 90 min at rt. After filtering off the resin, the

cleavage solution was diluted with chilled tert-butyl methyl ether to precipitate the peptide, which was separated by centrifugation, solubilized in water, and lyophilized.

30. Gausepohl, H.; Kraft, M.; Frank, R. W. Int. J. Pept. Protein Res. 1989, 34, 287.