

Available online at www.sciencedirect.com



Protein Expression and Purification 27 (2003) 109-114

Protein Expression Purification

www.elsevier.com/locate/yprep

Inhibition of tobacco etch virus protease activity by detergents

Arun K. Mohanty, Chad R. Simmons, and Michael C. Wiener*

Department of Molecular Physiology and Biological Physics, University of Virginia, Charlottesville, VA 22908-0736, USA

Received 3 June 2002, and in revised form 22 August 2002

Abstract

Affinity tags such as polyhistidine greatly facilitate recombinant protein production. The solubility of integral membrane proteins is maintained by the formation of protein–detergent complexes (PDCs), with detergent present at concentration above its critical micelle concentration (CMC). Removal of the affinity tag necessitates inclusion of an engineered protease cleavage site. A commonly utilized protease for tag removal is tobacco etch virus (TEV) protease. TEV is available in a recombinant form (rTEV) and frequently contains its own polyhistidine affinity tag for removal after use in enzymatic digestion. Proteolytic cleavage of the tagged domain is carried out by incubation of the protein with rTEV protease. We have observed that the efficiency of rTEV digestion decreases significantly in the presence of a variety of detergents utilized in purification, crystallization, and other biochemical studies of integral membrane proteins. This reduction in protease activity is suggestive of detergent-induced inhibition of rTEV. To test this hypothesis, we examined the effects of detergents upon the rTEV proteolytic digestion of a soluble fusion protein, α_1 platelet activating factor acetylhydrolase (PAFAH α_1). Removal of a hexahistidine amino-terminal affinity tag has been characterized in the presence of 16 different detergents at concentrations above their respective CMCs. Our data indicate that half of the detergents tested reduce the activity of rTEV and that these detergents should be avoided or otherwise accounted for during rTEV digestion of recombinant integral membrane proteins.

© 2002 Elsevier Science (USA). All rights reserved.

Biochemical and structural characterization of integral membrane proteins require multimilligram quantities of purified protein. Recombinant DNA technology has facilitated the design and development of various vector DNA based systems for high-level expression of foreign genes in different hosts. For the purification of recombinant proteins, various classical separation procedures are employed and are based on the physicalchemical properties of the protein, such as charge, size, and hydrophobicity. These procedures are often time consuming and laborious; therefore, simple and rapid alternatives for purification have been developed. The production of recombinant proteins containing polyhistidine tags has become a frequently used procedure for rapid purification of recombinant proteins [1,2]. This

* Corresponding author. Fax: +1-434-982-1616.

affinity tagging is readily performed by fusion of a cDNA that codes for polyhistidine (typically six to ten histidines) to the gene of interest in the expression vector, which yields a protein that can be detected and/or purified via immobilized metal affinity chromatography (IMAC) or anti-histidine antibodies. Purification of many bacterially expressed integral membrane proteins has been reported (for example, glucose transporter [3], diacylglycerol kinase [4], outer membrane iron siderophore transporter FhuA [5], nontypeable Haemophilus influenzae p5 outer membrane protein [6], CLC chloride channel homolog YadQ [7], and acyl-acyl carrier protein synthase [8]). Removal of the affinity tag from the protein of interest is frequently sought and is accomplished by inserting a site-specific protease cleavage site between the tag and the protein. The tag is then separated from the fusion protein by proteolysis after affinity chromatography. Many different proteases are used for cleavage including Factor Xa [9], thrombin [10,11], enterokinase [12], preScission [13], or tobacco etch virus

E-mail address: mwiener@virginia.edu (M.C. Wiener).

1	1	0	

Detergent	Detergent concentration during rTEV digestion (mM)	Detergent CMC (mM) ^a	Detergent chain length	Detergent type ^b	Digestion ^c
No detergent	_	_	_	_	С
APO-10	9	4.57 ^d	10	Ν	Ι
C_8E_4	20	7.2 ^e	8	Ν	С
DDMAB	9	4.3 ^d	12	Z	Ι
DHPC	4	1.4 ^f	7	Z	С
DM	5	1.8 ^e	10	Ν	С
DODMG	5	1.5 ^e	12	Z	Ι
DS	9	2.5 ^d	10	Ν	С
FC-12	5	1.5 ^e	12	Z	Ι
FOS-MEA-10	10	5.25 ^e	10	Z	С
HECAMEG	35	19.5 ^e	7	Ν	Ι
HEGA-10	20	7.0 ^e	10	Ν	С
LDAO	5	1.4 ^e	12	Z	Ι
LYSOPC-12	3	0.9^{f}	12	Z	С
NTM	6.5	3.2 ^e	9	Ν	С
OG	35	19.0 ^e	8	Ν	Ι
ZW 3-12	6.5	3.0 ^d	12	Z	Ι

Table 1 Effect of detergent on rTEV protease digestion

^a Detergent CMC values were obtained from the catalogs of Calbiochem, CA, Anatrace, OH, Avanti Polar Lipids, AL.

^b N–Neutral, Z–zwitterionic.

^cC-Complete, I-incomplete.

^d Detergent CMC values were obtained from the catalogs of Calbiochem, CA.

^e Detergent CMC values were obtained from the catalogs of Anatrace, OH.

^fDetergent CMC values were obtained from the catalogs of Avanti Polar Lipids, AL.

 $(\text{TEV})^1$ protease [14]. TEV protease is among the most widely used due to its high specificity and its activity over a broad temperature range [15]. It has been cloned as a polyhistidine tagged fusion protein [14] and has been engineered to increase its expression level in *Escherichia coli* [16].

The focus of our laboratory is structural biology (Xray crystallography) of integral membrane proteins. The proteins are typically purified as affinity tagged fusion proteins in buffers that contain various detergents at concentrations above their respective critical micelle concentrations (CMCs). A solution of purified membrane protein contains, in equilibrium, protein–detergent complexes (PDCs), free detergent micelles, and detergent monomers [17]. We have frequently observed incomplete tag removal from recombinant membrane proteins after treatment with rTEV protease. Variation of digestion time, digestion temperature, and amount of protease often had relatively little effect upon efficiency or yield. This effect suggests the possibility of inhibition of rTEV protease activity due to detergents at concentrations above their CMCs. To address this possibility, we examined the effects of detergents upon the rTEV protease cleavage of a polyhistidine affinity tag from the recombinant soluble protein α_1 platelet activating factor acetylhydrolase (PAFAH α_1) [18]. This protein has an amino hexahistidine tag with an rTEV protease cleavage site and is digested quantitatively by rTEV. The tag removal has been characterized in the presence of 16 different detergents. Our results indicate that certain detergents, namely; APO-10, DDMAB, DODMG, FC-12, HECAMEG, LDAO, OG, and ZW 3-12 (Table 1) can reduce rTEV digestion to varying degrees. These detergents may be avoided when using rTEV digestion as a method of tag removal from recombinant membrane proteins.

Materials and methods

Materials

The plasmid pHis-PAFAH α_1 encoding α_1 -platelet activating factor acetylhydrolase was provided by

¹ Abbreviations used: PDC, protein-detergent complex; CMC, critical micelle concentration; TEV, tobacco etch virus; rTEV, recombinant tobacco etch virus; PAFAH α_1 , α_1 platelet activating factor acetylhydrolase; IMAC, immobilized metal affinity chromatography; EDTA, ethylenediaminetetraacetic acid disodium salt dihydrate; LB, Luria-Bertani; IPTG, isopropyl-β-D-thiogalactopyranoside; SDS-PAGE, sodium dodecyl sulfate-polyacrylamide gel electrophoresis; LDS, lithium dodecyl sulfate; APO-10, dimethyldecylphosphine oxide; C₈E₄, tetraethyleneglycolmonooctylether; DDMAB, n-dodecyl-N,N-(dimethylammonio)butyrate; DHPC, 1,2-diheptanoyl-sn-glycero-3-phosphocholine; DM, n-decyl- β -D-maltopyranoside; DODMG, n-dodecyl-N,N-dimethylglycine; DS, n-decanoyl-β-D-fructofuranosylα-p-glucopyranoside; FC-12, n-dodecylphosphocholine; FOS-MEA-10, decyl-phospho-n-methylethanolamine; HECAMEG, methyl-6-O-(Nheptylcarbamoyl)-a-D-glucopyranoside; HEGA-10, decanoyl-N-hydroxyethylglucamide; LDAO, n-dodecyl-N,N-dimethylamine-N-oxide; LYSOPC-12, 1-lauroyl-sn-glycero-3-phosphocholine; NTM, n-nonylβ-D-thiomaltopyranoside; OG, *n*-octyl-β-D-glucopyranoside; ZW 3–12, 3-(dodecyldimethylammonio)-1-sulfonate.

Dr. Zygmunt Derewenda (University of Virginia). The *E. coli* strain BL21(DE3)pLysS was used for protein expression. Isopropyl-β-D-thiogalactopyranoside (IPTG) was obtained from Research Products International, IL. Detergents were purchased from Anatrace, OH; Avanti Polar Lipids, AL; or Calbiochem, CA. TransformAid transformation kit was from MBI Fermentas, MD. Ni-NTA Superflow metal affinity resin was from Qiagen, CA. Recombinant tobacco etch virus (rTEV) protease was from Life Technologies, MD. Novex NuPAGE (10%) Bis–Tris gels and SeeBlue Plus2 pre-stained protein molecular standard were from Invitrogen, CA. Pefabloc was purchased from Pentapharm, Switzerland.

Expression and purification of $PAFAH\alpha_1$

For protein expression, the plasmid pHis-PAFAH α_1 was transformed into the E. coli strain BL21(DE3)pLysS and colonies were selected on LB agar plates containing 100 µg/ml ampicillin and 34 µg/ml chloramphenicol. Cells from single drug-resistant colonies were grown overnight in 10 ml LB broth supplemented with the same antibiotics at 37 °C. The next morning, the cells were diluted into 1 L LB broth with appropriate antibiotics in a 2.8 L baffled Fernbach flask. The cells were grown at 37 °C to mid-log phase (A_{600} 0.5–0.6) and the gene was induced with 1 mM IPTG for 3 h. The cells were harvested by centrifugation and the cell pellet was resuspended in 50 ml of 50 mM NaH₂PO₄ (pH 8.0), 300 mM NaCl, 1 mM pefabloc, 1 mM PMSF, and 1 µg/ ml DNase. The cells were passed three times at 16,000 psi in a Spectronic Unicam 40K FRENCH pressure cell using a FRENCH pressure cell press. The lysate was centrifuged at 13,900g for 30 min in a Jouan MR1822 centrifuge to remove the cell debris and unlysed cells. The supernatant containing the PAFAH α_1 was loaded onto a 5ml bed volume Ni-NTA superflow metal affinity column at a flow rate of 1.0 ml/min. Before loading, the column was pre-equilibrated with buffer A (50 mM NaH₂PO₄, pH 8.0, 300 mM NaCl). The unbound protein was then washed with buffer A + 20 mMimidazole until the A_{280} came to the baseline. The proteins were then eluted with buffer A + 250 mM imidazole. The peak fractions were pooled and concentrated using an Amicon concentrator with a YM10 membrane. The concentrated protein was then dialysed against 20 mM Tris-Cl, pH 8.0, for 3 days using 10 kDa MWCO dialysis membrane.

rTEV protease digestion

rTEV protease digestion of the protein was carried out in a total volume of 50 µl containing $1 \times$ assay buffer (50 mM Tris–Cl, pH 8.0, 0.5 mM EDTA, and 1 mM DTT), 10 µg PAFAH α_1 , and 10 units rTEV protease. Experiments were performed at room temperature and at 30 °C. Sixteen different detergents (Table 1) were added to individual reaction mixture. The reaction was quenched after 6h by mixing with $4 \times$ NuPAGE LDS sample buffer (40% glycerol, 564 mM Tris base, 424 mM Tris-HCl, 8% LDS, 2.04 mM EDTA, 0.4% bromophenol blue, and 0.025% phenol red) and incubating in boiling water bath for 3 min. The degree of rTEV digestion was detected on SDS-PAGE. Each cleavage experiment was repeated four times. The quantity of the digested products was measured qualitatively by visualization and compared with the control experiment that was carried out without any detergent in the reaction. Reactions, identical to the detergent-free control, where no uncut PAFAH α_1 could be detected were referred to as complete (C) digestion. Reactions that yielded uncut PAFAH α_1 were referred to as incomplete (I) digestion.

Sodium dodecyl sulfate–polyacrylamide gel electrophoresis

SDS–PAGE [19] was performed on a NuPAGE 10% Bis–Tris gel with a Novex Xcell II mini-cell apparatus (Invitrogen, CA). The protein bands were stained by Coomassie brilliant blue R-250 and then destained by boiling the gels in water for 15–20 min.

Results

The objective of this study was to characterize the effects of detergents upon rTEV activity. The soluble test protein used for this study, α_1 subunit of platelet activating factor acetylhydrolase (PAFAH α_1) [18], has previously been cloned in the pHis-Parallel1 vector [20] and expressed in E. coli. The fusion protein was expressed from the plasmid pHis-PAFAH α_1 and purified using Ni-NTA column to homogeneity. The untagged protein has a calculated molecular mass of 26 kDa. However, the untagged protein runs as a 29 kDa and the polyhistidine-tagged fusion protein runs with a mass of approximately 32 kDa on SDS-PAGE (data not shown). For control experiments, the rTEV digestion of the PAFAH α_1 was carried out for 3 and 6h at both room temperature and 30 °C. Analyses of the digested products on SDS-PAGE gel revealed that the rTEV protease cleaves and quantitatively removes the tag from PAFAHa₁ (Fig. 1A, lanes 4-7). No significant difference in digestion was observed when the reactions were carried out for 3 h. vs. 6 h and at room temperature vs. 30 °C. Digestion experiments were then carried out in the presence of 16 different detergents (Table 1) for 6 h. The results of the cleavage experiments, shown in Fig. 1, are summarized in Table 1. Several of the detergents examined, notably APO-10, DDMAB, DODMG, FC-12, HECAMEG, LDAO, OG, and ZW 3-12 inhibit

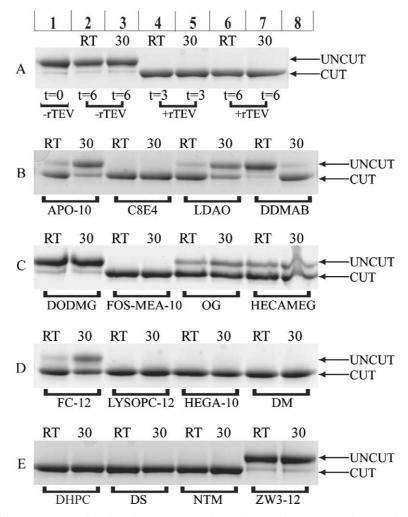


Fig. 1. SDS–PAGE analysis of rTEV protease digestion of PAFAH α_1 . Each reaction contains 10 µg PAFAH α_1 and 10 units (as defined in the Life Technologies catalog) rTEV protease. (A)–Control reactions carried out without added detergents. Lanes 1–3: no rTEV added. Lanes 4–7: rTEV at indicated time and temperature. t = 0, t = 3, and t = 6 denote time 0, 3, and 6 h, respectively. (B) to (E)–Reactions performed for 6 h in the presence of different detergents (marked underneath). For all panels: RT = room temperature, 30 = 30 °C, uncut and cut positions of the proteins are marked with arrows, lane positions are marked on top of (A).

rTEV digestion by at least a factor of 2 to 3. No inhibition in digestion was observed in C_8E_4 , DHPC, DM, DS, FOS-MEA-10, HEGA-10, LYSOPC-12, and NTM.

Discussion

Inefficient removal of an affinity tag in membrane proteins could occur by steric occlusion of the cleavage site by protein and/or detergent of the protein-detergent complex (PDC), or by an inhibitory effect of detergent upon protease activity. Steric occlusion effects are dependent upon the specific protein and detergent of a particular PDC; thus, these effects need to be assayed on a case-by-case basis. In this study, we sought to answer the more general question: do specific detergents at concentrations used for membrane protein biochemistry inhibit rTEV activity? Our experimental results indicate that eight of sixteen different detergents inhibit rTEV activity, as assayed by less efficient removal of a polyhistidine tag from PAFAHa₁. Detergent concentrations, listed in Table 1, are typical for use in integral membrane protein purification, crystallization, and other biochemical experiments. The specific chainlengths used for each of the given detergent head group 'classes' are typical for uses with integral membrane proteins. We utilized PAFAH α_1 as a test protein because as a soluble protein it will have less interaction with detergents (i.e., we do not expect PAFAH α_1 to form PDCs in the presence of detergents). We observe no simple correlation between the specific properties of a given detergent (charge, CMC, tail chainlength, head group structure, etc.) and its ability to inhibit rTEV protease activity. For example, some uncharged detergents (C₈E₄, DM, DS, HEGA-10, and NTM) do not inhibit rTEV digestion, while other uncharged detergents (APO-10, HECA-MEG, and OG) do inhibit digestion. Some of the detergents with lower CMCs (C₈E₄, DHPC, DM, DS, FOS-MEA-10, HEGA-10, LYSOPC-12, and NTM) do not inhibit rTEV digestion, while other low-CMC detergents (APO-10, DDMAB, DODMG, FC-12, LDAO, and ZW 3-12) do inhibit digestion. Higher CMC values could possibly be a factor in rTEV inhibition. The CMCs of all of the detergents except OG and HECA-MEG are between 0.9 and 7.2 mM, whereas OG and HECAMEG have CMCs of 19 and 19.5 mM, respectively, and do inhibit the cleavage. The chainlengths of all of the detergents are between seven and twelve carbons (methylenes and terminal methyl). As evident from Table 1, larger or smaller chainlengths do not play an obvious role in inhibition of rTEV protease activity. LYSOPC-12 has a 12 carbon chainlength and does not inhibit the cleavage; however, DDMAB, DODMG, FC-12, LDAO, and ZW 3-12 possess identical 12 carbon chainlengths but do inhibit the digestion. DHPC has a seven carbon chainlength and does not inhibit the reaction while HECAMEG, also of chainlength seven, does inhibit the digestion. The head group structures of all of the detergents are different and no particular structure of the detergents used is a simple factor in inhibition of rTEV activity.

In the most general case of membrane protein purification and crystallization, three different detergents may be required. One detergent is effective at solubilizing the protein from the cell membrane, another is effective for chromatography, and a third is used for crystallization. Each different detergent entails exchange of the protein into it. Our results indicate that, in this general scenario, a fourth detergent that does not inhibit rTEV protease may be required. Alternatively, certain detergents may need to be avoided during the digestion step, so as to eliminate the possibility of detergent-induced inhibition or inactivation of TEV protease, leading to incomplete digestion and tag removal. While steric occlusion of the protease site within the proteindetergent complex (PDC) is certainly a possibility, avoiding inhibitory detergents will enable this cause to be diagnosed and potentially addressed. Modifications of the protein construct (changing the linker, moving from N to C terminus, etc.) and/or exchanging into a different detergent may overcome this problem.

Acknowledgments

This research was supported by the National Institutes of Health research grant (GM-56251) and the National Aeronautics and Space Administration (NAG8-1832). A.K.M. was supported as a Postdoctoral Fellow of the American Heart Association (Mid-Atlantic Affiliate). We thank Dr. Zygmunt Derewenda for providing the pHis-PAFAH α_1 plasmid.

References

- J. Nilsson, M. Larsson, S. Stahl, P.A. Nygren, M. Uhlen, Multiple affinity domains for the detection, purification and immobilization of recombinant proteins, J. Mol. Recogn. 9 (1996) 585–594.
- [2] R. Janknecht, G. de Martynoff, J. Lou, R.A. Hipskind, A. Nordheim, H.G. Stunnenberg, Rapid and efficient purification of native histidine-tagged protein expressed by recombinant *vaccinia* virus, Proc. Natl. Acad. Sci. USA 88 (1991) 8972–8976.
- [3] U. Waeber, A. Buhr, T. Schunk, B. Erni, The glucose transporter of *Escherichia coli*. Purification and characterization by Ni⁺ chelate affinity chromatography of the IIBCGlc subunit, FEBS Lett. 324 (1993) 109–112.
- [4] F.W. Lau, J.U. Bowie, A method for assessing the stability of a membrane protein, Biochemistry 36 (1997) 5884–5892.
- [5] A.D. Ferguson, J. Breed, K. Diederichs, W. Welte, J.W. Coulton, An internal affinity-tag for purification and crystallization of the siderophore receptor FhuA, integral outer membrane protein from *Escherichia coli* K-12, Protein Sci. 7 (1998) 1636–1638.
- [6] D.C. Webb, A.W. Cripps, A method for the purification and refolding of a recombinant form of the nontypeable *Haemophilus influenzae* P5 outer membrane protein fused to polyhistidine, Protein Expr. Purif. 15 (1999) 1–7.
- [7] M.D. Purdy, M.C. Wiener, Expression, purification, and initial structural characterization of YadQ, a bacterial homolog of mammalian CIC chloride channel proteins, FEBS Lett. 466 (2000) 26–28.
- [8] J. Shanklin, Overexpression and purification of the *Escherichia coli* inner membrane enzyme acyl-acyl carrier protein synthase in an active form, Protein Expr. Purif. 18 (2000) 355–360.
- [9] D.B. Smith, K.S. Johnson, Single-step purification of polypeptides expressed in *Escherichia coli* as fusions with glutathione *S*-transferase, Gene 67 (1988) 31–40.
- [10] U.C. Vothknecht, C.G. Kannangara, D. von Wettstein, Expression of catalytically active barley glutamyl tRNAGlu reductase in *Escherichia coli* as a fusion protein with glutathione S-transferase, Proc. Natl. Acad. Sci. USA 93 (1996) 9287–9291.
- [11] K.R. Sticha, C.A. Sieg, C.P. Bergstrom, P.E. Hanna, C.R. Wagner, Overexpression and large-scale purification of recombinant hamster polymorphic arylamine *N*-acetyltransferase as a dihydrofolate reductase fusion protein, Protein Expr. Purif. 10 (1997) 141–153.
- [12] S.I. Choi, H.W. Song, J.W. Moon, B.L. Seong, Recombinant enterokinase light chain with affinity tag: expression from *Saccharomyces cerevisiae* and its utilities in fusion protein technology, Biotechnol. Bioeng. 75 (2001) 718–724.
- [13] S. Carr, J. Miller, S.E. Leary, A.M. Bennett, A. Ho, E.D. Williamson, Expression of a recombinant form of the V antigen of *Yersinia pestis*, using three different expression systems, Vaccine 18 (1999) 153–159.
- [14] T.D. Parks, K.K. Leuther, E.D. Howard, S.A. Johnston, W.G. Dougherty, Release of proteins and peptides from fusion proteins using a recombinant plant virus proteinase, Anal. Biochem. 216 (1994) 413–417.
- [15] W.G. Dougherty, J.C. Carrington, Expression and function of polyviral gene products, Annu. Rev. Phytopathol. 26 (1988) 123– 143.
- [16] R.B. Kapust, K.M. Routzahn, D.S. Waugh, Processive degradation of nascent polypeptides, triggered by tandem AGA codons, limits the accumulation of recombinant tobacco etch virus protease in *Escherichia coli* BL21(DE3), Protein Expr. Purif. 24 (2002) 61–70.

- [17] M. Zulauf, Detergent phenomena in membrane protein crystallization, in: H. Michel (Ed.), Crystallization of Membrane Proteins, CRC Press, Boca Raton, FL, 1991, pp. 53–72.
- [18] Y.S. Ho, L. Swenson, U. Derewenda, L. Serre, Y. Wei, Z. Dauter, M. Hattori, T. Adachi, J. Aoki, H. Arai, K. Inoue, Z.S. Derewenda, Brain acetylhydrolase that inactivates platelet-activating factor is a G-protein-like trimer, Nature 385 (1997) 89–93.
- [19] U.K. Laemmli, Cleavage of structural proteins during the assembly of the head of bacteriophage T4, Nature 227 (1970) 680-685.
- [20] P. Sheffield, S. Garrard, Z. Derewenda, Overcoming expression and purification problems of RhoGDI using a family of parallel expression vectors, Protein Expr. Purif. 15 (1999) 34–39.