

# Arg-Ser-<sup>775</sup>, <sup>792</sup> and <sup>823</sup> in Spacer Region of ADAMTS-18 Is Critical for Thrombin Cleavage

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Received 13 August 2014; revised 28 September 2014; accepted 13 October 2014

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## Abstract

Cleavage of ADAMTS-18 by thrombin represents a new mechanism of platelet thrombus clearance via the release of active ~45-kDa C-terminal fragments that induces oxidative platelet fragmentation. The exact cleavage sites remain unclear, but Arg (R)<sup>775</sup>/Ser (S)<sup>776</sup> in spacer region of ADAMTS-18 has been shown to be one of the cleavage sites of thrombin. Here, we demonstrate that R<sup>792</sup>/S<sup>793</sup> and R<sup>823</sup>/S<sup>824</sup> are also thrombin cleavage sites by sequence analysis, amino acid mutation and mass spectrometry assay. All these cleavage sites are thrombin-specific and insensitive to other enzymes tested (e.g. cathepsin D or trypsin). Simultaneous mutation of R<sup>775</sup>, <sup>792</sup>, <sup>823</sup> to S<sup>775</sup>, <sup>792</sup>, <sup>823</sup> in ADAMTS-18 completely abrogated the cleavage by thrombin and the generation of active C-terminal 45-kDa fragments. Together with previous study, a total of three thrombin-specific cleavage sites have been identified in spacer region of ADAMTS-18.

## Keywords

ADAMTS-18, Thrombin, Cleavage, Mass Spectrum

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## 1. Introduction

ADAMTS (a disintegrin and metalloproteinase domain, with thrombospondin type-1 modules) is a family of 19 secreted Zn-metalloproteinases, which have multidomain structural components in common [1]. These include an N-terminal signal peptide, followed by a pro-domain, a metalloproteinase catalytic domain with a zinc binding motif, a disintegrin-like domain, a central thrombospondin type-1-like repeat (TSR), a cysteine rich domain (high sequence homology), a spacer region, and a variable number of C terminal TSR repeats. This family plays important roles in several pathophysiological conditions mainly including arthritis [2], spermatogenesis [3], angiogenesis [4] [5], and thrombosis-related disease [6]. Noteworthy, most of these activities are related to proteolytic processing within their C-terminal regions [6]-[9].

ADAMTS-18 has the similar domain organization as other family members. ADAMTS-18 has been shown to be epigenetically silenced in multiple carcinomas and has tumor suppressor activity [10]. Mutation of ADAMTS-18 is strongly associated with colorectal cancer [11]. The data from National Center for Biotechnology Information (NCBI) subject's gene expression omnibus (GEO) also showed that ADAMTS-18 gene was differentially expressed in subjects with normal skeletal fracture versus subjects with nonunion skeletal fracture [12]. Therefore, it is also associated with bone mineral density (BMD) determination in the major human ethnic groups. Recently, some studies indicate that the ADAMTS-18 gene is also play a crucial role in early eye development [13].

Platelet integrin  $\alpha\text{IIb}\beta\text{3}$  (GPIIb/IIIa) is a heterodimeric receptor of the integrin family expressed at high density (50,000 - 80,000 copies/cell) on the platelet plasma membrane [14]. GPIIIa49-66 (CAPESIEFPVSEAREVLED) is a linear epitope of integrin subunit  $\beta\text{3}$  (GPIIIa) in its extracellular domain. We previously reported that the unique feature of the antibodies (Abs) against GPIIIa49-66 was their ability to induce reactive oxygen species (ROS) through the activation of 12-lipoxygenase and nicotinamide adenine dinucleotide phosphate oxidase (NADPH), leading to complement-independent platelet fragmentation [15] [16]. Recently, we revealed that ADAMTS-18 was the physiologic ligand of platelet GPIIIa49-66 [17]. Thrombin generated from the endothelium of vessel injury is able to cleave ADAMTS-18. The generated ~45-kDa C-terminal cleavage product of ADAMTS-18 becomes activated. It clusters the  $\beta\text{3}$  integrins and induces oxidative platelet fragmentation as we previously described anti-GPIIIa 49 - 66 Ab [17]. We have identified that R<sup>775</sup>/S<sup>776</sup> in spacer region of ADAMTS-18 is one of the potential cleavage sites of thrombin [18]. However, sequence analysis indicates that there still exist two same sites in spacer region neighboring R<sup>775</sup>/S<sup>776</sup> named R<sup>792</sup>/S<sup>793</sup> and R<sup>823</sup>/S<sup>824</sup>, which also generate similar ~45-kDa C-terminal products in theory when cleaved by thrombin. In this study, we have investigated other thrombin cleavage sites in spacer region of ADAMTS-18 through amino acid mutation and mass spectrometry assay.

## 2. Materials and Methods

### 2.1. Reagents

All reagents were obtained from Sigma (St. Louis, MO) unless otherwise designated. Full-length ADAMTS-18 cDNA coding sequence was purchased from ATCC and cloned into mammalian expression vector pBudCE4.1 from Invitrogen (Carlsbad, CA) [17] [18]. ADAMTS-18 peptides were synthesized by Sangon Biotech (Shanghai, China). The *in vitro* Transcend™ Biotinylated Translation Detection Systems was purchase from Promega (Madison, WI, USA).

### 2.2. *In Vitro* DNA Translation and Thrombin Cleavage Assay

Biotinylated-methionine-labeled ADAMTS-18 or its mutant was translated using an *in vitro* Transcend™ Biotinylated Translation Detection Systems following the protocol provided by the manufacturer. All the peptides or translated proteins were then digested by thrombin or cathepsin D or trypsin according to the protocol provided by the manufacture.

### 2.3. Immunoblotting

*In vitro* translation products were separated by 12% SDS/PAGE gels, transferred to a nitrocellulose membrane, and immunoblotted with horseradish peroxidase (HRP) conjugated avidin for 1 hour followed by washing with

PBST (0.1% Tween 20). The signal band was detected by chemiluminescence substrate [18].

## 2.4. Mass Spectrometry

Mass spectrometry was performed as previously described [18]. Briefly, for analysis of ADAMTS-18 cleavage products, a fresh mixture of enzyme and ADAMTS-18 peptide was submitted to molecular weight determination by Matrix assisted laser desorption ionization quadrupole time of flight (MALDI-QTOF) mass spectrometry (MS) (Applied Biosystems 4700 Proteomics Analyzer). To determine the amino acid sequences of newly observed peaks, MS/MS peptide *de novo* sequencing using a specific software program (Applied Biosystems DeNovo Explorer) was performed.

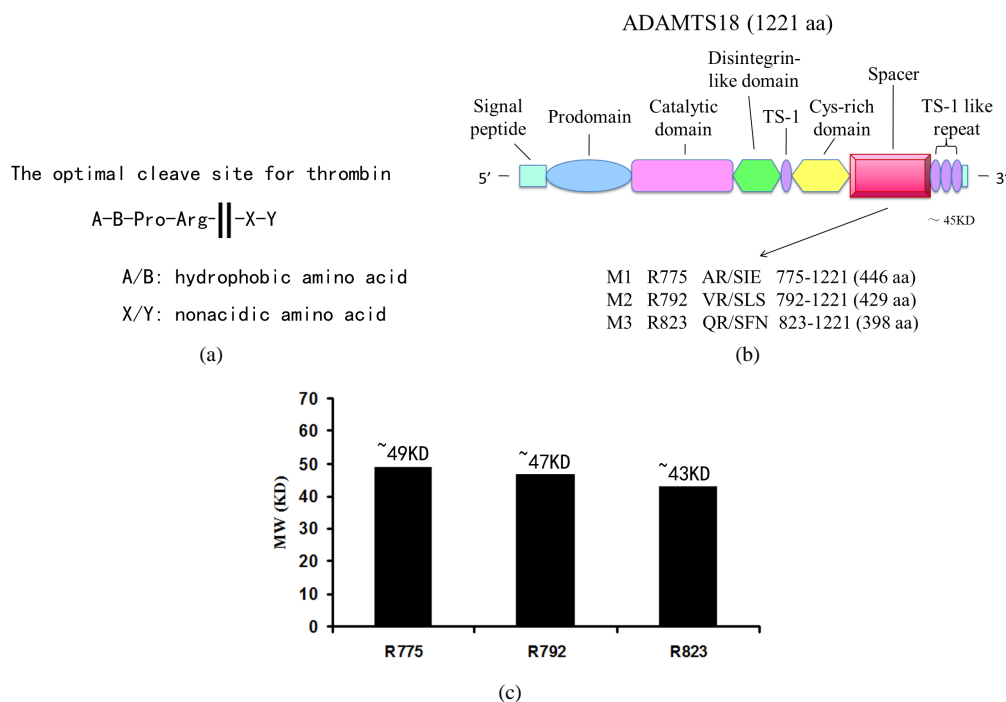
## 3. Results

### 3.1. Thrombin Cleavage of C-Terminal ADAMTS-18 on Several Sites

Previous study has shown that the full-length ADAMTS-18 is proteolyzed by thrombin and results in ~45-kDa C-terminal fragments releasing [17]. The optimal cleavage site for thrombin is R/X [X refers to nonacidic amino acid mainly including R, lys (K), His (H), and Ser (S)] (Figure 1(a)). We have demonstrated that R<sup>775</sup>/S<sup>776</sup> in spacer region of ADAMTS-18 is the potential cleavage site of thrombin [18]. However, analysis of the primary amino acid sequence of ADAMTS18 revealed that there exist three similar thrombin cleavage sites in ADAMTS-18 spacer region named R<sup>775</sup>/S<sup>776</sup>, R<sup>792</sup>/S<sup>793</sup> and R<sup>823</sup>/S<sup>824</sup> (Figure 1(b)). The possible molecular weight from these predicted sites to C terminal is ~49-, 47- and 43-kDa, respectively (Figure 1(c)). Therefore, it remained uncertain whether R<sup>792</sup>/S<sup>793</sup> and R<sup>823</sup>/S<sup>824</sup> were also the actual sites of proteolysis.

### 3.2. Susceptibility of Thrombin for R<sup>792</sup>/S<sup>793</sup> and R<sup>823</sup>/S<sup>824</sup> of C-Terminal ADAMTS-18

To explore these predictions, we synthesized peptides covering the other two putative cleavage sites. The P06594 (PGEFPPAGTTTFEYQRSFNRPERLYAPG) covers R<sup>823</sup>/S<sup>824</sup>. The initial molecular weight (MW) of

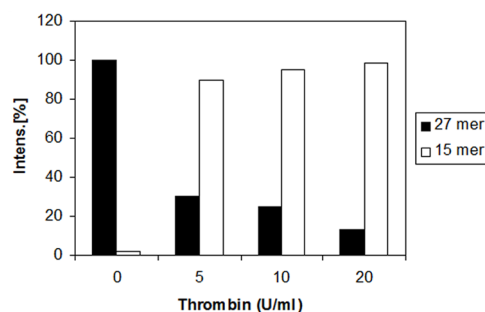
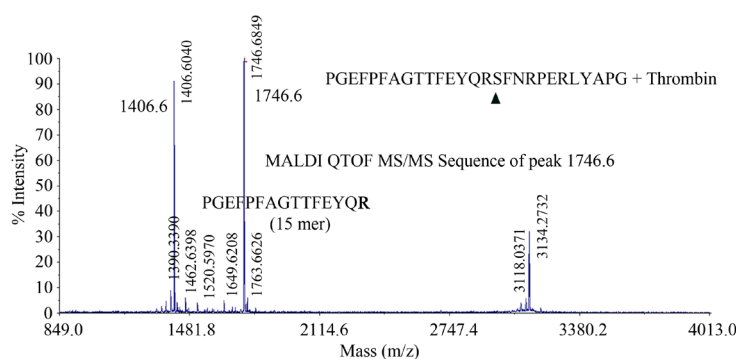
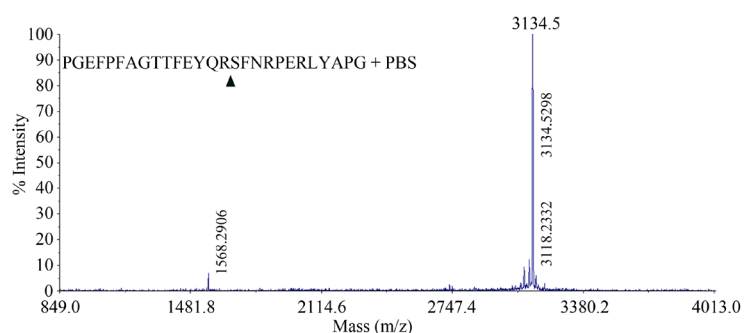


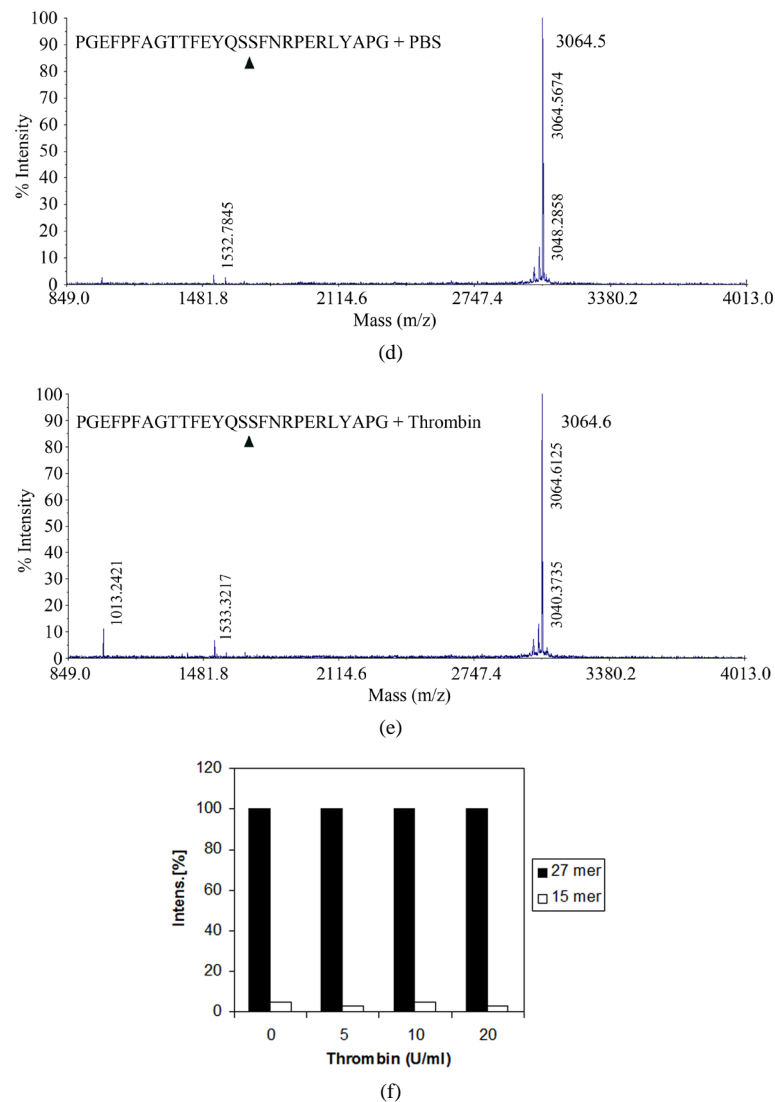
**Figure 1.** Putative thrombin cleavage sites in ADAMTS-18 spacer region. (a) The optimal cleave site for thrombin. (b) Diagram of ADAMTS-18 domain structure. Location of predicted thrombin cleavage sites after Arg (R)<sup>775</sup>, R<sup>792</sup> and R<sup>823</sup> are shown above. (c) The possible molecular weight from these predicted cleavage sites to C-terminal of ADAMTS-18.

P06594 is ~3134.5 Da when incubated with PBS buffer (Figure 2(a)). However, thrombin cleaved 27-mer P06594 at R/S site, producing 15-mer N terminal peptide PGEFPPFAGTTFEYQR (~1746.6 Da) and 12-mer C terminal peptide SFNRPERLYAPG (~1406.6 Da), respectively (Figure 2(b)). The generation of 15-mer peptide becomes obvious when the concentration of thrombin beyond 5 U/ml (Figure 2(c)). Consistently both PBS and thrombin had no effect on P06595 (PGEFPPFAGTTFEYQSSFNRPERLYAPG), in which R<sup>823</sup> was mutated to S<sup>823</sup> (Figure 2(d) and Figure 2(e)). The generation of 15-mer peptide completely abrogated when cleaved by various concentrations of thrombin (Figure 2(f)). Hirudin completely inhibited the generation of MW1746.6 and MW1406.6 peak suggesting the specificity of thrombin cleavage (Figure 3) Similar results were obtained with P06728 (ELQVSS SYLAVRSLSQKYYLTGGWSID), which covers R<sup>792</sup>/S<sup>793</sup> producing two peptide peaks (~1717.9 Da and 1351.52) at R<sup>792</sup>/S<sup>793</sup> site (Table 1). We also incubated these peptides with other enzyme cathepsin D or trypsin, and assayed by mass spectrometry. It demonstrated that these cleavage sites are thrombin-specific, and insensitive to cathepsin D or trypsin (Table 1).

### 3.3. Specificity of Thrombin for Site-Mutated ADAMTS-18 Full-Length Protein

Since R/S<sup>775, 792</sup> and <sup>823</sup> in spacer region of ADAMTS-18 are critical for thrombin cleavage, we further constructed mammalian expression vector in which all these susceptible sites were mutated to S/S<sup>-775, 792</sup> and <sup>823</sup> (Figure 4(a)).





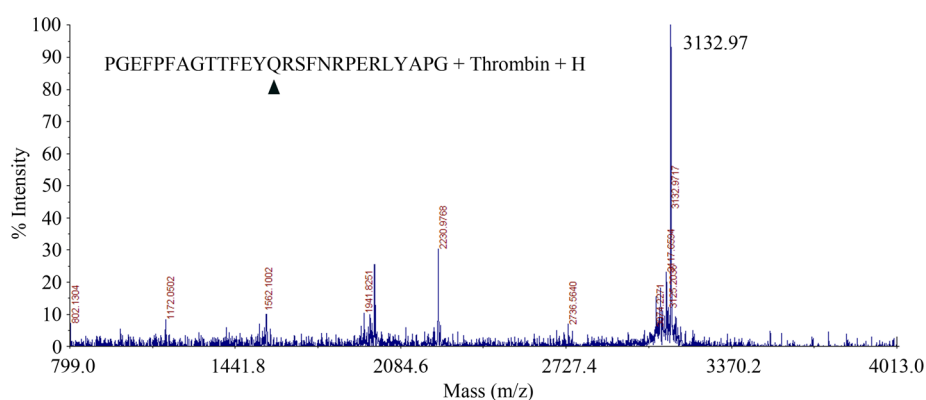
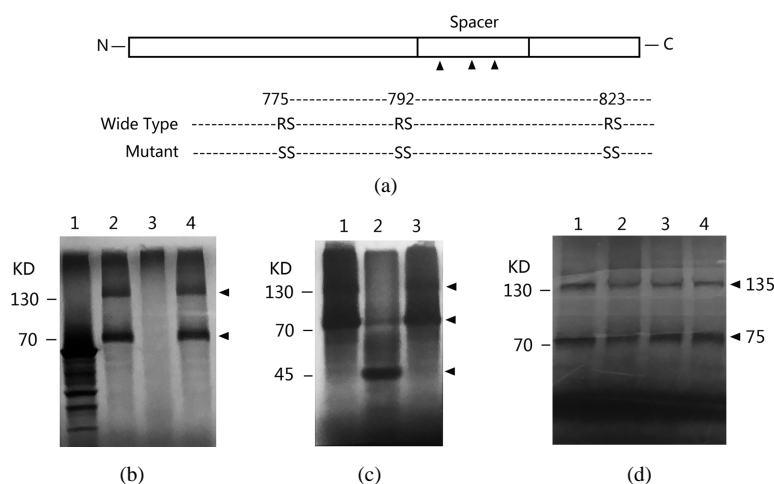
**Figure 2.** Susceptibility of thrombin for R<sup>823</sup>/S<sup>824</sup> site of ADAMTS18. (a) (b) Synthesized 27-mer ADAMTS-18 peptide P06594 containing R<sup>823</sup>/S<sup>824</sup> (~3134.5 Da) was incubated with PBS (a) or 5 U/ml thrombin (b) for 1 h. The putative thrombin cleavage site was confirmed by MALDI QTOF mass spectrometry. (c) The releasing of 15-mer N terminal peptide (MW 1746.6) when P06594 was cleaved by different concentration of thrombin at R<sup>823</sup>/S<sup>824</sup> site. (d) (e) Mutated 27-mer ADAMTS-18 peptide P06595 (~3064.5 Da, R<sup>823</sup> switches to S<sup>823</sup>) was incubated with PBS (d) or thrombin (e) in the same condition as P06594 and analyzed by mass spectrometry. Proteolysis after R<sup>823</sup> was prevented by substitution of the arginine (Arg, R) to serine (Ser, S). (f) No 15-mer N terminal peptide (MW 1746.6) was released when P06595 was cleaved by different concentrations of thrombin at S<sup>823</sup>/S<sup>824</sup> site.

Bio-methionine-labeled ADAMTS18 and site-mutant ADAMTS-18 were synthesized with *in vitro* translation system using the expression vector of pBudCe 4.1/ADAMTS-18. Both pBudCe 4.1/ADAMTS-18 (lane 2) and its mutant (lane 4) demonstrated two dominant bands of ~135 kDa and ~75 kDa. The ~135 band represented intact ADAMTS-18 (1221 amino acids), and ~75 kDa band does represent the short form of ADAMTS-18 since luciferase control (lane 1) and the empty vector (lane 3) did not transcribe these two bands (**Figure 4(b)**). The expression of ~75 kDa short form of ADAMTS-18 is consistent with our previous report [18]. **Figure 4(c)** demonstrates wide type ADAMTS-18 is proteolyzed by thrombin, and the cleavage fragment is about ~45-kDa. However, thrombin had no effect on mutated ADAMTS-18 in various concentrations (**Figure 4(d)**).

**Table 1.** Analysis of thrombin cleavage sites in ADAMTS-18 protein.

Number	Peptide location in ADAMTS-18	Sequence	Molecular weight	Molecular weight after thrombin digestion (R/S)	Molecular weight after cathepsin D or trypsin digestion
331941	762-791	NEYYPVVIIPAGARSSIEIQELQVSSSYLAV	3308.41	1447.52 + 1559.3	ND
331942	762-791	NEYYPVVIIPAGASSIEIQELQVSSSYLAV	2982.29	ND	ND
P06728	780-806	ELQVSSSYLAVRSLSQKYLLTGGWSID	3051.4	1351.52 + 1717.9	ND
P06729	780-806	ELQVSSSYLAVSSLSQKYLLTGGWSID	2982.29	ND	ND
P06594	808-834	PGEFPFAGTTFEYQRSFNRPERLYAPG	3134.5	1746.6 + 1406.6	ND
P06595	808-834	PGEFPFAGTTFEYQSSFNRPERLYAPG	3066.34	ND	ND

ND, no digestion.

**Figure 3.** Inhibition effect of hirudin on thrombin cleavage. Synthesized 27-mer ADAMTS18 peptide P06594 was incubated with 5 U/ml thrombin and equal amount of hirudin for 1 h and analyzed by mass spectrometry. Representative mass spectrometry map showed proteolysis after R<sup>823</sup> was completely inhibited by the addition of hirudin.**Figure 4.** Effect of thrombin on ADAMTS-18 mutant. (a) Diagram of ADAMTS-18 mutation sites in which R<sup>775</sup>, R<sup>792</sup> and R<sup>823</sup> were simultaneously mutated to S<sup>775</sup>, S<sup>792</sup> and S<sup>823</sup>. (b) *In vitro* translation. Lane 1, luciferase (~62 kDa); lane 2, pBudCE4.1/ADAMTS-18 (~135 kDa); lane 3, pBudCE4.1; lane 4, pBudCE4.1/ADAMTS-18 mutant (~135 kDa). (c) Wide-type ADAMTS-18 was incubated with thrombin and analyzed by immunoblotting. Lane 1, Bio-ADAMTS-18 alone; lane 2, Bio-ADAMTS-18 + 5 U/ml thrombin; lane 3, Bio-ADAMTS-18 + 5 U/ml thrombin + hirudin. (d) Bio-ADAMTS18 mutant was incubated with various concentrations of thrombin and analyzed by immunoblotting. Lane 1-4 refers to 5, 10, 20, 30 U/ml thrombin, respectively.

## 4. Discussion

Despite the similarity shared by ADAMTS family members, most differences among them are found in the C-terminal domains of the protein, suggesting that the C-terminal domains of ADAMTS may determine their *in vivo* location and substrate specificity [19]-[22]. C-terminal processing has been shown in ADAMTS-1 [19] [21], ADAMTS-4 [20] [22], ADAMTS-8 [4], ADAMTS-9 [5], and ADAMTS-13 [6]. This splicing will shed light on the biological function of these important proteins. Noteworthy, most of cleavage events occur within the spacer region [19]-[22].

We previously reported that cleavage of ADAMTS-18 by thrombin represent a novel mechanism for platelet thrombus clearance [17]. The release of the active 45-kDa C-terminal fragment could regulate thrombus size by inducing oxidative platelet fragmentation. In this study, we first revealed that the R<sup>775</sup>/S<sup>776</sup>, R<sup>792</sup>/S<sup>793</sup> and R<sup>823</sup>/S<sup>824</sup> in spacer region of ADAMTS-18 are critical for thrombin cleavage. This cleavage region is similar to those of the ADAMTS family members reported previously [19]-[22]. Physiologically, thrombin is generated rapidly, and at high local concentrations during the normal hemostatic response. We found that ADAMTS-18 was proteolyzed by thrombin at a high thrombin concentration, whereas low thrombin concentration had undetectable cleavage effect on ADAMTS-18 which mimics some physiological conditions, especially platelet thrombus formation. It is of interest in this regard that ADAMTS-13 has recently been shown to be inactivated by thrombin contributing to the loss of ADAMTS-13 VWF cleavage function [6]. Furthermore, ADAMTS-13 has been reported to limit platelet thrombus formation in a shear rate dependent platelet thrombus model on collagen, by its cleavage of ultra large VWF [23].

In present study, we also find ~75-kDa band which is from ADAMTS-18 cDNA in *in vitro* translation assays. Thrombin or other enzyme (cathepsin D or trypsin) had no effect on the generation of this band. Thus, it is likely other mechanism has been involved in the ADAMTS-18 processing.

## 5. Conclusion

In summary, this report provides a direct proof that the existence of C-terminal proteolytic cleavage sites of ADAMTS-18 by thrombin, has potential drug application in dissolution of arterial thrombi.

## Acknowledgements

This work was supported by the National Natural Science Foundation of China (No.81170481, 81200352); the Innovation Fund of Shanghai Municipal Education Commission (12zz040, 13YZ024), Shanghai Municipal Natural Science Foundation (12ZR1421100), The Key Construction Program of the National “985” project, and SRF for ROCS (to W.Z.), Doctoral Fund of Ministry of Education of China (20120073120113).

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