Mosquito-Derived Anophelin Sulfoproteins Are Potent Antithrombetics

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ABSTRACT: The anophelins are small protein thrombin inhibitors that are produced in the salivary glands of the Anopheles mosquito to fulfill a vital role in blood feeding. A bioinformatic analysis of anophelin sequences revealed the presence of conserved tyrosine residues in an acidic environment that were predicted to be post-translationally sulfated in vivo. To test this prediction, insect cell expression of two anophelin proteins, from Anopheles albimanus and Anopheles gambiae, was performed, followed by analysis by mass spectrometry, which showed heterogeneous sulfation at the predicted sites. Homogeneously sulfated variants of the two proteins were subsequently generated by chemical synthesis via a one-pot ligation—desulfurization strategy. Tyrosine sulfation of the anophelins was shown to significantly enhance the thrombin inhibitory activity, with a doubly sulfated variant of the anophelin from A. albimanus exhibiting a 100-fold increase in potency compared with the unmodified homologue. Sulfated anophelins were also shown to exhibit potent in vivo anticoagulant and antithrombotic activity.

INTRODUCTION

Hematophagous invertebrates have evolved highly effective mechanisms to facilitate the acquisition of a blood meal via the production of exquisitely potent and selective inhibitors of host coagulation factors, in particular the serine proteinase thrombin.1,2 These organism-evolved molecules have been reported to possess reduced toxicity and immunogenicity, privileged properties that are often difficult to design or predict in small-molecule thrombin inhibitors. It is therefore not surprising that molecules derived from blood feeding organisms have found utility in therapy, with the archetypal anticoagulant hirudin (from the medicinal leech Hirudo medicinalis)3 and structural analogues of this protein being used clinically for a range of thromboembolic disorders and postsurgery.4

One feature of these natural thrombin-inhibiting molecules that is often overlooked is the potential presence of post-translational modifications and the effect that these may have on the activity and/or stability of the native peptides and proteins. Interestingly, despite the fact that recombinant hirudin used clinically does not bear any modifications, the native leech protein was first identified with a tyrosine sulfate modification, which was shown to impart a ca. 10-fold improvement in thrombin inhibitory activity.5 We have recently discovered an important role of tyrosine sulfation for the thrombin inhibitory activity of two saliva-derived thrombin inhibitors, madanin-1 and chimadanin, from the bush tick Haemaphysalis longicornis.6 These two inhibitors were shown to exert their activity by binding to the active site and exosite II of human thrombin, with sulfation at two conserved tyrosine residues providing significant improvement in the thrombin inhibitory activity. This improved potency was attributed to enhanced binding of the inhibitor to exosite II of thrombin mediated by electrostatic interactions between the sulfated tyrosine residues and conserved basic residues on the enzyme, as identified through X-ray crystallography.7 On the basis of these findings, we now hypothesize that tyrosine sulfation could be a ubiquitous modification of salivary proteins from other
hematophagous organisms that could serve as a general mechanism for modulating anticoagulant activity during feeding.

The anophelins are an interesting family of thrombin-inhibiting proteins produced in the salivary glands of the *Anopheles* malaria mosquito vector. To date, the genomes of 16 *Anopheles* mosquitoes have been reported (Figure 1), leading to the identification of a number of anophelin protein homologues in “old-world” mosquitoes, e.g., *Anopheles funestus*, *Anopheles gambiae*, and *Anopheles stephensi*, as well as “new-world” mosquitoes such as *Anopheles albimanus* and *Anopheles darlingi*. Anophelin proteins that are recombinantly expressed in *Escherichia coli* have previously been shown to exhibit potent inhibitory activity against human thrombin via a binding mode that typically blocks the active site of thrombin and the N-terminus binds to exosite I.6,9 Guided by sequence analysis of a number of other peptides and proteins that are known to be post-translationally sulfated, we used a bioinformatics approach that have been identified as modulators of anticoagulant activity during feeding. 

While to date tyrosine sulfation has not been suggested or identified as a modification of mosquito salivary proteins, this analysis provided the impetus to test the hypothesis that the anophelins are natively sulfated and that this modification would directly affect the inhibitory activity of the proteins against thrombin. To test this hypothesis, we chose to investigate an “old-world” mosquito and a “new-world” mosquito as examples in order to probe the effect of tyrosine sulfation on the inhibition of thrombin by the family of anophelin proteins. For this purpose, we selected anophelins from *A. gambiae* and *A. albimanus* (herein denoted as AΔTY and AΔSH, respectively) that exhibited the most potent inhibition of thrombin in unmodified recombinant form from each family.6

In this study, we demonstrate that sulfation of AΔTY and AΔSH occurs in insect cells (by baculovirus-assisted recombinant expression) at the sites predicted in our bioinformatics analysis. We also demonstrate an efficient synthetic method to access homogeneously sulfated AΔTY and AΔSH through the use of ligation–desulfurization chemistry. Importantly, these synthetic sulfoproteins were shown to be significantly more potent thrombin inhibitors than the unmodified counterparts and possessed potent antithrombotic activity in an *in vivo* thrombosis model.

### RESULTS

**Anophelins Are Sulfated in Insect Cells.** Access to homogeneous samples of post-translationally modified proteins is challenging, as extremely low quantities of the proteins can typically be isolated from the natural source, in this case the salivary glands of the *Anopheles* mosquito. Typical prokaryotic expression systems lack the TPST enzymatic machinery to generate appropriately post-translationally modified molecules.13 Therefore, we first expressed AΔTY and AΔSH in a eukaryotic system to investigate whether the proteins could be sulfated *in vivo*. For this purpose, we used *Trichoplusia ni* insect cells as a model of the *Anopheles* mosquito. Specifically, codon-optimized sequences encoding AΔTY and AΔSH were designed as N-terminal fusions with the honeybee mellitin signal sequence in order to direct the recombinant proteins to the secretory pathway. Following expression, the cell medium containing the secreted proteins was analyzed by nanoliquid chromatography coupled to tandem mass spectrometry (nanoLC–MS/MS). Analysis of insect-cell-expressed AΔTY showed a heterogeneous population of sulfated protein with approximately 0.8% monosulfated and 41% disulfated variants (see Figure 2A and the Supporting Information, Table 1). MS/MS analysis of full length AΔTY with complementary fragmentation approaches, including higher-collisional dissociation (HCD) and electron transfer dissociation (ETD), confirmed the presence of sulfation via neutral loss but was unable to localize the sites of modification (Figure 2B). A tryptic digest of AΔSH revealed an N-terminal trypsin fragment
A. albimanus intact baculovirus extract

F. gambiae intact baculovirus extract

**Figure 2.** Analysis of A<sup>Ag</sup> and A<sup>Aa</sup> produced in *Trichoplusia ni* insect cells by nanoLC−MS/MS. (A) [M + 5H]<sup>5+</sup> extracted ion chromatograms and average precursor MS1 spectrum of full-length A<sup>Aa</sup> in the unmodified, mono-, and disulfated isoforms. (B) HCD MS/MS of disulfated A<sup>Aa</sup> [M + 5H + 2SO₃]<sup>5+</sup>. (C) In silico tryptic digestion of A<sup>Aa</sup> highlighting the potential sites of tyrosine sulfation. (D) Extracted ion chromatograms of synthetic and trypsin-digested monosulfated peptide APQYAPGDEPSYDEDTDDSDK of A<sup>Aa</sup>. (E) EThcD MS/MS of the monosulfated peptide LVENDTSITDEDYAAIEASLSETFNTAADPGR of A<sup>Aa</sup>. (F) [M + 8H]<sup>8+</sup> extracted ion chromatograms and average precursor MS1 spectrum of full-length A<sup>Ag</sup> in the unmodified and monosulfated isoforms. (G) HCD MS/MS of disulfated A<sup>Ag</sup> [M + 8H + 2SO₃]<sup>8+</sup>. (H) In silico tryptic digestion of A<sup>Ag</sup> highlighting the potential sites of tyrosine sulfation. (I) EThcD MS/MS of the monosulfated peptide GDVPTYDEEDFDEESLKP of A<sup>Ag</sup> (* indicates ions that contain SO₃<sup>−</sup>).*
Having established that A\textsuperscript{\textit{Ag}} and A\textsuperscript{\textit{Aa}} can be sulfated in vivo (albeit as heterogeneous mixtures), we next sought to investigate the effect of a given tyrosine sulfate modification on thrombin inhibitory activity, which necessitated access to homogeneously sulfated variants of the anophelins. Toward this end, we initially envisaged the use of amber-stop codon suppression,\textsuperscript{14} a methodology that has been used by Schultz and co-workers for the production of sulfated hirudin.\textsuperscript{15,16} Importantly, this technology enables ribosomal incorporation of sulfated tyrosine at a genetically encoded site using a mutated tRNA/tRNA synthetase pair and therefore removes the heterogeneity of enzymatic TPST-catalyzed sulfation observed in the insect cell expression system. Because in vivo expression with sulfotyrosine requires unusually high concentrations of the unnatural amino acid\textsuperscript{17} (presumably because of poor uptake by the cells), we chose to access the sulfated A\textsuperscript{\textit{Aa}} and A\textsuperscript{\textit{Ag}} through cell-free expression with amber codon incorporation of the sulfated tyrosine residues at the specific sites shown to be sulfated in the baculovirus system. Briefly, A\textsuperscript{\textit{Aa}} and A\textsuperscript{\textit{Ag}} were expressed in vitro supplemented with sulfotyrosine, optimized suppressor-tRNA,\textsuperscript{18} and purified sulfotyrosyl-tRNA synthetase\textsuperscript{19,20} or polyspecific p-cyanophenylalanyl-tRNA synthetase. The anophelin constructs were fused N-terminally to His\textsubscript{6}-tagged ubiquitin, which permitted affinity purification of the expressed protein and liberation of the native sequence through proteolytic cleavage with deubiquitinate.\textsuperscript{20} (see the Supporting Information for methods and characterization data). By means of this cell-free expression strategy, a homogeneous variant of the monosulfated A\textsuperscript{\textit{Ag}} Cfe1 (displaying sulfation at Tyr12) was generated, together with the truncated polypeptide in which the ribosomal synthesis stopped at the amber codon. Cfe1 could be easily separated from the truncated polypeptide via reversed-phase HPLC to generate pure monosulfated Cfe1. Unfortunately, attempts to express doubly sulfated A\textsuperscript{\textit{Aa}} were unsuccessful. Nonetheless, with the sulfated A\textsuperscript{\textit{Ag}} Cfe1 in hand, we next assessed the effect of sulfation at Tyr12 on the inhibitory activity against human \textalpha;-thrombin by measuring the rate of thrombin-catalyzed cleavage of the chromogenic substrate Tos-Gly-Pro-Arg-p-nitroanilide in the presence of Cfe1 (see the Supporting Information ). Importantly, we were able to demonstrate that Cfe1 was a significantly more potent thrombin inhibitor ($K_i = 1.13 \pm 0.21$ pM) than the unsulfated counterpart ($K_i = 5.50 \pm 1.26$ pM),\textsuperscript{9} thus validating our hypothesis that sulfation is capable of modulating the thrombin inhibitory activity of anophelins. However, as a result of the small quantities of A\textsuperscript{\textit{Ag}} produced (300 µg from a 10 mL cell-free reaction) coupled with the fact that in our hands doubly sulfated A\textsuperscript{\textit{Aa}} could not be accessed through this methodology, we sought an alternative means to access the entire family of differentially sulfated variants of the two proteins. For this purpose, we turned to a chemical synthesis approach as a means of preparing the entire family of sulfoforms for both A\textsuperscript{\textit{Aa}} and A\textsuperscript{\textit{Ag}} in sufficient quantities for in depth in vitro and in vivo studies.

\textbf{Chemical Synthesis of Homogeneously Sulfated A\textsuperscript{\textit{Aa}} and A\textsuperscript{\textit{Ag}} Proteins.} Syn1—Syn4 represented the differentially sulfated A\textsuperscript{\textit{Aa}} and A\textsuperscript{\textit{Ag}} targets for chemical synthesis. As both A\textsuperscript{\textit{Aa}} and A\textsuperscript{\textit{Ag}} exceed the typical polypeptide length limit for preparation by Fmoc-strategy solid-phase peptide synthesis (SPPS) (≈40 residues), it was envisioned that these could be accessed via convergent peptide ligation chemistry. Specifically, our synthetic strategy centered on the use of the native chemical ligation\textsuperscript{21}—desulfurization chemistry that has recently...
been developed for a range of thiol-derived amino acids.\textsuperscript{22−24} We began by designing a synthetic strategy that would enable access to the three possible sulfated variants of the 61-residue A\textsuperscript{Ag}. Toward this end, we envisaged disconnection near the middle of the sequence between Thr30 and Asp31, which would enable assembly through ligation−desulfurization chemistry at β-thiol aspartate.\textsuperscript{25} We conceived that this could be achieved in a one-pot reaction of three suitably functionalized peptide fragments. We envisaged that this could be achieved in a one-pot reaction of three suitably functionalized peptide fragments. With the target fragments in hand, the A\textsuperscript{Ag} sulfoforms (Syn2−4) were next assembled using a one-pot ligation−desulfurization strategy. Specifically, peptide thioester 5 or sulfoprotein library could be assembled from two N-terminal peptide thioester fragments (A\textsuperscript{Ag}1−30), 5 and 6, with tyrosine or sulfated tyrosine at Tyr12, respectively, and two C-terminal fragments (A\textsuperscript{Ag}31−61) bearing a β-thiol aspartate and a reactive TFET thioester on the C-terminus, A\textsuperscript{Ag}7−82. This one-pot ligation−desulfurization sequence provided synthetic A\textsuperscript{Ag}−thiol aspartate-containing peptide fragments 5−8 were readily synthesized by Fmoc-strategy SPPS and purified to homogeneity via reversed-phase HPLC (see the Supporting Information for synthetic details and characterization data). With the target fragments in hand, the A\textsuperscript{Ag} sulfoforms (Syn2−4) were next assembled using a one-pot ligation−desulfurization strategy. Specifically, peptide thioester 5 or sulfoprotein library could be assembled from two N-terminal peptide thioester fragments (A\textsuperscript{Ag}1−30), 5 and 6, with tyrosine or sulfated tyrosine at Tyr12, respectively, and two C-terminal fragments (A\textsuperscript{Ag}31−61) bearing a β-thiol aspartate and a reactive TFET thioester on the C-terminus, A\textsuperscript{Ag}7−82. This one-pot ligation−desulfurization sequence provided synthetic A\textsuperscript{Ag}−thiol aspartate-containing peptide fragments 5−8 were readily synthesized by Fmoc-strategy SPPS and purified to homogeneity via reversed-phase HPLC (see the Supporting Information for synthetic details and characterization data). With the target fragments in hand, the A\textsuperscript{Ag} sulfoforms (Syn2−4) were next assembled using a one-pot ligation−desulfurization strategy. Specifically, peptide thioester 5 or sulfoprotein library could be assembled from two N-terminal peptide thioester fragments (A\textsuperscript{Ag}1−30), 5 and 6, with tyrosine or sulfated tyrosine at Tyr12, respectively, and two C-terminal fragments (A\textsuperscript{Ag}31−61) bearing a β-thiol aspartate and a reactive TFET thioester on the C-terminus, A\textsuperscript{Ag}7−82. This one-pot ligation−desulfurization sequence provided synthetic A\textsuperscript{Ag}−thiol aspartate-containing peptide fragments 5−8 were readily synthesized by Fmoc-strategy SPPS and purified to homogeneity via reversed-phase HPLC (see the Supporting Information for synthetic details and characterization data).
with the chemoselective ligation between reactive sulfopeptide thioester 12 and bifunctional peptide fragment 13, which was carried out under standard buffer conditions (6 M Gn·HCl, 100 mM Na₂HPO₄, 10 mM TCEP, pH 6.2) in the absence of an external thiol additive and reached completion within 5 h as determined by HPLC−MS to afford ligation product 15 (Scheme 2; see the Supporting Information for the crude data). It should be noted that the shorter reaction time led to only partial (25%) loss of the neopentyl ester from the sulfated tyrosine residue. The ligation product was not isolated at this stage, but rather, TFET was added to the crude ligation reaction to activate the unreactive alkyl thioester on the C-terminus of 15 to generate the reactive S-trifluoroethyl thioester, followed by the addition of fragment 14 bearing an N-terminal cysteine residue to facilitate native chemical ligation. In this case, the ligation reaction required 16 h to reach completion and occurred with concomitant deprotection of all of the remaining neopentyl ester. All that remained for the completion of the synthesis was desulfurization of the non-native β-thiol aspartate and cysteine residues to Asp18 and Ala51, respectively. The crude reaction mixture was therefore treated with VA-044, TCEP, and reduced glutathione at 37 °C, and after 16 h the reaction had reached completion as judged by HPLC−MS analysis to afford the A⁸⁶ sulfoprotein Syn1 in

Figure 3. Tyrosine sulfation of A⁸⁴ and A⁸⁶ significantly improves thrombin inhibition and prolongs blood coagulation in vitro. (A, B) Dose response curves for the inhibition of α-thrombin activity by increasing concentrations of (A) unsulfated A⁸⁴ and synthetic sulfated variants Syn2−4 and (B) recombinant A⁸⁶ (cE5)⁹ and synthetic sulfated variant Syn1. (C, D) Dose response curves for the inhibition of γ-thrombin activity by increasing concentrations of (C) unsulfated A⁸⁴ and doubly sulfated variant Syn4 and (D) recombinant A⁸⁶ (cE5)⁹ and synthetic sulfated variant Syn1. (E) Inhibition constants (Kᵢ) for A⁸⁴ and A⁸⁶ sulfoproteins, determined by fitting the inhibited steady-state velocity data to the Morrison model. The given Kᵢ values ± SEM are representative of two independent experiments. Also shown are the thrombin times (TTs), measuring the clotting time of human plasma in the presence of different A⁸⁴ and A⁸⁶ sulfoproteins (at 5 nM). In the absence of inhibitor, the TT was 21.3 s (mean of four replicates), and TT values were not evaluated past 140 s. The TT values reported are means of two independent determinations. Errors are depicted as standard deviations from two independent measurements.
Sulfation Modulates the Thrombin Inhibitory Activity of the Anopheles. Having successfully prepared sulfated Anopheles (Syn1) and the three sulfated variants of Aa (Syn2–4), we next assessed the in vitro inhibition of human α-thrombin by the synthetic sulfoproteins to evaluate the effect of tyrosine sulfation on the activity. The inhibitory potencies of Syn1 and Syn 4 were also assessed against human γ-thrombin, which has a disrupted exosite I. Thus, screening against both α- and γ-thrombin was used to provide an indirect measure of the mode of binding of the inhibitors to thrombin, i.e., whether the anopheles may exhibit enhanced exosite II binding when sulfated.28,29 Inhibition of the amidolytic activities of α- and γ-thrombin by Syn1–4 was assessed using the kinetic assay described above by measuring proteolytic cleavage of the chromogenic substrate Tos-Gly-Pro-Arg-p-nitroanilide (see Figure 3). As expected, on the basis of the data obtained for Cfe1, Try12 sulfation of Aa in Syn1 led to a mild enhancement in the thrombin inhibitory activity (Ki = 1.12 ± 0.23 pM) compared with the unsulfated Aa counterpart (Ki = 5.50 ± 1.26 pM) (Figure 3B,E). A more dramatic effect was observed when sulfation was introduced to Aa in Syn2–4 (Figure 3A,E). Specifically, sulfation at Tyr12 in Syn2 led to a 7-fold improvement in α-thrombin inhibition (Ki = 16.7 ± 1.2 pM for Syn2 vs Ki = 128.3 ± 20.0 pM for unsulfated Aa). Monosulfation at Tyr34 in Syn3 provided a more pronounced improvement in activity over the unmodified Aa (Ki = 7.7 ± 1.1 pM). However, sulfation at both Tyr12 and Tyr34 in Syn4 led to a synergistic improvement in activity with a Ki of 1.7 ± 0.6 pM. Interestingly, while unsulfated Aa and sulfated Syn1 lost 2 and 3 orders of magnitude activity against γ-thrombin (Figure 3D,E), strongly suggesting an inhibitory mode involving exosite I binding, unsulfated Aa and doubly sulfated Syn4 only lost 48–24-fold activity against γ-thrombin (Figure 3C,E). This may suggest that Aa might overcome the decrease in affinity brought about by the disruption of exosite I by establishing an additional interaction with exosite II. Having shown that sulfation of the anopheles led to an improvement in thrombin inhibitory activity in vitro, we next assessed how the sulfated variants affected the time for thrombin-catalyzed blood coagulation using a clinical thrombin time (TT) assay. Gratifyingly, when used at 5 nM concentration, both doubly sulfated Aa (Syn4, TT = 72.5 s) and sulfated Aa (Syn1, TT ≥ 140 s) led to a significant increase in thrombin time over the unmodified counterparts (37 and 64 s for unmodified Aa and Aa, respectively).

Anopheles Sulfoproteins Possess Potent Antithrombotic Activity in Vivo. Having shown that sulfation of Aa and Aa significantly improved the thrombin inhibitory potency and anticoagulant activity in vitro, we next investigated the in vivo antithrombotic activity of the most potent synthetic variants, Syn1 and Syn4. We initially confirmed that sulfated Aa and Aa retained potent inhibitory activity against mouse thrombin by assessing the impact of these inhibitors on the in vivo mouse activated partial thromboplastin time (aPTT), a measure of the time taken for clotting to occur via the intrinsic pathway. Syn1

Figure 4. Effect of thrombin inhibition in vitro and antithrombotic effect of Aa Syn4 and Aa Syn1 in a needle injury thrombus model. (A) Dose response curves of activated partial thromboplastin time (aPTT) in pooled CS7BL/6 plasma for Syn4 and Syn1. (B, C) Time courses of changes in (B) platelet thrombus volume and (C) fibrin total fluorescence intensity over 16 min pre- and post-injection of Syn4 (blue) and Syn1 (red). (D) Representative confocal fluorescence images depicting platelet thrombus and fibrin formation on injured endothelium with no inhibitor, Syn4, and Syn1. Data points represent mean ± SEM of three to five independent pooled plasma samples for the aPTT assay and three independent animals with four to seven injuries each for needle injury experiments, with hirudin as a positive control (see the Supporting Information).
and Syn4 prolonged the aPTT in a concentration-dependent manner (Figure 4A) over a similar dose range required to inhibit human thrombin. To determine the dose requirements of Syn1 and Syn4 to produce an anticoagulant effect in vivo, we performed ex vivo aPTT assays on mouse plasma post-i.v. injection of Syn1, Syn4, or hirudin as a control. Syn1 and Syn4 each prolonged the aPTT in a concentration-dependent manner (see the Supporting Information). The increase in aPTT correlated well with the prolongation in tail bleeding time (see the Supporting Information), confirming the ability of these peptides to counter the hemostatic function of thrombin in vivo. On the basis of the ex vivo aPTT data, we employed therapeutically relevant doses of each inhibitor (typically a 2–3-fold prolongation of the aPTT, i.e., 25.4 × 10⁻² μmol/kg for A₄⁶ Syn4 and 44.3 × 10⁻² μmol/kg for A₆⁶ Syn1) to assess their antithrombotic potentials in vivo. For these studies, we employed a localized needle injury model in the mesenteric venous circulation of mice that leads to the formation of highly reproducible mural thrombi composed of platelets and fibrin, which can be visualized via Alexa 649 αGP1bβ and Alexa 546 αfibrin, respectively. 50 Treatment with the doubly sulfated A₄⁶ Syn4 and monosulfated A₆⁶ Syn1 resulted in major reductions in platelet thrombus volume (Figure 4B) that coincided with reduced formation of fibrin polymers (Figure 4C), culminating in significant reduction of the total thrombus size in both treatment groups (Figure 4D; see the Supporting Information for raw data). Importantly, this potent in vivo antithrombotic activity of sulfated A₄⁶ and A₆⁶ suggests that these molecules may prove useful as leads for the development of effective direct thrombin inhibitors that operate through a novel binding mode compared with those currently used in the clinic. Studies toward this end will be the focus of future work within our laboratories.

**DISCUSSION**

Hematophagous organisms produce a suite of potent inhibitors of the blood coagulation cascade to facilitate blood feeding activities. A number of thrombin-inhibiting peptides and proteins have recently been identified in the salivary glands of a variety of blood feeders, including leeches, ticks, and flies. Post-translational modifications made to these proteins have largely been overlooked, presumably because of the paucity of material that can be isolated and characterized from these small organisms. Previous biochemical characterization of the mosquito-derived anophelins, 6,7 similar to tick salivary proteins, 31 relied on recombinant inhibitors expressed in prokaryotic systems that do not possess the requisite machinery to install PTMs specific to secreted eukaryotic proteins. It is therefore likely that the thrombin inhibitory activity and, by extension, the anticoagulant and antithrombotic potency have been underestimated compared with the activity of the proteins produced natively in the salivary glands. A key finding that post-translational sulfation of tyrosine residues on specific leech and tick proteins significantly improves the thrombin inhibitory activity by 1–3 orders of magnitude exemplifies the importance of post-translational modifications for the modulation of bioactivity. 5,32

Tyrosine sulfation has yet to be observed on salivary proteins from mosquitoes, a possibility that we explored in this work. A bioinformatic approach was employed to predict the presence of this post-translational modification on the anophelins, the thrombin-inhibiting proteins from the *Anopheles* mosquito. Expression of an anophelin from the "new-world" mosquito *A. albimanus* and from the "old-world" mosquito *A. gambiae* in insect cells followed by nanoLC–MS/MS analysis unequivocally demonstrated that these proteins can be sulfated at the predicted tyrosine sites in eukaryotic cells, albeit as heterogeneous mixtures. Small quantities of pure monosulfated A₄⁶ (Cef1) could be generated in a cell-free expression system via amber stop-codon suppression technology, and this material was used to show that sulfation improved the thrombin inhibitory activity of the protein. While the cell-free expression method served as a useful screening tool in this study, the low yields, coupled with the inability to access A₄⁶ bearing two sulfation sites, led to exploration of an alternative means to access differentially sulfated variants of A₄⁶ and A₆⁶ proteins, namely, total chemical synthesis. By means of a one-pot native chemical ligation–desulfurization manifold, the three homogeneously sulfated homologues of A₄⁶ (Syn2–4) and sulfated A₆⁶ (Syn1) were generated in multimilligram quantities in good overall yields, enabling the role of sulfation on thrombin inhibitory and anticoagulant activity to be assessed. Sulfation of A₄⁶ at residues Tyr12 and Tyr34 (Syn4) showed the most dramatic effect, with a 100-fold increase in thrombin inhibition (Kᵢ = 1.7 pM), while A₆⁶ sulfated at Tyr12 (Syn1) led to a 5-fold improvement in activity (Kᵢ = 1.1 pM). The two sulfated anophelins showed differing inhibitory activities against γ-thrombin, which may suggest that the proteins can also associate with exosite II of thrombin.

Both Syn1 and Syn4 exhibited potent anticoagulant activity in a clinical thrombin time assay, prolonged aPTT in a dose-dependent manner ex vivo, and were able to abrogate clot formation in an in vivo needle injury model of thrombosis. These results lay the foundation for the study of these molecules, as well as sulfated anticoagulants from other bloodfeeders, as novel antithrombotic leads. Indeed, our findings now provide the impetus to investigate salivary proteins from other species of mosquito with a view to discovering potent bioactive molecules whose activity is modulated by tyrosine sulfation.

**ASSOCIATED CONTENT**

Supporting Information

The Supporting Information is available free of charge on the ACS Publications website at DOI: 10.1021/acscentsci.7b00612.

Thrombin inhibition data, ligation traces, ex vivo aPTT data, tail bleeding data, needle injury data, and experimental procedures (PDF)

Supporting Information, Table 1 Anophelin from *Anopheles albimanus* (UniProtKB - Q9NJS1) peptides identified by nanoLC-MS/MS following expression in *Trichoplusia ni* insect cells (XLSX)

Supporting Information, Table 2 Anophelin from *Anopheles gambiae* (UniProtKB - Q7Q3R9) peptides identified by nanoLC-MS/MS following expression in *Trichoplusia ni* insect cells (XLSX)

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Notes

The authors declare no competing financial interest.

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