

## Fusion Proteins with Anticoagulant and Fibrinolytic Properties: Functional Studies and Structural Considerations

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### ABSTRACT

In an effort to combine the benefits of fibrinolytics, such as staphylokinase, with those of thrombin inhibitors for the prevention of vessel reocclusion after vascular injury, we have produced several chimeric proteins with plasminogen-activating and thrombin-inhibiting properties. Fusion proteins were constructed consisting of the modules staphylokinase (Sak), the factor Xa cleavage site, and various dipetalin (Dip) domains (H<sub>6</sub>-Sak-Dip-I+II, H<sub>6</sub>-Sak-Dip-I, and H<sub>6</sub>-Sak-Dip-II). Sak stimulates fibrinolysis via activation of plasminogen, whereas dipetalin is a two-domain, Kazal-type inhibitor of thrombin. NMR spectroscopy of the fusion proteins revealed that the molecular structures of the modules are retained in the fusion protein and that no significant interactions occur between the modules in terms of their functionally relevant regions. In enzymatic thrombin inhibition tests and blood coagulation assays (thrombin, prothrombin, and activated partial thromboplastin times), no

significant differences in anticoagulant capacity were observed between the fusion protein H<sub>6</sub>-Sak-Dip-I+II and isolated Dip-I+II, even at nanomolar concentrations. Similar results (i.e., the inhibition of thrombin-induced platelet aggregation and the inhibition of thrombin-induced vascular relaxation) were obtained when the cellular thrombin effects were studied. The fusion protein containing Dip-I has less but still significant thrombin inhibitory effects compared with those of H<sub>6</sub>-Sak-Dip-I+II. In contrast, the H<sub>6</sub>-Sak-Dip-II protein failed to inhibit thrombin in each of the assays used. The plasminogen-activating and fibrinolytic activities of the fusion proteins are similar to those of wild-type Sak. The individual dipetalin domains do not activate plasminogen. In conclusion, the fusion protein H<sub>6</sub>-Sak-Dip-I+II is a bifunctional molecule able to activate fibrinolysis via plasminogen activation and inhibit blood coagulation via direct inhibition of thrombin.

Progress in the therapy of thromboembolic diseases, besides interventional cardiology, can be attributed to drug intervention in blood coagulation and fibrinolysis. To this end, effective inhibitors of blood coagulation are available, especially thrombin inhibitors, such as heparins and cumarins. The pharmacokinetic and -dynamic properties of low molecular weight synthetic inhibitors, as well as their thrombin specificity, have not yet been optimized (Hauptmann and Sturzebecher, 1999). Proteins with thrombin inhibitory potency previously isolated from hematophagous animals exhibit an extremely high specificity for serine proteinases (Markwardt, 1994a,b). A representative of this class of substances is hirudin, which is now introduced in clinical therapy (Markwardt, 1994c). Other proteins also belonging to the Kazal-type thrombin inhibitor class, such as rhodniin (Friedrich et al., 1993) and dipetalin (Guhrs et al., 1996), have not yet reached the clinical setting.

Plasminogen activators convert the zymogen plasminogen into plasmin, which initiates the lysis of blood clots. Staphylokinase (Sak), a plasminogen activator originally isolated from *Staphylococcus aureus*, exhibits a high thrombolytic efficacy (Collen and Van de Werf, 1993). Recent reports on staphylokinase-related research (Thomson, 1999; Okada et al., 2000; Wong and White, 2000; Goldhaber, 2001; Moons et al., 2001; Sazonova et al., 2001) demonstrate the growing interest in the development of Sak-based plasminogen activators. In addition, Sak is presently undergoing clinical trials (Armstrong et al., 2000; Heymans et al., 2000; Laroche et al., 2000) as a potential drug for thrombolytic treatment.

Despite successful lytic therapy of thromboembolic disorders, such as acute myocardial infarction, reocclusion of the damaged vessels frequently reduces the therapeutic effect. Because there is a high procoagulatory potential with increased thrombin liberation at the injured site of the vessel,

**ABBREVIATIONS:** Sak, staphylokinase; Dip-I, N-terminal domain of dipetalin; Dip-II, dipetalin second domain; Dip-I+II, dipetalin consisting of the two N-terminal domains; H<sub>6</sub>-Sak, staphylokinase with six His residues in N-terminal position and Gln through Leu followed by the FXa cleavage site (Ile-Glu-Gly-Arg) at the C terminus; FXa, activated coagulation factor X; HSQC, heteronuclear single-quantum correlation; PGF<sub>2α</sub>, prostaglandin F<sub>2α</sub>; S-2251, synthetic chromogenic substrate for plasmin; PAGE, polyacrylamide gel electrophoresis; TT, thrombin time; PT, prothrombin time; aPTT, activated partial thromboplastin time.

the simultaneous administration of fibrinolytics and thrombin inhibitors would be a reasonable step in preventing re-occlusion (Turpie et al., 1995). This concept encouraged us to combine both activities in one active compound by formation of fusion proteins. Several attempts to design such proteins with combined plasminogen-activating and thrombin-inhibiting activity have been reported (Szarka et al., 1999; van Zyl et al., 2000; Szemraj et al., 2001). In most of these studies, hirudin was used in the fusion proteins as a C-terminal or N-terminal module when fused to Sak. Additional components to improve targeting were included in the fusion proteins (e.g., the incorporation of a tissue-type plasminogen activator kringle domain for targeting to fibrin or of an RGD sequence motif for platelet binding) (Szemraj et al., 2001).

The arbitrary combination of modules with desired functions, however, often does not take into account structural aspects. Due to molecular interactions of the individual components, possible variations of protein structure and of influence on functionally relevant regions are rarely considered. Limitations in the functional efficacies of these designed fusion proteins may be explained along these lines.

In this report, we present functional and structural studies of fusion proteins consisting of the plasminogen activator staphylokinase and the thrombin inhibitor dipetalin. The construction of the fusion protein was based on rational aspects derived from our previous studies on structure and function of the individual modules of staphylokinase (Ohlenschlager et al., 1998; Parry et al., 1998; Schlott et al., 1998) and dipetalin. This two-domain thrombin inhibitor was isolated from the predatory insect *Dipetalogaster maximus* (Guhrs et al., 1996), and its structure was characterized in our laboratories (Schlott et al., 2002). In the present study, the anticoagulant activities of the fusion proteins H<sub>6</sub>-Sak-Dip-I, H<sub>6</sub>-Sak-Dip-II, and H<sub>6</sub>-Sak-Dip-I+II and the isolated dipetalin domains were measured using global coagulation tests. Furthermore, the inhibitory effects on thrombin-induced cellular events, such as platelet aggregation and relaxation of prostaglandin F<sub>2α</sub> (PGF<sub>2α</sub>)-precontracted porcine pulmonary arteries, were compared. We used an assay with the chromogenic substrate S-2251 and the fibrin plate method to assess the influence of the purified proteins on plasminogen activation and fibrinolysis. NMR experiments were performed to assess the structural integrity of the modules in the fusion protein and determine conformational changes in functionally relevant molecular sites.

## Materials and Methods

**Protein Expression and Purification.** The H<sub>6</sub>-Sak-Dip-I+II, H<sub>6</sub>-Sak-Dip-I, and H<sub>6</sub>-Sak-Dip-II fusion proteins were produced recombinantly by transforming *Escherichia coli* TG1 cells with the expression plasmids *pMEXH<sub>6</sub>-Sak42D-(QL)-FXa-Dip-I+II*, *pMEXH<sub>6</sub>-Sak42D-(QL)-FXa-Dip-I*, and *pMEXH<sub>6</sub>-Sak42D-(QF)-FXa-Dip-II*, respectively. Cell cultivation, stimulation of expression, cell harvesting, and the preparation of cell extracts were performed as described by Schlott et al. (1994). Fusion protein purification was achieved by a uniform, multistep chromatographic procedure: two repetitions of metal-chelating chromatography using Ni(II)-chelating Sepharose (Amersham Biosciences, Freiburg, Germany) and Ni-nitrilotriacetic acid agarose (QIAGEN GmbH, Hilden, Germany) were followed by gel filtration (Superdex 75 HR 16/60 column; Amersham Biosciences) and anion exchange chromatography (MonoQ HR 5/5 column; Amersham Biosciences). The cleavage of the fusion proteins by FXa (New England

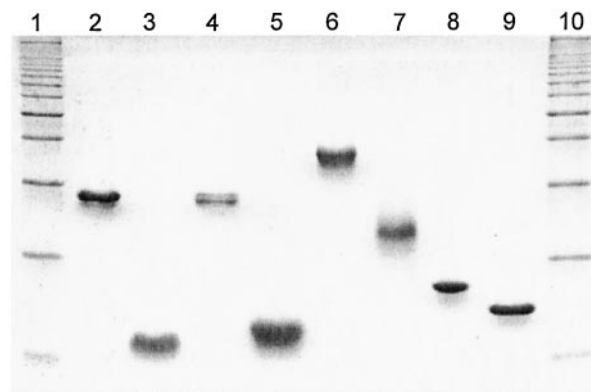
Biolabs, Schwalbach, Germany) was performed as described by Schlott et al. (1997). Separation of the individual dipetalin domains from H<sub>6</sub>-Sak was performed by metal-chelating Ni-nitrilotriacetic acid chromatography (QIAGEN). Final Dip-domain purification from the column flow-through was achieved by gel filtration. After being eluted from the metal-chelate column, the H<sub>6</sub>-Sak protein was purified by cation exchange chromatography (MonoS HR 5/5 column; Amersham Biosciences). The purity and identity of the isolated proteins was confirmed by SDS-PAGE (Fig. 1), matrix-assisted laser desorption/ionization-mass spectrometry, and N-terminal sequencing (data not shown). For preparation of the <sup>15</sup>N-labeled fusion protein, the culture medium was supplemented with <sup>15</sup>NH<sub>4</sub>Cl (Cambridge Isotopes Laboratories, Inc., Andover, MA) as described by Ohlenschlager et al. (1997, 1998). The protein isolation procedure was the same as detailed above. After adding 35 μl of D<sub>2</sub>O (Cambridge Isotopes Laboratories, Inc.), the sample had a volume of 600 μl in a sealable NMR tube, which yielded a final concentration of 1.0 mM U-[<sup>15</sup>N]-H<sub>6</sub>-Sak-Dip-I. All chemicals (i.e., buffer substances and components for SDS-PAGE) were of the highest quality commercially available.

**NMR Spectroscopy.** Two-dimensional [<sup>1</sup>H-<sup>15</sup>N]-HSQC experiments (Bodenhausen and Ruben, 1980) were recorded at 15°C on an INOVA 750-MHz four-channel NMR spectrometer (Varian, Inc., Palo Alto, CA). The NMR spectra were processed with the VNMR software (Varian, Inc.) and analyzed using the program XEASY (Bartels et al., 1995).

**Clotting Assays.** The thrombin time (TT), prothrombin time (PT), and activated partial thromboplastin time (aPTT) were measured using a Thrombotrack 8 coagulometer (Immuno, Heidelberg, Germany). Commercially available test kits (Immuno, Vienna, Austria) were used. All measurements were carried out in duplicate according to the guidelines of the manufacturer.

**Activation of Plasminogen and Fibrinolytic Activity.** Activation of plasminogen (final concentration, 1.5 μM) induced by the proteins tested (final concentration, 5 nM) was assayed at 37°C in 0.1 M phosphate buffer, pH 7.4, containing 0.1% (v/v) Tween 80. Aliquots (5 μl) were withdrawn at different time intervals (0–30 min) and diluted 50-fold in a 1 mM solution of the chromogenic plasmin substrate S-2251. The plasmin generated was determined at different time intervals by measuring the change in absorbance at 405 nm over a period of 1 min.

Kinetic analysis of plasminogen activation was performed as described by Collen et al. (1993b). Initial activation rates were obtained from plots of concentration versus activation time of plasmin generated. The kinetic constants  $K_M$ ,  $k_{cat}$ , and catalytic efficiency  $k_{cat}/K_M$  were calculated using the Lineweaver-Burk plot. Measurement of fibrinolytic activity using fibrin plates was performed according to the method of Astrup and Müllertz (1952).



**Fig. 1.** 13.75% SDS-PAGE of the purified fusion proteins and isolated dipetalin domains. Lanes 1 and 10, 10-kDa protein calibration mixture (Invitrogen, Carlsbad, CA) (the lowest band refers to 10 kDa); lane 2, H<sub>6</sub>-Sak-Dip-I; lane 3, Dip-I; lane 4, H<sub>6</sub>-Sak-Dip-II; lane 5, Dip-II; lane 6, H<sub>6</sub>-Sak-Dip-I+II; lane 7, Dip-I+II; lane 8, H<sub>6</sub>-Sak; and lane 9, Sak42D.

**Plasma Clot Lysis Time.** To 100  $\mu\text{l}$  of human citrated plasma, 100  $\mu\text{l}$  of the proteins tested ( $\text{H}_6\text{-Sak-Dip-I+II}$  and  $\text{H}_6\text{-Sak}$ ; final concentration, 100 nM) were added. The determination of the clot lysis time was performed as two-step process with a Thrombotrack 4 coagulometer, which allows measurement of both clot formation and fibrinolysis. After the addition of 50  $\mu\text{l}$  of thrombin (final concentration, 80–200 nM), clots were induced within <10 s, subsequently, and the lysis time was measured in the same experimental system over a period of 15 min.

**Platelet Aggregation.** Platelet aggregation was monitored using an aggregometer AFACT 4 (Labor GmbH, Ahrensburg, Germany). Washed platelets were obtained from peripheral, citrate-anticoagulated blood of healthy volunteers according to Glusa et al. (1997). Measurement of ADP- and collagen-induced platelet aggregation was carried out with platelet-rich plasma. The platelet count was adjusted to  $3 \times 10^8$  platelets/ml. Proteins tested (final concentrations, 0.5–100 nM) were added to the platelet suspension 3 min before the addition of aggregation-inducing agents. Changes in light transmission of the platelet suspension were recorded continuously for a maximum of 10 min. The extent of aggregation was determined by measuring the maximum amplitude of an increase in light transmission. Percentage values were derived from the ratio of the extent of aggregation in samples with the test compounds compared with those without.

**Vascular Relaxation Studies on Isolated Vessels.** Porcine lungs were obtained from the local slaughterhouse. Small branches of pulmonary arteries were carefully prepared, cut into rings (2 to 3 mm long and 1.5 to 2 mm wide), fixed between two L-shaped platinum hooks in a 10-ml organ bath filled with modified Krebs-Henseleit solution at 37°C (Glusa et al., 1996) and continuously gassed with 95%  $\text{O}_2/5\%$   $\text{CO}_2$ . Changes in tension were recorded isometrically. Resting tension was adjusted to 20 mN throughout each experiment. After an initial stabilization period of 60 min, the rings were stimulated at intervals of 45 min, once with KCl (45 mM) and three times with  $\text{PGF}_{2\alpha}$  (3  $\mu\text{M}$ ), until the contractile response had become constant. The integrity of the endothelium was assessed functionally by measuring the relaxation after application of bradykinin to a final concentration of 10 nM. In endothelium-denuded vessels, this relaxation was absent. The relaxant response to thrombin was studied when the contraction had reached a plateau after the addition of  $\text{PGF}_{2\alpha}$ . Dipetalins and fusion proteins were added to the organ bath 5 min before thrombin.

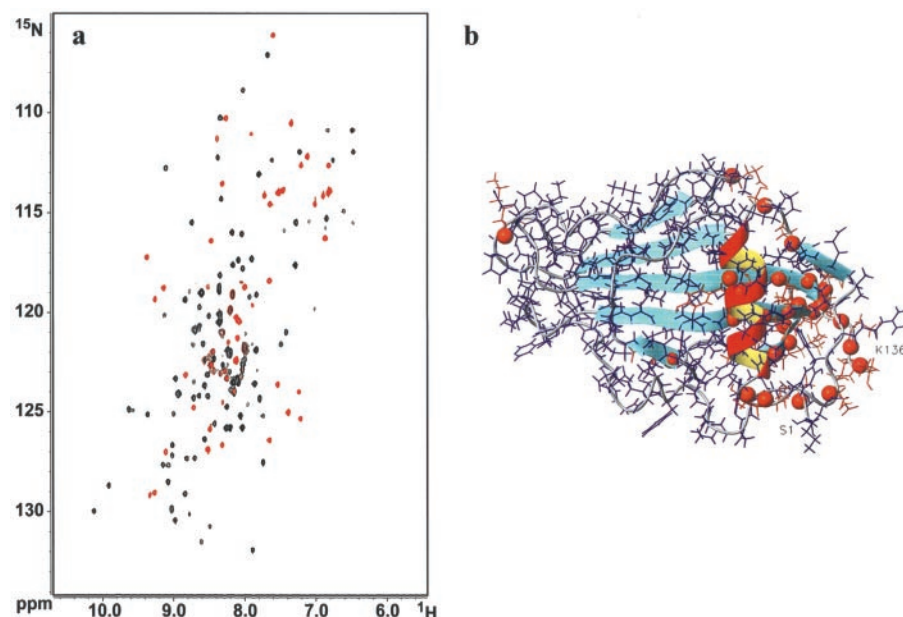
**Data Analysis.** Data are represented as mean  $\pm$  S.E.M. for  $n$  separate experiments. Concentration-effect curves were fitted using

the computer program Origin (OriginLab Corp., Northampton, MA). Comparison of means was made using Student's  $t$  test modified according to the Bonferroni method. Differences were considered statistically significant at  $p < 0.05$ .

## Results

**NMR Spectroscopy of the Fusion Proteins.** NMR spectroscopy was used to identify structural changes in the fused modules of the proteins  $\text{H}_6\text{-Sak-Dip-I}$  and  $\text{H}_6\text{-Sak-Dip-I+II}$ . The comparison of  $[\text{H}-^{15}\text{N}]$ -HSQC data of Sak (Ohlenschlager et al., 1997) and Dip-I (Schlott et al., 2002) with the spectrum of the respective fusion protein identifies residues affected. For the sake of clarity, this approach is shown in Fig. 2a for  $\text{H}_6\text{-Sak-Dip-I}$ . The  $[\text{H}-^{15}\text{N}]$ -HSQC spectrum of  $\text{H}_6\text{-Sak-Dip-I}$  consists of the sum of signal sets observed for the individual protein components. Only a few residues exhibited larger chemical shift variations in the  $^1\text{H}$  and  $^{15}\text{N}$  dimensions. Figure 2b shows a mapping of these residues onto the staphylokinase solution structure (Ohlenschlager et al., 1998). With two exceptions ( $\text{Lys}^{96}$  and  $\text{Glu}^{46}$ ), all affected residues are located in the vicinity of the C terminus of the staphylokinase part of the fusion protein as expected because of the short linker element of six amino acids between staphylokinase and the dipetalin modules. A similar observation is made in the  $[\text{H}-^{15}\text{N}]$ -HSQC spectrum of  $\text{H}_6\text{-Sak-Dip-I+II}$ , which can be described as the sum of the spectra of the three contributing domains. The  $[\text{H}-^{15}\text{N}]$ -HSQC spectra also indicate that Sak and the dipetalin domains in the fusion protein display their native folds. In addition, only minor interactions between the plasminogen-activating and the thrombin-inhibiting modules take place, as shown by the low number of resonances shifted.

**Plasminogen Activation and Fibrinolytic Activity.** Using chromogenic substrate tests, it was shown that the fusion proteins (listed in Table 1) had a time course of plasminogen activation that was similar to that of the wild-type Sak and  $\text{H}_6\text{-Sak}$  (Fig. 3). Differences at the 5-min data point were not statistically significant. From 10 min onward, the plasmin generation rate stabilized at a steady-state level. In



**Fig. 2.** a,  $[\text{H}-^{15}\text{N}]$ -HSQC spectrum of the  $\text{H}_6$ -[staphylokinase]-QL-IEGR-[dipetalin-I] fusion protein. The cross peaks originating from the dipetalin-I and staphylokinase domains are shown in red and black, respectively. b, mapping of the residues experiencing a higher deviation in the chemical shift values in the  $[\text{H}-^{15}\text{N}]$ -HSQC spectrum onto the solution structure of staphylokinase (nitrogen atoms and side chains are highlighted by orange spheres and bonds, respectively). The figure was produced using the MOLMOL program (Koradi et al., 1996).

contrast to the fusion proteins, the isolated dipetalin domains did not activate plasminogen (Fig. 3). The kinetic data of plasminogen activation were nearly identical for the fusion proteins H<sub>6</sub>-Sak and Sak (data not shown). In addition, the fibrinolytic activity of fusion proteins was estimated using the fibrin plate assay (Fig. 4). The fusion proteins elicited a concentration-dependent fibrinolysis that did not differ statistically from that of Sak and H<sub>6</sub>-Sak. Hence, the fibrinolytic activity of the Sak module was not affected by the presence of additional modules in the fusion proteins.

**Anticoagulant Effects.** To evaluate the anticoagulant effects of the dipetalin domains and fusion proteins, the TT, aPTT, and PT were measured. As shown in Fig. 5a, a significant prolongation of the TT (final thrombin concentration, 20 nM) was produced by Dip-I+II and H<sub>6</sub>-Sak-Dip-I+II at concentrations >10 nM. Concentrations of H<sub>6</sub>-Sak-Dip-I and Dip-I greater than 10-fold higher were necessary to significantly increase the TT. For H<sub>6</sub>-Sak-Dip-II and Dip-II, no TT prolongation was achieved even when their concentrations were raised to more than 1 μM. The effect of H<sub>6</sub>-Sak on TT was negligible (Fig. 5a). The extent of TT prolongation by the proteins tested correlated with their respective K<sub>i</sub> values, reflecting the thrombin-inhibitory capacity in enzymatic tests (see Table 1).

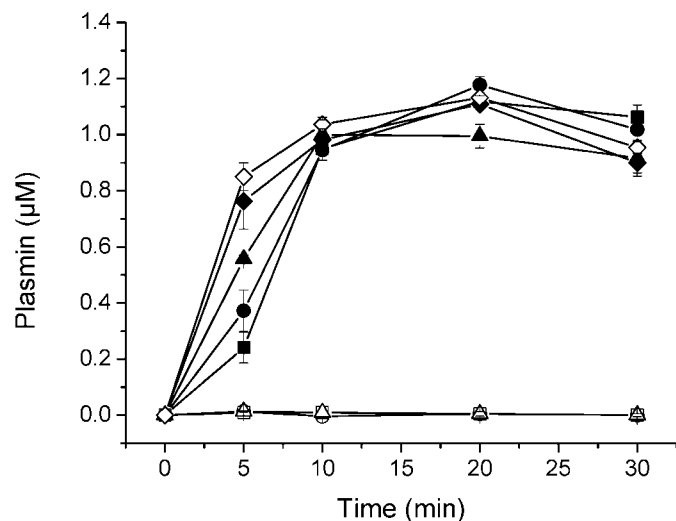
The increase in the aPTT (Fig. 5b) confirmed the thrombin-

TABLE 1

Predicted molecular masses derived from the primary structure, masses determined by mass spectroscopy, and the K<sub>i</sub> values of the respective proteins for the interaction with thrombin

	Primary Structure	MALDI-MS	K <sub>i</sub>
	Da	M <sup>+</sup> H <sup>+</sup>	pM
H <sub>6</sub> -Sak-Dip-I	23,167	23,264	353
Dip-I	6,083	6,077	75
H <sub>6</sub> -Sak-Dip-II	23,717	23,750	≥353
Dip-II	6,598	6,576	≥353
H <sub>6</sub> -Sak-Dip-I + II	29,096	29,158	0.91
Dip-I + II	12,011	11,995	0.78
H <sub>6</sub> -Sak	17,102	17,175	≥353
Sak42D	15,583	N.D.	N.D.

N.D., not determined; MALDI-MS, matrix-assisted laser desorption ionization-mass spectrometry.



**Fig. 3.** Activation of plasminogen (final concentration, 1 μM) as a function of time by Sak42D (◇), H<sub>6</sub>-Sak (◆), H<sub>6</sub>-Sak-Dip-I+II (●), Dip-I+II (○), H<sub>6</sub>-Sak-Dip-I (■), Dip-I (◻), H<sub>6</sub>-Sak-Dip-II (▲), and Dip-II (△) (final concentrations, 5 nM each). Data shown are mean ± S.E.M.; n = 5.

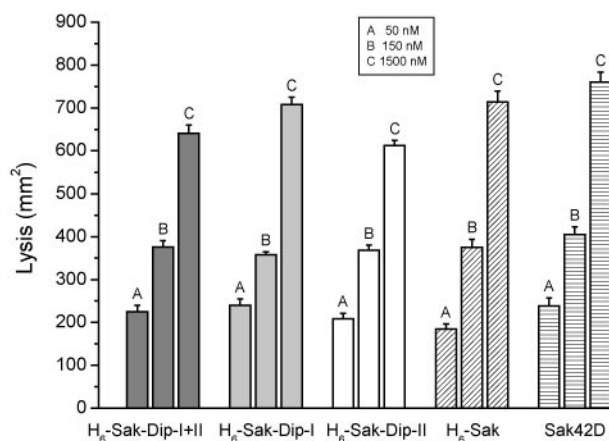
inhibitory potency of Dip-I+II and H<sub>6</sub>-Sak-Dip-I+II. In contrast, Dip-II, Dip-I, and the respective fusion proteins caused significantly weaker anticoagulant effects. The H<sub>6</sub>-Sak did not affect the aPTT.

As shown in Fig. 5c, a significant prolongation of the PT was observed only in the presence of Dip-I+II and H<sub>6</sub>-Sak-Dip-I+II. However, concentrations of 300 nM were required to inhibit coagulation.

**Plasma Clot Lysis Time.** In presence of H<sub>6</sub>-Sak (100 nM), a clot was formed 4 to 7 s after the addition of 80 to 200 nM thrombin (Fig. 6a). In this system, clot lysis was completed after 608 ± 8 s (Fig. 6b). Addition of H<sub>6</sub>-Sak-Dip-I+II (100 nM) to the plasma required higher thrombin concentrations (>80 nM) for inducing coagulation. At 90 nM thrombin, a clot was present after 25.1 ± 4.4 s, whereas at 100 nM, clot formation time was below 10 s (Fig. 6a). The subsequent clot lysis time was not significantly different from that measured in the presence of H<sub>6</sub>-Sak or wild-type Sak (Fig. 6b). In control experiments, the thrombin-induced clot was stable against lysis over the period of 15 min, which rules out the contribution of endogenous plasminogen activators.

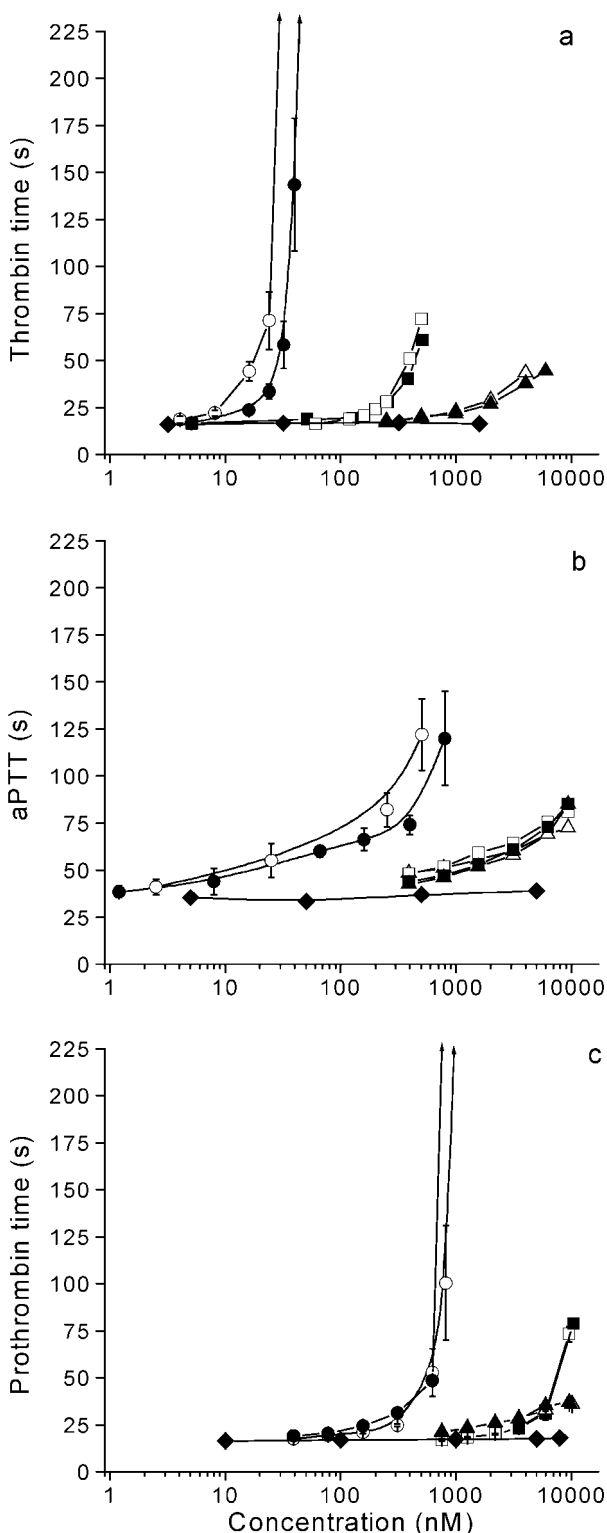
**Inhibition of Thrombin-Induced Platelet Aggregation.** Dip-I+II and H<sub>6</sub>-Sak-Dip-I+II strongly inhibited thrombin-induced (1 nM) platelet aggregation (Fig. 7). A significant inhibitory effect was obtained at a concentration as low as 1 nM, whereas 20-fold higher concentrations were required to obtain similar inhibition of aggregation by Dip-I and H<sub>6</sub>-Sak-Dip-I (Fig. 7). Dip-II and H<sub>6</sub>-Sak-Dip-II produced no significant inhibitory effects on thrombin-induced platelet aggregation at comparably high concentrations (data not shown). In addition, the fusion proteins did not affect ADP- and collagen-induced aggregation.

**Influence on Vascular Relaxation.** In porcine pulmonary arteries with intact endothelium, thrombin (1 nM) caused a reversible relaxation of PGF<sub>2α</sub>-precontracted vessels of 84 ± 5% (n = 20). As shown in Fig. 8, Dip-I+II and H<sub>6</sub>-Sak-Dip-I+II proved to be potent inhibitors of thrombin-induced, endothelium-dependent relaxation. Dip-I and H<sub>6</sub>-Sak-Dip-I showed similar results, but 10× higher concentrations were necessary to obtain significant inhibitory effects. In contrast to these findings, no inhibition of relaxation was obtained with Dip-II, H<sub>6</sub>-Sak-Dip-II, and H<sub>6</sub>-Sak. Thus, the present experiments confirm that the dipetalin domains and



**Fig. 4.** Concentration-effect curves for fibrinolysis by H<sub>6</sub>-Sak-Dip-I, H<sub>6</sub>-Sak-Dip-II, H<sub>6</sub>-Sak-Dip-I+II, H<sub>6</sub>-Sak, and Sak on fibrin plates after 20 h. Data are given as mean ± S.E.M.; n = 8–9.

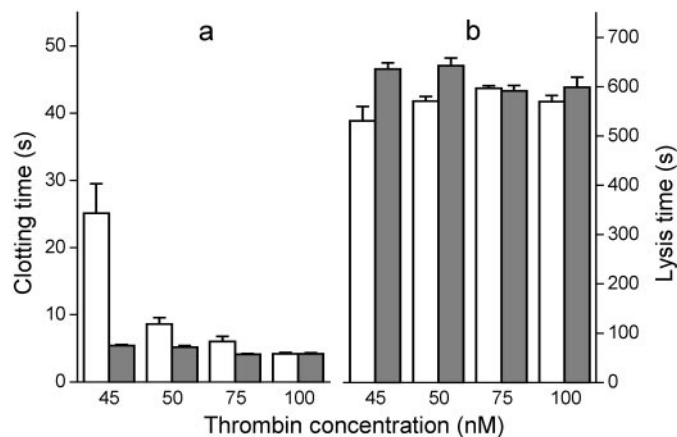
fusion proteins containing these domains block cellular effects of thrombin in a way that correlates with the inhibition of the proteolytic activity of thrombin.



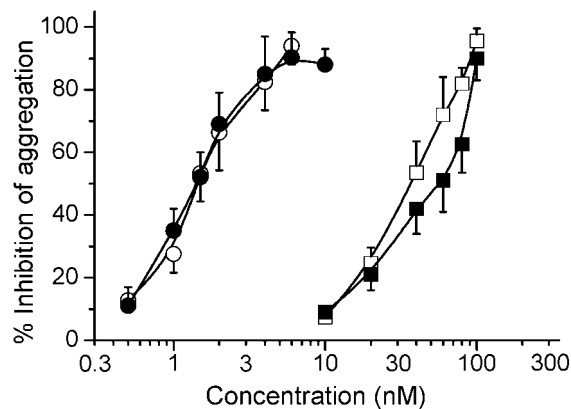
**Fig. 5.** Changes in TT (a, control:  $16 \pm 1$  s), aPTT (b, control:  $41 \pm 2$  s), and PT (c, control:  $17 \pm 1$  s) after preincubation of human plasma with H<sub>6</sub>-Sak-Dip-I+II (●), Dip-I+II (○), H<sub>6</sub>-Sak-Dip-I (■), Dip-I (□), H<sub>6</sub>-Sak-Dip-II (▲), Dip-II (△), and H<sub>6</sub>-Sak (◆). Data shown are mean  $\pm$  S.E.M.;  $n = 6$ .

### Discussion

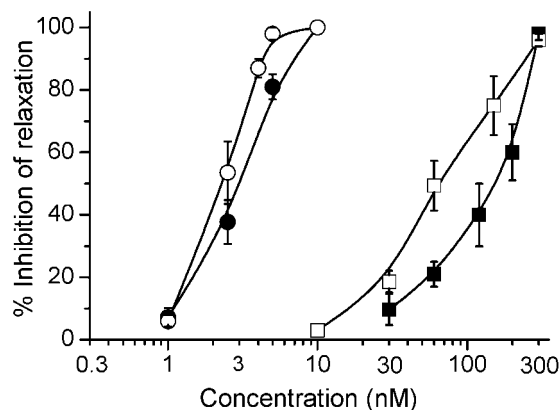
The synthesis of fusion proteins is a feasible way of designing multifunctional compounds of pharmacological interest. Therapy of thromboembolic disorders can be improved by the application of compounds that simultaneously dissolve a thrombus and inhibit the de novo formation of blood clots



**Fig. 6.** Plasma clot formation times (a) and clot lysis times (b) induced by H<sub>6</sub>-Sak-Dip-I+II (□) and H<sub>6</sub>-Sak (■). Data are given as mean  $\pm$  S.E.M.;  $n = 20$ .



**Fig. 7.** Concentration-response relationships for the inhibition of thrombin-induced (1 nM) aggregation of washed human platelets by H<sub>6</sub>-Sak-Dip-I+II (●), Dip-I+II (○), H<sub>6</sub>-Sak-Dip-I (■), and Dip-I (□). Data shown are mean  $\pm$  S.E.M.;  $n = 4-5$ .



**Fig. 8.** Concentration-response relationships for the inhibition of thrombin-induced (1 nM) endothelium-dependent relaxation of PGF<sub>2 $\alpha$</sub> -precontracted porcine pulmonary arteries by H<sub>6</sub>-Sak-Dip-I+II (●), Dip-I+II (○), H<sub>6</sub>-Sak-Dip-I (■), and Dip-I (□). Data shown are mean  $\pm$  S.E.M.;  $n = 5$ .

(Collen and Lijnen, 1995; van Zyl et al., 1997). These goals can be achieved by the combination of a thrombin inhibitor and a plasminogen activator. However, the results obtained to date (i.e., with hirudin N- or C-terminally fused to staphylokinase) have not been convincing.

The outcome of the present study of a new fusion protein that combines the advantageous effects of staphylokinase and the Kazal-type inhibitor dipetalin may indicate a benefit of this protein in therapeutic application. The construction of this Sak-Dip fusion protein was based on this rationale: staphylokinase is a globular protein and the smallest plasminogen activator currently known, with high efficacy in plasminogen activation and fibrinolysis (Collen et al., 1993a; Collen and Van de Werf, 1993); dipetalin is an efficient thrombin inhibitor composed of two molecular domains that are flexible due to an interdomain linker peptide. NMR data demonstrate that the folding of the individual domains of Dip is independent.

Our previous studies (Gase et al., 1996) have shown that Sak can be elongated by adding amino acids to the C terminus without any loss in its plasminogen-activating potency. Therefore, the dipetalin domains were C-terminally fused to Sak by a flexible linker element of six residues. This segment, together with the two flexible Dip domains, was designed to reduce steric hindrance between the individual components and, hence, also minimize restrictions on the bifunctional characteristics.

Some authors argue that the N-terminally fused Sak should be protected against proteolytic activities of plasmin (Szemraj et al., 2001). However, the products of proteolytic processing, mainly Sak $\Delta$ N10, arise during plasminogen activation in any case. Furthermore, we have shown that this N-terminal processing is an essential step in the activation process (Schlott et al., 1997, 1998). The N-terminal extension by a His tag to optimize the protein purification had no disadvantageous effect on the Sak function.

Finally, there was no evidence for an increase in affinity for fibrin when RGD sequences or kringle domains were inserted into a fusion protein (van Zyl et al., 2000; Szemraj et al., 2001). This approach would not seem to be productive, because Sak itself acts in a fibrin-specific manner (Collen et al., 1993b).

The rational design of an optimized bifunctional fusion protein was supplemented by structural studies using NMR spectroscopy. Comparison of the [ $^1\text{H}$ - $^{15}\text{N}$ ]-HSQC spectrum of the fusion protein with the spectra of Sak (Ohlenschlager et al., 1997) and Dip-I (Schlott et al., 2002) shows that the modules in the fusion protein exhibit the same globular fold. The three main areas of Sak identified as important for biological function (Silence et al., 1995) [i.e., residues 1–12 (N terminus), residues around Lys<sup>50</sup>, and residues in the  $\alpha$ -helix from Glu<sup>65</sup> to Asp<sup>69</sup>] are not affected, as demonstrated by the absence of pronounced chemical shift changes in the NMR spectrum of the fusion protein. A similar situation exists for Dip-I, where only a few residues show changes in resonance frequencies, indicating that the core-structural elements are not affected by domain interactions. It is known from heteronuclear relaxation data from a previous study (Schlott et al., 2002) that a higher conformational flexibility is observed at the N terminus and at the four C-terminal residues of the Dip-I module constituting the linker to the Dip-II domain. It also must be assumed that the Sak-Dip-I linker consisting of the six residues QLIEGR does not introduce conformational restrictions. Thus, these flexible linkers allow an independent reorientation of the modules Sak, Dip-I, and Dip-II. Consequently, the NMR results are consis-

tent with the retention of the plasminogen-activating and thrombin-inhibiting properties in the fusion protein.

The present functional studies provide evidence that the fusion proteins, like their individual modules, exhibit both anticoagulant and fibrinolytic effects. The functional experiments comprise global clotting and fibrinolysis tests as well as thrombin-induced platelet aggregation and vascular relaxation. The clotting assays confirm the strong anticoagulant activity of the domain Dip-I+II. Generally, in all tests, including the cellular experiments, the thrombin inhibitory potency of the domains Dip-I and Dip-II was less than that of Dip-I+II. It was previously shown in tests with chromogenic substrates that the combination of Dip-I and Dip-II did not exceed the efficacy of Dip-I alone. Therefore, Dip-II seems to be important for thrombin inhibition only when it is linked to the Dip-I domain via a flexible linker peptide, as indicated from the structural NMR studies (Schlott et al., 2002). Knowledge of the tertiary structure of Dip-II, currently under investigation, is required to clarify whether Dip-II binds to the thrombin anion-binding exosite 1.

There were no significant differences between the anticoagulant activities of the fusion proteins with Sak and the individual Dip domains. On the other hand, the Sak fusion proteins are active as plasminogen activators and fibrinolytic agents with the same potency as the wild-type Sak, whereas the protein domains without Sak are ineffective. Thus, the functional studies confirm the structural NMR results with the fusion proteins as discussed above. Among the different coagulation tests, the TT is the most sensitive method to test the anticoagulant effect of H<sub>6</sub>-Sak-Dip-I+II and Dip-I+II. Higher concentrations of the fusion proteins were required to prolong the aPTT or PT. For comparison, the anticoagulant effects of H<sub>6</sub>-Sak-Dip-I+II and Dip-I+II are in the same concentration range as that for hirudin, the well-known, most potent recombinant thrombin inhibitor (Markwardt, 1994c).

Moreover, it was of interest to demonstrate whether the fusion proteins also inhibited thrombin-induced cellular effects mediated by stimulation of protease-activated receptors. Thrombin is the most potent agonist of platelet activation, and at very low concentrations, it causes human platelet aggregation that can be blocked by H<sub>6</sub>-Sak-Dip-I+II and Dip-I+II at concentrations of the same order of magnitude as found with hirudin (Glusa, 1991) or triabin (Noeske-Jungblut et al., 1995; Glusa et al., 1997). Thrombin-induced, endothelium-dependent relaxation was also inhibited by H<sub>6</sub>-Sak-Dip-I+II and Dip-I+II with the same potency observed for the inhibition of aggregation. Because the same thrombin concentration (1 nM) was used for the inhibition of aggregation and relaxation, the concentration-response curves for the inhibition of both effects had a similar shape. The present results with H<sub>6</sub>-Sak-Dip-I+II and Dip-I+II correlate well with the results for the inhibition of these effects by hirudin and triabin, whereas hirudin had slightly greater effects on the inhibition of thrombin (Markwardt, 1991). Triabin is a thrombin anion-binding exosite 1 inhibitor of thrombin that inhibits the cellular effects, probably by interfering with the thrombin recognition site of protease-activated receptor 1, thereby preventing the cleavage of the N terminus of the receptor.

There were no significant differences between the abilities of the fusion proteins and wild-type Sak to activate plasminogen. These findings were corroborated by the fibrin plate assay. The lysis zones induced by all proteins tested were the same size as

those produced by wild-type Sak. Thus, the plasminogen-activating and fibrinolytic properties remain unchanged in the fusion proteins compared with those of wild-type Sak and H<sub>6</sub>-Sak.

To demonstrate whether the fusion protein is capable of simultaneously discharging its two separate functions (i.e., the inhibition of thrombin and the activation of plasminogen), plasma clot lysis tests were performed. In this test system, H<sub>6</sub>-Sak caused a complete lysis of the thrombin-induced clots without interference with the clotting time. In the presence of the fusion protein H<sub>6</sub>-Sak-Dip-I+II, the clot formation was induced when the thrombin concentration exceeded the capacity of Dip-I+II to bind thrombin, but the subsequent clot lysis was in the same range as seen with H<sub>6</sub>-Sak. Thus, the fusion protein retains its bifunctionality when thrombin is bound, thereby providing evidence for the formation of the ternary thrombin/H<sub>6</sub>-Sak-Dip-I+II/plasminogen complex. This has to be expected when also considering the strong interaction of the dipetalin module with thrombin as shown by a  $K_D$  value in the picomolar range (Schlott et al., 2002). In contrast, H<sub>6</sub>-Sak stimulates only the clot lysis, whereas an interaction with thrombin should be excluded because of its  $K_D \gg 10^{-5}$  M.

The present study demonstrates that the fusion proteins containing Sak and various dipetalin domains exhibit fibrinolytic activity that is comparable with that of wild-type Sak. H<sub>6</sub>-Sak-Dip-I+II and Dip-I+II proved to be potent thrombin inhibitors. The functional results were supported by NMR experiments demonstrating that in the fusion proteins, the molecular structures of the individual modules are retained primarily unchanged. In conclusion, the fusion protein H<sub>6</sub>-Sak-Dip-I+II provides a combined mode of action and hence may be of benefit for the treatment of thromboembolic disorders.

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