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Binding of Thrombin to Glycoprotein Ib Accelerates the Hydrolysis of Par-1 on Intact Platelets*

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The activation of human platelets by α-thrombin is mediated at least in part by cleavage of protease-activated G-protein-coupled receptors, PAR-1 and PAR-4. Platelet glycoprotein Ibα also has a high affinity binding site for α-thrombin, and this interaction contributes to platelet activation through a still unknown mechanism. In the present study the hypothesis that GpIbα may contribute to platelet activation by modulating the hydrolysis of PAR-1 on the platelet membrane was investigated. Gel-filtered platelets from normal individuals were stimulated by α-thrombin, and the kinetics of PAR-1 hydrolysis by enzyme was followed with flow cytometry using an anti-PAR-1 monoclonal antibody (SPAN 12) that recognizes only intact PAR-1 molecules. This strategy allowed measurement of the apparent k_{cat}/K_m value for thrombin hydrolysis of PAR-1 on intact platelets, which was equal to $1.5 \pm 0.1 \times 10^7$ M^{-1} sec^{-1}. The hydrolysis rate of PAR-1 by thrombin was measured under conditions in which thrombin binding to GpIb was inhibited by different strategies, with the following results. 1) Elimination of GpIbα on platelet membranes by mocarhagin treatment reduced the k_{cat}/K_m value by about 6-fold. 2) A monoclonal anti-GpIb antibody reduced the apparent k_{cat}/K_m value by about 5-fold. 3) An oligonucleotide DNA aptamer, HD22, which binds to the thrombin heparin-binding site (HBS) and inhibits thrombin interaction with GpIbα, reduced the apparent k_{cat}/K_m value by about 5-fold. 4) Displacement of α-thrombin from the binding site on GpIb using PPACK-thrombin reduced the apparent k_{cat}/K_m value by about 5-fold, and 5) mutation at the HBS of thrombin (R98A) caused a 5-fold reduction of the apparent k_{cat}/K_m value of PAR-1 hydrolysis. Altogether these results show that thrombin interaction with GpIb enhances the specificity of thrombin cleavage of PAR-1 on intact platelets, suggesting that GpIb may function as a "cofactor" for PAR-1 activation by thrombin.

Platelet activation by the coagulation protease α-thrombin plays a crucial role in physiologic hemostatic processes and in thrombotic diseases. The activation of human platelets by thrombin is mediated by at least two receptors belonging to the family of protease-activated receptors (PARs),[1] *i.e.* PAR-1 and PAR-4 (1–2). These receptors are activated upon cleavage by thrombin and mediate transmembrane signaling by coupling to G-proteins (1–2). α-Thrombin also binds with high affinity to the platelet glycoprotein Ib (GpIb) that belongs to the leucine-rich repeat family of proteins (3). Thrombin binding to GpIb contributes to platelet activation by the enzyme, as demonstrated by the finding that Bernard-Soulier platelets, which lack the GpIb-IX-V complex, have a delayed response to thrombin stimulation (4). In addition, several *in vitro* studies have demonstrated that the inhibition of thrombin binding to GpIb by different strategies causes a reduction in thrombin-induced platelet activation (5–9).

The mechanism by which the binding of α-thrombin to GpIb contributes to platelet activation is not clear. Numerous studies have shown that a proteolytic-active enzyme is required to activate platelets. PPACK-thrombin, which retains its ability to bind to GpIb, does not induce platelet aggregation (10). Moreover, GpIb does not undergo cleavage by thrombin. On the other hand, the cleavage of G-protein-coupled PARs seems to be essential in platelet activation and transmembrane signaling. The finding that thrombin binding to GpIb involves a distinct thrombin domain, the HBS, which is far from the thrombin catalytic site and the fibrinogen recognition site (7–9), would suggest that a ternary complex thrombin·GpIb·PAR-1 may form on the platelet membrane that could be responsible for optimal hydrolysis and signal transduction.

In the present study, the hypothesis that thrombin binding to GpIb may affect the hydrolysis of PAR-1 by the enzyme on intact platelets was investigated. The hydrolysis of PAR-1 was evaluated as a paradigm to construct a model where GpIb acts as a cofactor for PAR(s) cleavage.

EXPERIMENTAL PROCEDURES

Materials—Human α-thrombin was purified and characterized as previously reported (11). Mutant thrombin R98A, which contains an alanine substitution at Arg-98 (thrombin B-chain numbering),[2] and recombinant wild-type (WT) human thrombin were obtained and characterized as described previously (12). The mutant form retains its catalytic activity, although its ability to interact with heparin was severely impaired, as demonstrated by *in vitro* studies on heparin-

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[1] The abbreviations used are: PAR, protease-activated receptor; PE, phycoerythrin; PPACK, *O*-phenylalanine-proline-arginine-chloromethylketone; WT, wild-type; HBS, heparin binding site; mAb, monoclonal antibody; HPLC, high performance liquid chromatography.

[2] Amino acid residues were numbered according to the thrombin sequence where the first amino acid of the B-chain was designated as number 1. (Arg-98 corresponds to Arg-101 in the chymotrypsin numbering system.)

catalyzed thrombin inhibition by anti-thrombin III. PPACK-thrombin was obtained and characterized as previously reported (13).

Mocarhagin was purified from cobra venom, as described previously (14), at the Baker Medical Research Institute, Praharan, Australia. HD22, a single-stranded DNA oligonucleotide with the sequence 5′-AGTCCGTGGTAGGGCAGGTTGGGGTGACT-3′, which binds with high affinity to the heparin binding site of thrombin (15), was a kind gift of Prof. J. I. Weitz, (McMaster University, Hamilton, Ontario).

The PAR-1-(38–60) peptide, LDPRSFLLRNPNDKYEPFWEDEE, was synthesized and characterized by mass spectrometry at Primm s. r. l. (Milan, Italy). The monoclonal antibody LJ1b10, which is able to selectively inhibit thrombin-GpIb interaction, was a generous gift from Dr. Zaverio Ruggeri (The Scripps Research Institute, La Jolla, CA).

Preparation of Platelets—Platelets from normal donors were obtained by gel filtration of platelet rich plasma onto Sepharose 2B columns (25 × 1 cm) equilibrated with a buffer containing 20 mM Hepes, 135 mM NaCl, 5 mM KCl, 5 mM glucose, 0.2% albumin, pH 7.4. EDTA (1-mM final concentration) was added to PRP prior to gel filtration to avoid activation during washing procedures. The platelet count was adjusted to $1 \times 10^5/\mu$l with washing buffer in all the experiments.

GpIb-depleted platelets were prepared by using the cobra venom metalloproteinase, mocarhagin, which selectively cleaves GpIb between Glu-282 and Asp-283 residues, according to a previously reported method (9). Briefly, gel-filtered platelets were incubated with 10 μg/ml mocarhagin and 1 mM Ca^{2+} for 20 min at 37 °C. The mocarhagin activity was stopped by 2 mM EDTA. An aliquot of intact platelets (*i.e.* not exposed to mocarhagin) from the same donor was subjected to the same incubation with 1 mM Ca^{2+} for 20 min at 37°, addition of 2 mM EDTA and was used as a control. Evaluation of GpIb cleavage was performed by flow cytometry using the fluorescein isothiocyanate (FITC)-conjugated anti-GpIb monoclonal antibody CD42b (SZ2 clone) (Immunotech, Marseille, France), whose epitope on GpIbα is lost following mocarhagin treatment (5).

Measurement of PAR-1 Hydrolysis by Thrombin on Intact Platelets—Gel-filtered platelets, intact or GpIb-depleted, were exposed to α-thrombin, whose final concentration ranged from 1 nM to 10 nM in different experiments. At different times (from 15 to 600 s), aliquots of 50 μl of stimulated platelets were drawn into tubes containing 100 nM hirudin, which abolished the thrombin activity. The tubes were placed in ice to stop internalization of cleaved PAR-1 molecules (16).

In different experiments, intact platelets were stimulated by α-thrombin in the presence of either 130 μg/ml anti-GpIb SZ2 mAb, 400 nM HD22 aptamer, or 140 nM PPACK-thrombin.

In the experiments using the R98A thrombin mutant and the recombinant WT human thrombin, gel-filtered platelets were stimulated by the enzymes at a concentration of 1 nM.

The presence of intact PAR-1 molecules on the platelet membrane at different times after thrombin stimulation was measured by using a phycoerythrin (PE)-conjugated anti-PAR-1 mAb, SPAN12 clone (Immunotech). SPAN12 recognizes the NH_2-terminal peptide of PAR-1 residues 35–46 (NATLDPR↓SFLLR), where "↓" indicates the cleavage site by thrombin. This mAb reacts only with uncleaved PAR-1 molecules (16). In preliminary experiments, PE-SPAN12 was added to 1×10^6 platelets at increasing amounts (0.5, 1, 1.5, 2, 2.5, and 3 μg) for 30 min at 4 °C. Platelet suspensions were subsequently washed in phosphate-buffered saline/EDTA at 1500 rpm for 5 min. An optimal resolution of control and test histograms was obtained with 2 μg of anti-PAR-1 mAb/1×10^6 platelets. Thus, this saturating dose was chosen for subsequent experiments. Background fluorescence was determined using a PE-conjugated isotype-matched irrelevant mAb.

At the end of stimulation by thrombin, 2 μg of SPAN-12 was added to each tube containing platelets and hirudin. After incubation at 4 °C for 30 min, platelets were washed in phosphate-buffered saline/EDTA, and samples were run through a FACScan flow cytometer (Becton Dickinson, Mountain View, CA) equipped with an argon laser emitting at 488 nm. PE signals were collected and recorded at 575 nm; gain setting stability was verified daily with Calibrite Beads™® (Becton Dickenson). A minimum of 20,000 events were acquired in list mode using CellQuest™ software (Becton Dickenson); forward (FSC) and side (SSC) scatter were collected with logarithmic amplification, and fluorescent emissions were collected on a 4-decade logarithmic scale. Levels of silver expression were measured in terms of the geometric mean of specific fluorescence.

Measurement of PAR-1-(38–60) Peptide Hydrolysis by WT Thrombin and R98A Thrombin—Hydrolysis of the PAR-1-(38–60) peptide by thrombin was followed by measuring the release of the peptide LDPR, resulting from the cleavage of the NH_2 terminus of PAR-1, according to a previously described method (7). Briefly, 0.5 μM PAR-1-(38–60) peptide was incubated with 0.1 nM WT thrombin or 0.1 nM R98A thrombin in HEPES (10 mM), NaCl (0.15 M), polyethylene glycol M_r 6000 (0.1%) pH 7.5 at 25°. At time intervals (1, 2, 3, 4, 8, 12, and 15 min) the reaction was stopped with 0.3 M $HClO_4$, and the cleaved peptide was measured by reversed-phase HPLC, using a 250 × 4.6 mm RP-304 column (Bio-Rad).

Experimental concentrations of PAR-1-(38–60) peptide cleaved at time t (P_t), were fitted to the following equation,

$$P_t = P_\infty(1 - \exp(-k_{obs}t)) \quad \text{(Eq. 1)}$$

where P_∞ is the peptide concentration at $t = \infty$ and k_{obs} is the pseudo first-order rate of PAR-1 hydrolysis, equal to $e_0 \times k_{cat}/K_m$ (e_0 is the thrombin concentration).

Aggregometry Studies—Gel-filtered platelets were suspended in HEPES buffer, as detailed above, containing 2 mM $CaCl_2$ and used at a final count of 200,000/μl. Platelet aggregation by thrombin was studied using a 4-channel PACKS-4 aggregometer (Helena Laboratories, Sunderland, UK), according to the Born method. In some experiments, platelets were stimulated by recombinant human WT thrombin and R98A thrombin at concentrations ranging from 0.39 nM to 50 nM. In other experiments, platelets were stimulated by WT thrombin at concentrations ranging from 0.625 to 20 nM, or by R98A thrombin at concentrations ranging from 3.125 to 100 nM, in the absence and in the presence of monoclonal antibody LJIb10 (0.15 mg/ml, final concentration). The velocity of absorbance change was measured and expressed as percent/min.

RESULTS

Measurement of Thrombin Hydrolysis of PAR-1 on Intact Platelets—Measurement of PAR-1 hydrolysis by α-thrombin was accomplished by a cytofluorimetric method, using a fluorescent monoclonal antibody, SPAN-12, that recognizes only the intact NH_2-terminal portion of the receptor. After cleavage, the mAb does not interact with the receptor, so that disappearance of the mAb signal reflects the hydrolytic reaction. Internalization of the receptor, which could also lead to loss of signal, has been shown to occur only for cleaved PAR-1 molecules (16–18). Under the conditions of the study, using intact gel-filtered platelets, the concentration of PAR-1 present on the platelet membrane (100–2000 copies of PAR-1/platelet, Refs. 19–20) is much lower (nanomolar) than the K_m value of its hydrolysis by thrombin (micromolar range), so that the kinetics of PAR-1 cleavage can be fitted to an exponential equation, whose rate constant, k_{obs}, is proportional to the k_{cat}/K_m value of thrombin-PAR-1 hydrolysis, according to the following equation (21).

$$k_{obs} = e_0 k_{cat}/K_m \quad \text{(Eq. 2)}$$

In the experimental setup, the fluorescent signal given by the SPAN-12 mAb was monitored as a function of time at fixed thrombin concentrations. Although the antibody staining procedure is relatively long compared with PAR-1 cleavage kinetics at the concentrations of thrombin used, this limitation was overcome by performing the staining on ice and using high concentrations of hirudin to completetly inhibit thrombin activity. Fluorescence signals measured as a function of time were fitted to the following equation,

$$Fl_t = Fl_0 \exp(-k_{obs}t) + Fl_\infty \quad \text{(Eq. 3)}$$

where Fl_t is the fluorescence at time t, Fl_0 is the initial, Fl_∞ is the final fluorescence value, and k_{obs} is the observed rate constant for the single exponential decay. Knowing the enzyme concentration and using Eq. 2, the k_{cat}/K_m value could be calculated. Additional experiments were carried out to confirm the validity of this experimental approach. From Eq. 2 it follows that if the k_{obs} value actually reflects the k_{cat}/K_m value of the hydrolytic reaction, then it must depend on the enzyme concentration.

Thus, the observed rate constant was measured at different thrombin concentrations, ranging from 0.5 to 8 nM. The above

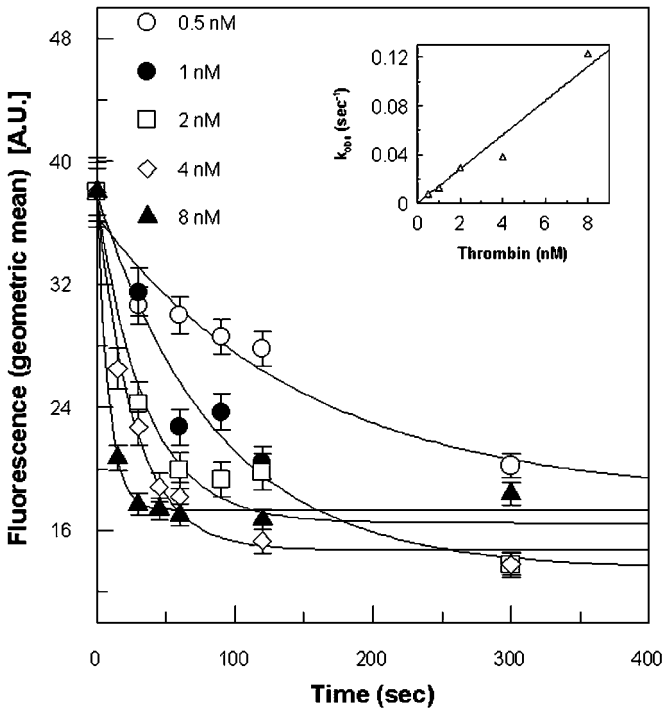

FIG. 1. **Kinetics of PAR-1 cleavage by different thrombin concentrations, measured as a loss of SPAN12 mAb fluorescence over time.** The experimental conditions reported under "Experimental Procedures" included 60,000 gel-filtered platelets/μl and 0.12 μg/ml of the mAb. *Solid lines* are drawn according to Eq. 3 with the bestfit k_{obs} values: (○), $6.6 \pm 0.6 \times 10^{-3}$ sec^{-1}; (●), $1.2 \pm 0.3 \times 10^{-2}$ sec^{-1}; (□), $2.9 \pm 0.6 \times 10^{-2}$ sec^{-1}; (◇), $3.7 \pm 0.4 \times 10^{-2}$ sec^{-1}; (▲), $1.2 \pm 0.3 \times 10^{-1}$ sec^{-1}. Data are presented as mean ± S.E. from two different determinations. In the *inset,* the experimental values of k_{obs} pertaining to PAR-1 cleavage on intact platelets are plotted as a function of thrombin concentration, according to Eq. 2. The *straight line* was drawn according to the bestfit k_{cat}/K_m value of $1.5 \pm 0.1 \times 10^7$ M^{-1} sec^{-1}.

analysis assumes that the concentration of the uncleaved receptor does not change during the time course of the experiments. To test this hypothesis, control experiments were carried out with a different mAb, WEDE-15, directed against the COOH-terminal domain of the PAR-1 cleavage site. Using thrombin in the nanomolar range, only a decrease in WEDE-15 binding to gel-filtered platelets was observed, consistent with an internalization process of the hydrolyzed PAR-1 receptor, which has been previously reported (16–18). This implies that over the time course of the experiments, newly exposed receptors (present in the surface connecting system) did not significantly alter the total PAR-1 concentration and that loss of WEDE-15 binding to platelets is likely because of an internalization process involving the cleaved receptor molecules. These findings therefore allow calculation of the apparent k_{cat}/K_m value pertaining to thrombin-PAR-1 interaction as outlined above.

As shown in Fig. 1, the pseudo first-order rate constant of PAR-1 cleavage increased as a function of α-thrombin concentration ranging from 0.5 to 8 nM, consistent with the canonical Michaelis scheme for serine protease activity that predicts a linear relation between the catalytic rate and the enzyme concentration (Eq. 2). The *inset* in Fig. 1 demonstrates this relationship with the slope of the straight line expressing the apparent k_{cat}/K_m value, which is equal to $1.5 \pm 0.1 \times 10^7$ M^{-1} sec^{-1}. This value is similar to that for thrombin hydrolysis of the PAR-1-(38–60) peptide in solution (see below), supporting the validity of the cytofluorimetric strategy used in this investigation.

Effect of Inhibiting Thrombin-GpIb Interaction on Hydrolysis of PAR-1 in Intact Platelets—The effect of inhibiting thrombin-GpIb interaction on the enzyme hydrolysis rate of PAR-1 was evaluated by five different experimental strategies: 1) elimination of the thrombin binding site on GpIbα by mocarhagin treatment of gel-filtered platelets, 2) use of a monoclonal antibody SZ2, which binds to GpIbα and inhibits thrombin interaction, 3) use of the DNA aptamer HD22, which specifically interacts with the heparin binding site (HBS) of thrombin and inhibits enzyme binding to GpIbα, 4) use of a thrombin mutant, R98A, which bears a perturbation of the HBS structure, and 5) use of PPACK-thrombin in competition experiments with α-thrombin.

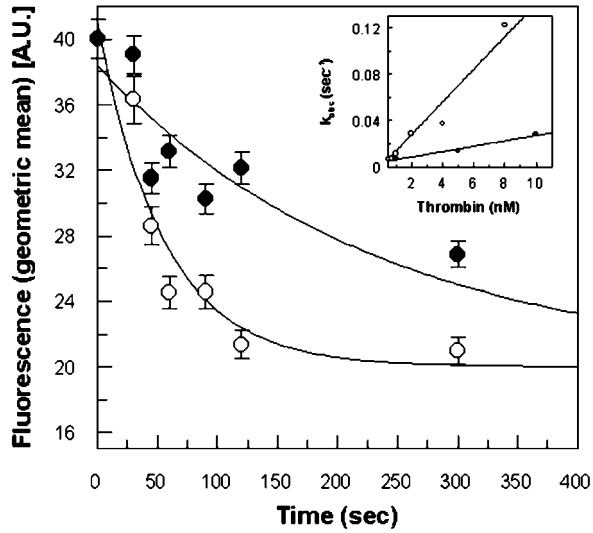

FIG. 2. **Measurement of the k_{obs} value pertaining to PAR-1 hydrolysis on intact and mocarhagin-treated platelets.** Experimental conditions were similar to those reported in the legend to Fig. 1. Intact (○) and mocarhagin-treated (●) (10 μg for 10 min at 37 °C) platelets were exposed to 1 nM α-thrombin, and the cleaved PAR-1 was estimated cytofluorimetrically by the SPAN 12 mAb, as described under "Experimental Procedures." The *solid lines* were drawn by nonlinear regression according to Eq. 3, with the bestfit k_{obs} values: (○), $1.8 \pm 0.3 \times 10^{-2}$ sec^{-1}; (●), $0.3 \pm 0.07 \times 10^{-2}$ sec^{-1}. Data are presented as mean ± S.E. from two different determinations. In the *inset,* the experimental values of k_{obs} pertaining to PAR-1 cleavage on mocarhagin-treated (●) and, for comparison, intact platelets (○) are plotted as a function of thrombin concentration, according to Eq. 2. The *straight lines* were drawn according to the bestfit k_{cat}/K_m value: (○), $1.5 \pm 0.1 \times 10^7$ M^{-1} sec^{-1}; (●), $2.8 \pm 0.3 \times 10^6$ M^{-1} sec^{-1}.

The removal of the NH_2-terminal 1–282 region of GpIbα by mocarhagin severely impaired the PAR-1 hydrolysis by thrombin. As shown in Fig. 2, the k_{obs} value for PAR-1 hydrolysis by 1 nM α-thrombin was reduced by about 6-fold in GpIb-depleted platelets compared with untreated platelets. The *inset* in Fig. 2 shows that the k_{cat}/K_m value of PAR-1 hydrolysis in mocarhagin-treated platelets, which was $2.8 \pm 0.3 \times 10^6$ M^{-1} sec^{-1}, decreased 5.4-fold in comparison with untreated platelets. Similar results were obtained by using two different competitive inhibitors of thrombin binding to GpIb, the mAb SZ2, which interacts with the thrombin binding site on GpIbα (5, 22), and the DNA aptamer HD22, which interacts with the thrombin HBS. Fig. 3 clearly shows that in both cases a roughly 5–6-fold reduction in k_{obs} was obtained using a large excess of the inhibitors. Although the targets of the inhibitors were different, the effect was the same, as in both cases the thrombin-GpIb interaction was inhibited. Altogether these results show that inhibition of thrombin binding to GpIbα causes a marked reduction of the apparent catalytic specificity constant of the thrombin-PAR-1 interaction.

The findings reported above raise the question of whether thrombin interaction with GpIbα might induce an intracellular

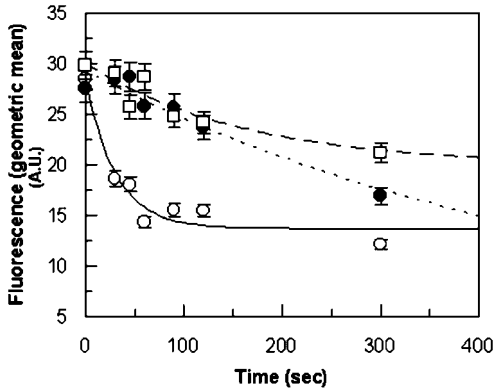

FIG. 3. **Measurement of the k_{obs} value pertaining to PAR-1 hydrolysis in the presence of inhibitors of thrombin-GpIb interaction.** Quantification of PAR-1 hydrolysis was accomplished as reported in the legend to Fig. 1, using 2 nM α-thrombin, but in the presence of 400 nM HD22 aptamer (●)or 130 μg/ml anti-GpIb SZ2 mAb (□), both inhibiting the thrombin-GpIb interaction. The kinetics of PAR-1 hydrolysis in the absence of any inhibitor, but in the presence of 130 μg/ml human IgG used as control, is reported as well (○). Data are presented as mean ± S.E. from two different determinations. The *lines* were drawn by nonlinear regression according to Eq. 3, with the bestfit k_{obs} values: (○), 3.2 ± 0.6 × 10^{-2} sec^{-1} (*solid line*); (●), 0.48 ± 0.06 × 10^{-2} sec^{-1} (*dashed line*); (□), 0.6 ± 0.09 × 10^{-2} sec^{-1} (*dotted line*).

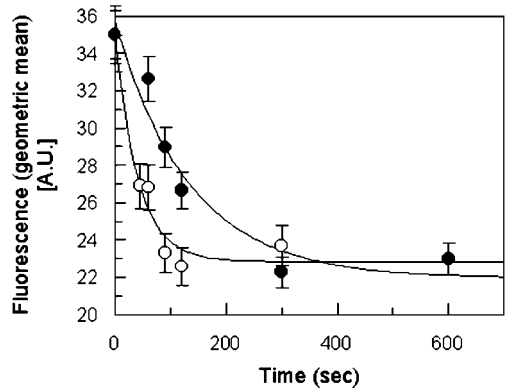

FIG. 4. **Effect of displacement of α-thrombin binding to GpIb by high PPACK-thrombin concentration on PAR-1 hydrolysis.** Kinetics of PAR-1 hydrolysis, as described in the legend to Fig. 1, using 1 nM α-thrombin, in the absence (○) or presence (●) of 140 nM PPACK-thrombin. Data are presented as mean ± S.E. from two different determinations. *Solid lines* were drawn by nonlinear fitting according to Eq. 3, with the bestfit k_{obs} values: (○), 1.6 ± 0.4 × 10^{-2} sec^{-1}. (●), 0.6 ± 0.08 × 10^{-2} sec^{-1}.

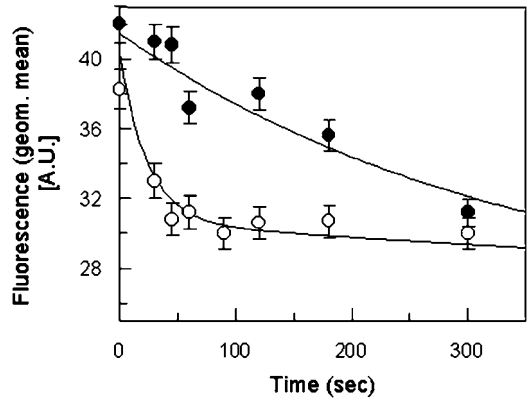

FIG. 5. **Measurement of the k_{obs} value pertaining to PAR-1 hydrolysis by wild-type and the R98A thrombin mutant.** Kinetics of PAR-1 cleavage by wild-type (○) and the R98A thrombin (●) at 1 nM concentration. Gel-filtered platelets were used at a concentration of 60,000/μl. Data are presented as mean ± S.E. from two different determinations. The *solid lines* were drawn by nonlinear regression according to Eq. 3, with the bestfit k_{obs} values: (○), 1.9 ± 0.2 × 10^{-2} sec^{-1}, (●), 0.34 ± 0.05 × 10^{-2} sec^{-1}.

signal that could alter the interaction of thrombin with PAR-1, for instance through liberation of a second messenger molecule acting on the expression/conformation of PAR-1 molecules. PPACK-thrombin, which is catalytically inactive, yet still able to interact with GpIb, did not cause aggregation of gel-filtered platelets, even at 200 nM and did not induce any intracytoplasmic Ca^{2+} flux (data not shown), in accordance with numerous previous reports (6, 10). On the other hand, competition experiments showed that a high concentration of PPACK-thrombin (140 nM), by displacing α-thrombin from GpIbα, reduced by about 3-fold the apparent k_{cat}/K_m value of PAR-1 hydrolysis on intact platelets, as shown in Fig. 4. Again, this experiment is in accord with the other functional experiments described above and corroborates the hypothesis that thrombin-GpIb interaction is able to enhance the specificity of thrombin cleavage of PAR-1 on intact platelets.

This hypothesis was further supported by the finding that a thrombin mutant, R98A, bearing an alanine substitution in the HBS of thrombin at Arg-98, showed a similar reduction of the k_{obs} value of PAR-1 hydrolysis compared with recombinant WT human thrombin, as shown in Fig. 5. In control experiments, this diminished activity of PAR-1 hydrolysis on platelets could not be attributed to an intrinsic reduction of the catalytic efficiency of the thrombin mutant. Solution experiments employing the PAR-1-(38–60) peptide, bearing both the cleavage and the recognition site for thrombin (23), demonstrated that thrombin R98A cleaved the solution peptide with a k_{cat}/K_m that was slightly higher than that of WT thrombin, as shown in Fig. 6. This finding is consistent with the hypothesis that the reduction of the k_{cat}/K_m value of PAR-1 hydrolysis on intact platelets is likely because of a defective interaction of the thrombin mutant with GpIbα. Moreover, the biological effect of this mutation on platelet activation can be seen in Fig. 7, which shows that the EC_{50} value for platelet aggregation by R98A is roughly 10-fold higher compared with WT thrombin.

Effect of Anti-GpIb mAb LJIb10 on Platelet Aggregation by WT Thrombin and R98A Mutant Thrombin—These experiments were carried out to evaluate whether the thrombin HBS could be involved in the interaction with other thrombin receptors. PAR-1 was already demonstrated not to be involved in HBS ligation (6–9), but PAR-4 could potentially contain a binding site for the thrombin HBS, although a close inspection of the PAR-4 primary sequence (24) does not show a negatively charged domain to support this hypothesis. The mAb LJ1b10 specifically inhibits the interaction of thrombin with GpIbα, without affecting the binding of von Willebrand factor to GpIbα (22, 25). The use of this mAb allows one to rule out a potential inhibitory effect on the aggregation of gel-filtered platelets that could be attributed to an impaired interaction of GpIb with platelet von Willebrand factor, which is released upon thrombin stimulation.

As shown by Fig. 8*A*, platelets stimulated by WT thrombin had a rightward shift in the aggregometric dose-response curve in the presence of 0.15 mg/ml LJIb10 (with EC_{50} values of 4.43 ± 0.4 nM and 10.15 ± 0.77 nM, respectively). This finding is in agreement with the hypothesis that specific inhibition of thrombin binding to GpIb causes a reduced platelet response to the agonist. In contrast, the dose-response curve obtained by stimulating platelets with thrombin mutated at the HBS (Fig. 8*B*) was not affected at all by the presence of the mAb (with EC_{50} values of 23.5 ± 2.8 nM and 22.1 ± 5 nM, respectively). This result is in agreement with the concept that the thrombin-GpIb interaction involves the enzyme HBS, as the LJ-Ib10 mAb could not induce any inhibition of the R98A thrombin-induced platelet activation. This result would also suggest that the

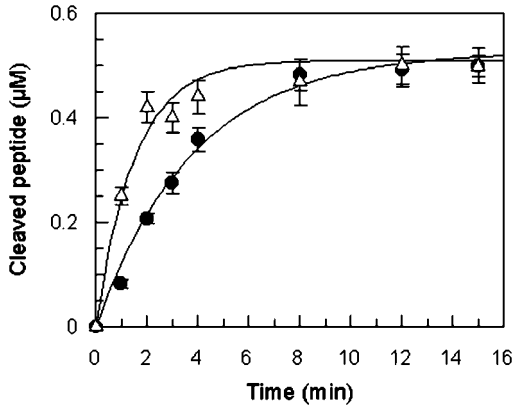

FIG. 6. **Measurement of the k_{cat}/K_m value pertaining to the PAR-1-(38–60) peptide hydrolysis by wild-type and the R98A thrombin mutant.** Hydrolysis of the PAR-1-(38–60) peptide was measured by the HPLC method, using 0.1 nM wild-type (●) and R98A thrombin mutant (△) and 0.5 μM peptide. The experimental points are the mean of two determinations. *Solid lines* were drawn by nonlinear regression according to Eq. 1, with the bestfit k_{obs} values: (●), 4.3 ± 0.3 × 10^7 M^{-1} sec^{-1}, (△), 7 ± 0.8 × 10^7 M^{-1} sec^{--1}.

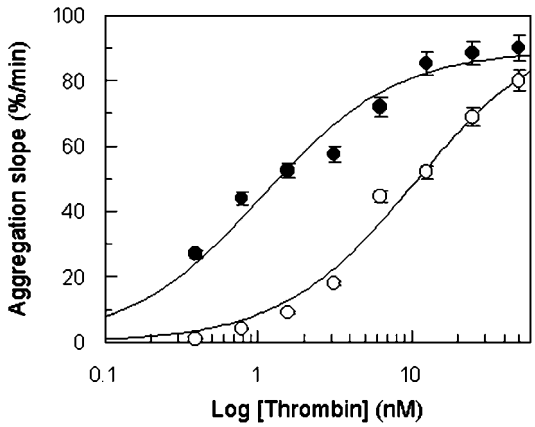

FIG. 7. **Platelet aggregation capacity of the wild-type and the R98A thrombin mutant.** Gel-filtered platelets used at 200,000/μl were exposed to different concentrations of wild-type (●) or R98A thrombin mutant (○). Data are presented as mean ± S.E. from two different determinations. The *solid lines* were drawn by nonlinear regression with the bestfit EC_{50} values equal to 1.1 ± 0.2 and 10 ± 2 nM for the wild-type and the R98A thrombin mutant, respectively.

thrombin HBS is involved only in GpIb binding and not in the interaction with other platelet receptors, such as PAR-4.

DISCUSSION

In this study, the role of GpIbα in the hydrolysis of PAR-1 by thrombin and in thrombin-induced platelet activation was examined. GpIbα binds thrombin with high affinity and contributes to platelet activation by the enzyme; however, there is no evidence that thrombin ligation to GpIb *per se* is able to trigger platelet activation. Results from the present study show that GpIbα can function as a cofactor for PAR-1 cleavage and activation in human platelets. In fact, by directly measuring the hydrolysis of PAR-1 on intact platelets, it was possible to evaluate the effect of the inhibition of thrombin binding to GpIbα on PAR-1 cleavage. The cytofluorimetric strategy used to detect PAR-1 hydrolysis on platelets allowed measurement of the apparent specificity constant, k_{cat}/K_m, pertaining to thrombin hydrolysis of the receptor. It is noteworthy that the value measured in intact cells is similar to that for hydrolysis of the PAR-1-(38–60) peptide in solution, as confirmation of the validity of the experimental method. Interestingly, the inhibition of thrombin interaction with GpIb on platelets, obtained by different experimental strategies, consistently showed a 5- to

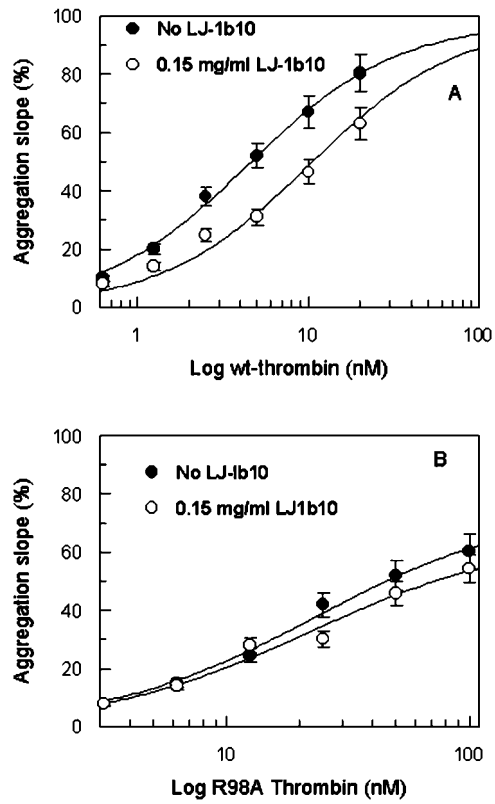

FIG. 8. **Effect of the anti-GpIb mAb LJIb10 on platelet aggregation by WT and R98A mutant thrombin.** Aggregation of gel-filtered platelets induced by WT thrombin (*A*) and the R98A thrombin mutant (*B*) was measured in the absence (●) and presence (○) of the LJ-Ib10 mAb, as described under "Experimental Procedures." Data are presented as mean ± S.E. from two different determinations. *Solid lines* were drawn using the bestfit EC_{50} values: 4.43 ± 0.4 nM and 10.15 ± 0.77 nM for WT-thrombin (in the absence and in the presence of 0.15 mg/ml LJ-Ib10, respectively); 23.5 ± 2.8 nM and 22.1 ± 5 nM for the R98A mutant (in the absence and in the presence of 0.15 mg/ml LJ-Ib10, respectively).

6-fold reduction of the specificity rate constant of PAR-1 hydrolysis by thrombin. This finding might suggest that in the absence of GpIb on the platelet membrane, the thrombin-PAR-1 interaction is partially hampered or less productive, given that the k_{cat}/K_m value is much lower than that measured with the PAR-1-(38–60) peptide in solution.

Thrombin bound to GpIbα via its HBS, whose blockade caused a reduction in both PAR-1 hydrolysis and platelet aggregation. That the HBS is not directly involved in the interaction with PAR-1 was demonstrated by the experiment showing that the HBS mutant thrombin, R98A, cleaves the PAR-1-(38–60) peptide in solution with an apparent k_{cat}/K_m similar to or even higher than that pertaining to WT thrombin. Platelet aggregation by R98A thrombin was not sensitive to the presence of the anti-GpIb mAb LJ-Ib10, whereas the aggregation by WT thrombin showed a rightward-shift of the dose-response curve (Fig. 8). In the former case, in fact, thrombin binding to GpIb was already impaired by HBS perturbation, whereas in the latter case use of the mAb blocked the GpIb contribution to platelet aggregation. The effect of the anti-GpIb mAb on the aggregation by WT thrombin is in agreement with the inhibitory effect of the mAb on PAR-1 activation by thrombin via the inhibition of enzyme binding to GpIb.

Because inhibition of the thrombin-GpIb interaction, obtained through different methods, caused in all cases a reduction of the PAR-1 hydrolysis rate, this finding was interpreted as a consequence to a positive linkage between thrombin binding to GpIb and the catalytic interaction of this enzyme com-

plex with PAR-1. It was previously shown that GpIbα in solution does not alter the kinetic constants of hydrolysis of the PAR-1-(38–60) peptide (7, 26). This implies that membrane phenomena are responsible for the effect observed using intact platelets.

One possible mechanism of action of GpIb could be that this transmembrane glycoprotein mediates a signal transduction event that could modify the membrane and/or PAR-1-folding, so that PAR-1 would be more activatable by thrombin. However, experiments with PPACK-thrombin did not confirm this hypothesis. In fact, intraplatelet Ca^{2+} flux was not observed using PPACK-thrombin that binds to GpIb but does not cleave PAR-1 (data not shown). Moreover, when PPACK-thrombin was used along with α-thrombin, it caused, as shown in Fig. 4, a 3-fold reduction of the apparent k_{cat}/K_m value pertaining to PAR-1 cleavage, in agreement with the effect of the other inhibitors of thrombin-GpIb binding. PPACK-thrombin would have caused an enhancement of PAR-1 cleavage, if a positive intracellular signal were generated. It is postulated that von Willebrand factor binding to GpIb induces signal transduction (27), whereas this phenomenon has not yet been demonstrated for thrombin binding to GpIb. Accordingly, very recent findings have indicated that thrombin-GpIb interaction is a necessary but not sufficient condition to induce a procoagulant capacity in the platelet membrane (28). In addition to thrombin binding to GpIb, the procoagulant platelet activity has been demonstrated to arise from both the involvement of the GpIIb-IIIa complex and the platelet-platelet interaction as well (28).

It may be hypothesized that GpIb would enhance the productive collisions between the enzyme and the substrate, PAR-1, on the membrane surface, essentially acting as a catalyst for the reaction. This hypothesis hinges on the structural properties of the components involved in the interaction. The formation of a ternary thrombin·GpIb·PAR-1 complex can be hypothesized, as GpIb binds to the thrombin HBS, whereas PAR-1 interacts with both the exosite referred to as fibrinogen recognition site and the catalytic pocket (6, 9, 23). The positive effect of GpIb interaction with thrombin might be considered as a template function, which could enhance the number of productive collisions between the enzyme and the PAR-1 substrate. The mechanisms through which this effect takes place is not in the realm of this study. Further studies are needed to demonstrate experimentally the formation of the ternary thrombin·GpIb·PAR-1 complex, as well as to unravel some structural issues pertaining to the components of this complex. GpIb is in fact an elongated molecule with a longitudinal axis of ~550 Å (29). Because the thrombin binding site on GpIbα and the NH_2-terminal PAR-1 domain are expected to be located at roughly 300 and 65–70 Å from the membrane surface, respectively, it has to be demonstrated how a ternary thrombin·GpIb·PAR-1 adduct could form on the platelet membrane.

From a physical standpoint, one can reasonably assume that the kinetics of thrombin binding to GpIb is faster than kinetics of formation of the thrombin·PAR-1 Michaelis adduct. Thus, although the association rate constants of thrombin·GpIb and thrombin·PAR-1 may be similar, the concentration of GpIb is at least 1–2 orders of magnitude higher than that of PAR-1 on the platelet membrane (19–20), and thus the bimolecular interaction of thrombin with GpIb is faster than the formation of the thrombin·PAR-1 adduct. Hence GpIb may function as a cofactor for PAR-1 activation by thrombin *in situ*. It is not clear from this investigation whether this cofactor activity is exclusively mediated by GpIb alone, or through more complex interactions involving the entire glycoprotein adduct, GpIb-IX-V. GpV in fact is known to be cleaved by thrombin, but its role in platelet activation remains unknown (30).

The cofactorial function of GpIb would resemble the one recently identified for thrombin interaction with PAR-3 and PAR-4 on mouse platelets (31). Similarly to GpIb for human platelets, PAR-3 in mouse platelets does not mediate transmembrane signaling, but its loss inhibits the mouse platelet activation by low thrombin concentrations. The model for PAR-3 function predicts that this receptor binds thrombin that remains available on platelet membrane to cleave and activate nearby PAR-4 molecules. Although PAR-3 and GpIb are completely different molecules, they might share a cofactorial function for PARs activation. This model may be of interest for human platelets, because it introduces the concept that cofactors for PARs activation might regulate the specificity of response to proteases of target cells. Regulation of cofactor function, rather than that of the receptor itself, might thus become crucial in modulating the effects of proteases on cells. This concept seems particularly to fit for proteins and enzymes that do not bear phospholipid binding sites. Membrane surface is one of the most relevant cofactors usually involved in strongly accelerating coagulation reactions (32). Many coagulation factors, such as Factor V, and Factor VIII, operating on a membrane surface, bear specific phospholipid binding sites. The interaction of thrombin with its PAR-1 substrate, inserted in the platelet membrane, could be hampered by the lack in the thrombin molecule of a domain capable of binding to membrane phospholipids. The high affinity interaction of thrombin with GpIb could overcome this limitation. The thrombin-GpIb interaction could pay the energetic cost to favor an otherwise hampered interaction between the enzyme and its macromolecular substrate. Likewise, an interesting model for this kind of cofactorial function of protease receptors is that recently described for the endothelial Protein C receptor involved in activating Protein C along with the thrombin·thrombomodulin complex on the surface of endothelial cells (33).

At this point one might question whether the 5–6-fold increase of the k_{cat}/K_m value of PAR-1 hydrolysis caused by thrombin interaction with GpIb could be of physiological relevance. The present data cannot indicate whether the increase of the k_{cat}/K_m value arises from either an increase of k_{cat}, or a decrease of K_m value, or else a combination of both phenomena. The present study shows that, under physiological conditions, thrombin cleaves PAR-1 according to a pseudo first-order kinetics. Under this condition, whatever the mechanism, an increase of 5–6-fold of the k_{cat}/K_m value of PAR-1 hydrolysis leads to a 5–6-fold increase of the net velocity of its cleavage, according to Eq. 2. Although the GpIb effect on PAR-1 activation is not dramatic, if compared with other similar phenomena of the blood coagulation system (33), it could likely be physiologically relevant. In fact, the PAR-1 shut-off is a very rapid process after cell activation by thrombin (34), and thus a very efficient enzyme interaction with PAR-1 molecules is needed to generate an optimal amount of activated receptors required for a full cell activation.

The results from the present and previous studies show that α-thrombin binding to GpIbα has a net prohemostatic effect, as not only is this interaction able to enhance the hydrolysis of PAR-1 on the platelet membrane, but also protects the enzyme from the heparin-catalyzed inhibition by anti-thrombin III (9). The demonstration that the specific inhibition of thrombin-GpIb interaction leads to reduced thrombin cleavage of PAR-1 on intact platelets, might open the way to new strategies for specific modulation of platelet responses to thrombin stimulation in different clinical settings.

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Binding of Thrombin to Glycoprotein Ib Accelerates the Hydrolysis of Par-1 on Intact Platelets

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