# Specific Binding of Integrin $\alpha v\beta 3$ to the Fibrinogen $\gamma$ and $\alpha_E$ Chain C-Terminal Domains<sup>†</sup>

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Received November 20, 1998; Revised Manuscript Received March 8, 1999

ABSTRACT: Integrin  $\alpha v \beta 3$ , a widely distributed fibrinogen receptor, recognizes the RGD<sup>572-574</sup> motif in the  $\alpha$  chain of human fibrinogen. However, this motif is not conserved in other species, nor is it required for  $\alpha v \beta$ 3-mediated fibrin clot retraction, suggesting that fibringen may have other  $\alpha v \beta$ 3 binding sites. Fibrinogen has conserved C-terminal domains in its  $\alpha$  (E variant),  $\beta$ , and  $\gamma$  chains (designated  $\alpha_E C$ ,  $\beta C$ , and  $\gamma C$ , respectively), but their function in cell adhesion is not known, except that  $\alpha IIb\beta 3$ , a platelet fibrinogen receptor, binds to the  $\gamma$ C HHLGGAKQAGDV $^{400-411}$  sequence. Here we used mammalian cells expressing recombinant  $\alpha v\beta 3$  to show that recombinant  $\alpha_E C$  and  $\gamma C$  domains expressed in bacteria specifically bind to  $\alpha v\beta 3$ . Interaction between  $\alpha v\beta 3$  and  $\gamma C$  or  $\alpha_E C$  is blocked by LM609, a functionblocking anti- $\alpha v\beta 3$  mAb, and by RGD peptides.  $\alpha v\beta 3$  does not require the HHLGGAKQAGDV<sup>400-411</sup> sequence of  $\gamma C$  for binding, and  $\alpha_E C$  does not have such a sequence, indicating that the  $\alpha \nu \beta 3$  binding sites are distinct from those of  $\alpha \text{IIb}\beta 3$ . A small fragment of  $\gamma \text{C}$  (residues 148–226) supports  $\alpha \text{v}\beta 3$  adhesion, suggesting that an  $\alpha v\beta 3$  binding site is located within the  $\gamma$  chain 148-226 region. We have reported that the CYDMKTTC sequence of  $\beta 3$  is responsible for the ligand specificity of  $\alpha v \beta 3$ .  $\gamma C$  and  $\alpha_E C$  do not bind to wild-type  $\alpha v\beta 1$ , but do bind to the  $\alpha v\beta 1$  mutant ( $\alpha v\beta 1$ -3-1), in which the CYDMKTTC sequence of  $\beta 3$  is substituted for the corresponding  $\beta 1$  sequence CTSEQNC. This suggests that  $\gamma C$  and  $\alpha_E C$  contain determinants for fibrinogen's specificity to  $\alpha v \beta 3$ . These results suggest that fibrinogen has potentially significant novel  $\alpha v \beta 3$  binding sites in  $\gamma C$  and  $\alpha_E C$ .

Fibrin interaction with integrin  $\alpha v \beta 3$  expressed on endothelial cells is important for angiogenesis associated with wound healing and tumorigenicity (1, 2).  $\alpha v\beta 3$  expression and fibrin generation increase in microvessels after focal cerebral ischemia (3). Thus,  $\alpha v \beta 3$ -fibrin(ogen) interaction is of biological significance and is a potential target for modulating these processes. Fibrinogen is a 340 kDa glycoprotein that consists of two identical disulfide-linked subunits. Each subunit is composed of three nonidentical polypeptide chains:  $\alpha$ ,  $\beta$ , and  $\gamma$  (4). The  $\beta$  and  $\gamma$  chains have conserved C-terminal domains (designated  $\beta C^1$  and  $\gamma C$ , respectively). The crystal structure of the isolated  $\gamma$ C domain (5), as well as that of the  $\gamma C$  and  $\beta C$  domains in the fibrinogen D fragment (6), revealed that both domains are similarly folded. A minor 420 kD form of fibrinogen (fibrinogen-420) has an alternative extended form of the  $\alpha$ 

American Heart Association fellowship 98-84 (to K.Y.). This is

chain ( $\alpha_E$ ), which has a C-terminal domain (designated  $\alpha_E C$ ) whose sequence and fold are highly homologous to those of the  $\beta C$  and  $\gamma C$  domains (7, 8). Although several functions of the  $\beta C$  and  $\gamma C$  domains have been well defined, the function of the  $\alpha_E C$  domain in fibrinogen-420 remains unknown.

Integrin  $\alpha v\beta 3$  is a fibringen receptor that is found in a wide range of cell types including endothelial cells, fibroblasts, leukocytes, and tumor cells. It is widely accepted that  $\alpha v \beta 3$  recognizes the RGD<sup>572–574</sup> sequence of the fibringen  $\alpha$  chain in  $\alpha v\beta$ 3-mediated cell adhesion (9, 10). However, the  $\alpha$  chain RGD<sup>572-574</sup> sequence is not conserved or is absent in fibrinogen from other species including primate. Rat, mouse, or bovine fibringen has RGD<sup>252-254</sup> instead of RGD<sup>572-574</sup> (11, 12), and rhesus monkey or pig fibrinogen has no RGD sequence in the  $\alpha$  chain (11). Therefore, fibrinogen that has no α chain RGD sequence should have another  $\alpha v\beta 3$  binding motif.  $\alpha v\beta 3$  has been shown to be critically involved in endothelial (or tumor) cell-mediated fibrin clot retraction (13, 14); interestingly, the fibrinogen  $\alpha$  chain RGD<sup>95–97</sup> and RGD<sup>572–574</sup> sequences and the  $\gamma$  chain AGDV<sup>408–411</sup> sequence are not required for this process (14, 15). These results suggest that other unknown  $\alpha v\beta 3$  binding sites are involved in fibrin clot retraction and cell adhesion.

In the present study, we discovered that the fibrinogen C-terminal domains ( $\gamma C$  and  $\alpha_E C$ ) support  $\alpha \nu \beta 3$ -mediated adhesion, using recombinant C-terminal domains. Since the C-terminal dodecapeptide sequence of  $\gamma C$  (HHLGGAK-QAGDV<sup>400-411</sup>) is not required for  $\gamma C$  binding to  $\alpha \nu \beta 3$ , the

<sup>(</sup>fibrinogen-420) has an alternative extended form of the α

† This work was supported by National Institute of Health Grants GM47157 and GM49899 (to Y.T.) and HL-56051 (to L.M.) and

Publication No. 11504-VB from The Scripps Research Institute.

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 $<sup>^1</sup>$  Abbreviations: CHO, Chinese hamster ovary;  $\alpha_E C,$  fibrinogen  $\alpha_E$  chain variant C-terminal domain;  $\beta C,$  fibrinogen  $\beta$  chain C-terminal domain;  $\gamma C,$  fibrinogen  $\gamma$  chain C-terminal domain; FITC, fluorescent isothiocyanate; mAb, monoclonal antibody; SDS-PAGE, sodium dodecyl sulfate-polyacrylamide gel electrophoresis.

 $\alpha\nu\beta3$  binding site in  $\gamma C$  is distinct from that of integrin  $\alpha IIb\beta3$ , a platelet fibrinogen receptor that requires the HHLGGAKQAGDV $^{400-411}$  sequence (ref 16, and references therein). These results suggest that fibrinogen has novel  $\alpha\nu\beta3$  binding sites in the  $\gamma C$  and  $\alpha_E C$  domains that may be biologically significant.

### **EXPERIMENTAL PROCEDURES**

Antibodies. LM609 (to  $\alpha v\beta 3$ ) (9) was provided by D. Cheresh (The Scripps Research Institute, La Jolla, CA). PT25-2 (to  $\alpha IIb\beta 3$ ) (17) was provided by M. Handa and Y. Ikeda (Keio University, Tokyo, Japan). MAb 13 (to human  $\beta 1$ ) (18) was a kind gift from K. Yamada (NIH, Bethesda, MD).

CHO Cells Expressing Different Human Integrins. Untransfected CHO cells express endogenous  $\alpha 5$ ,  $\alpha v$ , and  $\beta 1$ , but not  $\beta 2$  or  $\beta 3$ .  $\alpha IIb\beta 3$ -CHO cells express human  $\alpha IIb\beta 3$  and hamster  $\alpha v$ /human  $\beta 3$  hybrid (19).  $\beta 1$ -CHO cells express hamster  $\alpha v$  (or  $\alpha 5$ )/human  $\beta 1$  hybrid (20).  $\beta 3$ -CHO cells express hamster  $\alpha v$ /human  $\beta 3$  hybrid (20).  $\beta 1$ -3-1-CHO cells express the  $\alpha v\beta 1$ -3-1 mutant described in ref 20.

Recombinant Fibrinogen C-Terminal Domains. The fibringen C-terminal domains,  $\alpha_E C$ ,  $\gamma C$ , and its truncated mutant,  $\gamma$ C/399t, were produced in *Escherichia coli* using the pET-21a+ expression vector. The cDNA fragments encoding the fibrinogen C-terminal domains ( $\alpha_E C$ , residues 612-847 of the  $\alpha E$  chain;  $\gamma C$ , residues 151-411 of the  $\gamma$ chain; and  $\gamma$ C/399t, residues 151–399 of the  $\gamma$  chain) were amplified by polymerase chain reaction. Fibrinogen  $\gamma$  chain cDNA (ATCC59710) was used as a template for  $\gamma$ C, and a human liver cDNA library (Clontech) was used as templates for α<sub>E</sub>C. The primers used were 5'-GGGGATCCAAAGAT-TGTCAAGACATTGCC-3' and 5'-CGGAATTCTTAAA-CGTCTCCAGCCTG-3' for  $\gamma$ C, and 5'-GGAATTCCATAT-GGACTGTGATGATGTCCTCC-3' and 5'-ACCGCTCG-AGCTATTGGGTCACAAGGGGCC-3' for  $\alpha_E$ C. The cDNA fragments were subcloned into the BamHI/EcoRI site ( $\gamma$ C) and the NdeI/XhoI site (α<sub>E</sub>C) of PET21a+ vector. The cDNA fragments were completely sequenced to confirm that no errors occurred during amplification. A stop codon was introduced by mutagenesis at position 400 for the  $\gamma$ C/399t mutant. Synthesis of  $\gamma C$ , the  $\gamma C/399t$  mutant, and  $\alpha_E C$ , and purification and refolding of recombinant proteins, were performed as previously described (21). To confirm the refolding of the proteins, fluorescence measurements of thermal unfolding were performed as described (21).

Preparation of the Recombinant y 148-226 Fragment. We used SDS-PAGE to analyze the lysate of the bacterial cells that produce a mutant  $\gamma C$  (148-411) in which Asp199-Gly200 is mutated to Gly-Ala (22), and found that the pellet contained full-length  $\gamma C$  (148–411) and a substantial amount of a 9 kDa fragment. This fragment was immunopositive with antifibrinogen polyclonal antibody, suggesting that it represents a proteolytically truncated  $\gamma C$  mutant. The fragment was separated from the full-length γC mutant by sizeexclusion chromatography on Superdex 75 in 8 M urea and then refolded according to the protocol described earlier for wild-type  $\gamma$ C (148–411) (21). NH<sub>2</sub>-terminal sequence analysis of the full-length 9-kDa fragment and its tryptic fragments separated by HPLC revealed that it corresponds to the  $\gamma$ 148– 226 region containing the Asp199-Gly200 to Gly-Ala mutation.

Fluorescence measurements of thermal unfolding were performed in an SLM 8000-C fluorometer by monitoring either intrinsic fluorescence intensity at 370 nm, or the ratio of the intensity at 370 nm to that at 330 nm, with excitation at 280 nm as described earlier (21).

SDS-PAGE was carried out as previously described (*23*). *Adhesion Assay*. Adhesion assays were performed as previously described (*24*). Hepes-Tyrode buffer (10 mM HEPES, 150 mM NaCl, 12 mM NaHCO<sub>3</sub>, 0.4 mM NaH<sub>2</sub>-PO<sub>4</sub>, 2.5 mM KCl, 0.1% glucose, 0.02% BSA, and 1 mM Mg<sup>2+</sup>, pH 7.4) was used instead of Dulbecco's modified Eagle medium. In some experiments, cells were preincubated with 250  $\mu$ M RGD peptide or anti-integrin monoclonal antibodies.

Ligand Binding Assay. Fibrinogen and recombinant C-terminal domains were labeled with fluorescein-isothiocy-anate (FITC) as described (25). Cells (1–1.5  $\times$  10<sup>6</sup> cells) were incubated with soluble FITC-labeled fibrinogen, recombinant  $\gamma C$ , or recombinant  $\alpha_E C$ , in 100  $\mu L$  of Dulbecco's modified Eagle medium for 30 min at room temperature. The activating anti- $\alpha IIb\beta 3$  mAb PT25-2 was used to activate  $\alpha IIb\beta 3$ . Cells were washed with ice-cold medium and analyzed by cell sorter.

#### **RESULTS**

Preparation and Characterization of the Recombinant Fibrinogen C-Terminal Domains. To study the involvement of the fibringen C-terminal domains in  $\alpha v \beta 3$ /fibringen interaction, we produced in E. coli recombinant C-terminal domains. These include wild-type  $\gamma C$  (residues 151–411 of the  $\gamma$  chain), the truncated mutants  $\gamma$ C/399t (residues 151– 399 of the  $\gamma$  chain), and  $\alpha_E C$  (residues 612–847 of the  $\alpha_E$ chain). All of the recombinant fibrinogen C-terminal domains used were more than 90% homogeneous as revealed by SDS-PAGE (Figure 1A and data not shown). Since all of the recombinant domains were expressed in a bacterial system, contained disulfides, and were subjected to the refolding procedure, it was necessary to verify their structural integrity. Like the well-characterized recombinant  $\gamma$ C (148– 411) (21), both wild-type  $\gamma C$  and mutant  $\gamma C/399t$  exhibited fluorescence spectra with maximum at 344 nm (Figure 1B), which is consistent with the presence of a compact structure. When heated in the fluorometer while the fluorescence intensity at 370 nm was monitored they both exhibited a sigmoidal transition (Figure 1C) that was very similar to that of  $\gamma C$  (148–411). The refolded  $\alpha_E C$  domain exhibited fluorescence spectra at an even shorter wavelength with a maximum at 338 nm (Figure 1B). The sigmoidal transition in  $\alpha_E C$  monitored by the fluorescence intensity was less pronounced, but it became obvious when the ratio of fluorescence intensity at 370 nm to that at 330 nm was monitored upon heating (Figure 1D). These results indicate that the recombinant proteins used in this study are properly folded.

Interaction between  $\beta 3$  Integrins and the Recombinant C-Terminal Domains. It has been reported that the platelet fibrinogen receptor  $\alpha \text{IIb}\beta 3$  binds to  $\gamma \text{C}$  (148–411) (21). We examined the ability of our recombinant  $\gamma \text{C}$  (151–411) and  $\alpha_E \text{C}$  to bind to  $\alpha \text{IIb}\beta 3$ . We tested FITC-labeled recombinant  $\gamma \text{C}$  and  $\alpha_E \text{C}$  to see if they would bind to  $\alpha \text{IIb}\beta 3$ -CHO cells in the presence of mAb PT25-2, which specifically activates

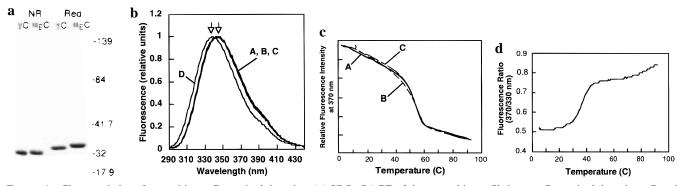


FIGURE 1: Characteristics of recombinant C-terminal domains. (a) SDS-PAGE of the recombinant fibrinogen C-terminal domains  $\gamma C$  and  $\alpha_E C$  on 10% gel under reducing (Red) and nonreducing (NR) conditions. Gel was stained with Coomassie brilliant blue and destained. (b) The fluorescent spectra of recombinant  $\gamma C$  (148-411) (A), recombinant  $\gamma C$  (residues 151-411) (B), its truncated mutant,  $\gamma C$ /399t (C), and recombinant  $\alpha_E C$  (residues 612-847) (D). Arrows indicate fluorescence intensity maximum at 344 nm (A, B, and C) or at 338 nm (D). (c) Fluorescence-detected thermal denaturation of recombinant  $\gamma C$  (148-411) (A), recombinant  $\gamma C$  (residues 151-411) (B), and its truncated mutant,  $\gamma C$ /399t (C). The experiments were performed in 100 mM Gly, pH 8.6, containing 0.5 mM Ca<sup>2+</sup>. (d) Fluorescence-detected thermal denaturation of recombinant  $\alpha_E C$  under the same conditions as described above. These results suggest that the recombinant proteins are properly folded.

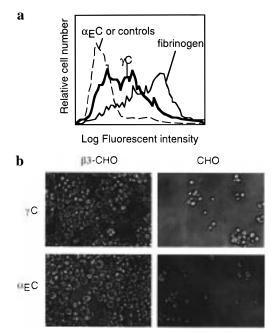


FIGURE 2: Interaction of  $\gamma C$  and  $\alpha_E C$  domains with different  $\beta 3$  integrins. (a) Binding of FITC-labeled  $\gamma C$  to  $\alpha IIIb\beta 3$ -CHO cells. Cells were incubated with soluble FITC-labeled recombinant  $\gamma C$  or fibrinogen in the presence of the activating anti- $\alpha IIIb\beta 3$  mAb PT25-2 and analyzed by cell sorter. Binding of  $\gamma C$  and fibrinogen was not detected in the absence of PT25-2. Binding of  $\alpha_E C$  was not detected, even in the presence of PT25-2. (b) Recombinant  $\gamma C$  and  $\alpha_E C$  adhere to  $\beta 3$ -CHO cells that express  $\alpha v \beta 3$ , but do not adhere to CHO cells that do not express  $\alpha v \beta 3$ . Wells were coated with recombinant  $\gamma C$  and  $\alpha_E C$  (at  $50~\mu g/mL$  coating concentration). After gently rinsing the wells once with buffer to remove unbound cells, we observed bound cells by phase contrast microscope (200×). Note that  $\beta 3$ -CHO cells do not spread on  $\gamma C$  or  $\alpha_E C$ . Untransfected CHO cells did not attach to  $\gamma C$  or  $\alpha_E C$ .

 $\alpha IIb\beta 3$  (but not  $\alpha v\beta 3$ ). As shown in Figure 2A, recombinant  $\gamma C$  binds to  $\alpha IIb\beta 3$ -CHO cells, but  $\alpha_E C$  does not. We did not detect any significant binding of FITC-labeled soluble  $\gamma C$  or  $\alpha_E C$  to  $\beta 3$ -CHO cells (data not shown).

To determine whether recombinant  $\gamma C$  and  $\alpha_E C$  interact with  $\alpha v \beta 3$ , we used  $\beta 3$ -CHO cells that express  $\alpha v \beta 3$  (but not  $\alpha IIb\beta 3$ ). Parent CHO cells do not express  $\alpha v \beta 3$ . As shown in Figure 2B,  $\beta 3$ -CHO cells adhered to recombinant  $\gamma C$  and  $\alpha_E C$ , but parent CHO cells did not.  $\beta 3$ -CHO cells

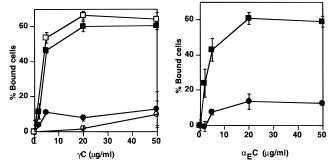


FIGURE 3: Adhesion of CHO cells and  $\beta3$ -CHO cells to recombinant  $\gamma C$  and  $\alpha_E C$  as a function of ligand concentration. Wells of 96-well microtiter plates were coated with increasing concentrations of  $\gamma C$ ,  $\gamma C$  (148–411), or  $\alpha_E C$  (up to 50  $\mu g/m L$ ). CHO cells (circles) and  $\beta3$ -CHO cells (squares) on  $\gamma C$  (151–411, closed circles or squares) or  $\gamma C$  (148–411, open circles or squares). The data are expressed as mean  $\pm$  sd of three experiments. The data suggest that adhesion of  $\beta3$ -CHO cells to these recombinant proteins saturates at a 20  $\mu g/m L$  coating concentration.

did not spread on the recombinant C-terminal domains. Adhesion of  $\beta$ 3-CHO cells to recombinant  $\gamma$ C and  $\alpha_E$ C was saturated at a coating concentration of 20  $\mu$ g/mL (Figure 3), indicating that recombinant  $\gamma$ C and  $\alpha_E$ C are equivalent in supporting  $\alpha v \beta 3$  adhesion. Similarly,  $\beta$ 3-CHO cells adhered to a well-characterized recombinant  $\gamma$ C (148–411) (Figure 3) (21). Adhesion of  $\beta$ 3-CHO cells to these proteins was completely inhibited by RGD peptides, EDTA, and LM609, a function-blocking anti- $\alpha v \beta 3$  mAb (Figure 4A). We also found that M21 human melanoma cells that express natural  $\alpha v \beta 3$  adhere to these domains, and that this adhesion is completely blocked by LM609 (Figure 4B). These results indicate that  $\alpha v \beta 3$  (recombinant or natural) specifically interacts with these C-terminal domains.

 $\alpha\nu\beta 3$  Does Not Require the HHLGGAKQAGDV<sup>400-411</sup> Sequence for Adhesion to  $\gamma C$ . The fact that the  $\alpha_E$  chain does not have the dodecapeptide-like sequence, but still supports  $\alpha\nu\beta 3$  adhesion, suggests that  $\alpha\nu\beta 3$  adhesion to  $\gamma C$  does not depend on the dodecapeptide sequence. To define the role of the  $\gamma C$  C-terminal region in  $\alpha\nu\beta 3$  binding, we examined the effects of truncating the C-terminal portion of  $\gamma C$  (Figure 5). We found that the  $\gamma C$  mutant with truncation

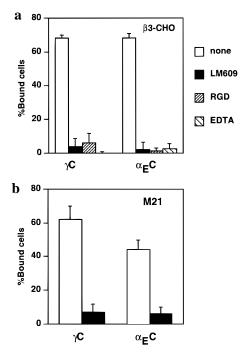


FIGURE 4: Specificity of adhesion of  $\beta$ 3-CHO cells (a) and M21 melanoma cells (b) to  $\gamma C$  and  $\alpha_E C.$  The adhesion assay was performed as described in the legend to Figure 2. Wells were coated with 50  $\mu$ g/mL  $\gamma$ C or  $\alpha$ <sub>E</sub>C. LM609 at 250× dilution of ascites, 250 µM RGD peptide, or 2mM EDTA (instead of 1 mM MgCl<sub>2</sub>) was used. The data are expressed as mean  $\pm$  sd of three experiments. The data suggest that adhesion of  $\beta$ 3-CHO and M21 cells to  $\gamma C$  and  $\alpha_E C$  is specifically mediated by integrin  $\alpha v \beta 3$ .

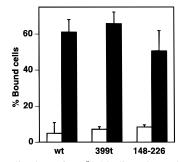


FIGURE 5: Localization of  $\alpha v \beta 3$  binding sites within  $\gamma C$ . Wildtype recombinant  $\gamma C$ , the  $\gamma C/399t$  truncation mutant, and a small  $\gamma$ C fragment (residues 148–226) were used for coating wells at 50  $\mu$ g/mL: CHO cells (open bar);  $\beta$ 3–CHO cells (solid bar). Adhesion assays were performed as described in the legend to Figure 3. The data are expressed as mean  $\pm$  sd of three experiments. The data suggest that the HHLGGAKQAGDV<sup>400-411</sup> sequence of  $\gamma$ C is not required for adhesion to  $\alpha v\beta 3$  and that an  $\alpha v\beta 3$  binding site is located within a region spanning residues 148-226.

of the complete dodecapeptide sequence HHLGGAKQ-AGDV<sup>400-411</sup> (399t) still supported adhesion of  $\beta$ 3-CHO cells. These results suggest that  $\alpha v \beta$ 3-mediated adhesion to  $\gamma C$  is not dependent on the HHLGGAKQAGDV<sup>400-411</sup> sequence. This is in contrast to previous reports that  $\alpha \text{IIb}\beta 3$ mediated platelet aggregation requires the AGDV<sup>408-411</sup> sequence of  $\gamma C$  (ref 16 and references therein). We also tested the recombinant fibringen y chain 148–226 fragment (Asp199-Gly200 is mutated to Gly-Ala) and found that  $\beta$ 3-CHO cells bound to this fragment. These results suggest that an  $\alpha v \beta 3$  binding site is located within the  $\gamma$  chain 148–226 region.

The  $\gamma C$  and  $\alpha_E C$  Domains Direct Fibrinogen's  $\alpha v \beta 3$ Specificity. We recently identified a region of the  $\beta$  subunit

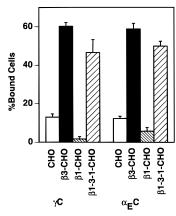


FIGURE 6:  $\gamma C$  and  $\alpha_E C$  are recognized by the  $\alpha v \beta 1$ -3-1 mutant. but not by  $\alpha v\beta 1$ .  $\beta 1$ -CHO cells express  $\alpha v\beta 1$ , but not  $\alpha v\beta 3$ .  $\beta 3$ -CHO cells express both  $\alpha v \beta 1$  and  $\alpha v \beta 3$ .  $\beta 1$ -3-1-CHO cells express  $\alpha v\beta 1$ -3-1.  $\alpha v\beta 3$  recognizes fibringen, but  $\alpha v\beta 1$  does not. The  $\alpha v \beta 1$ -3-1 mutant recognizes fibringen, although the anti- $\beta 1$ function-blocking antibody blocks this interaction. Adhesion assays were performed as described in the legend of Figure 3. The data are expressed as mean  $\pm$  sd of three experiments. The data suggest that recombinant  $\gamma C$  and  $\alpha_E C$  (which have no RGD sequence) support  $\alpha v \beta 1$ -3-1 adhesion, suggesting that these domains contain determinants for the  $\alpha v \beta 3$  specificity of fibrinogen.

that is critical for the ligand specificity of integrins  $\alpha v \beta 1$ and  $\alpha v\beta 3$  (20). Integrin  $\alpha v\beta 3$  recognizes fibrinogen, von Willebrand factor, vitronectin, and fibronectin, while  $\alpha v \beta 1$ recognizes only fibronectin. When the sequence CTSEQNC (residues 187–193) of  $\beta$ 1 is replaced with the corresponding CYDMKTTC sequence of  $\beta$ 3, the ligand specificity of  $\alpha v \beta$ 1 is altered; the mutant ( $\alpha v\beta 1$ -3-1) recognizes the same ligands as  $\alpha v \beta 3$ . We studied whether the  $\alpha v \beta 1$ -3-1 mutant adheres to  $\gamma C$  and  $\alpha_E C$ . We found that  $\beta 1$ -3-1-CHO cells do adhere to recombinant  $\gamma C$  and  $\alpha_E C$ , but control  $\beta$ 1-CHO cells do not (Figure 6). Adhesion of  $\alpha v \beta 1$ -3-1 to the C-terminal domains was blocked by mAb 13, a function blocking anti- $\beta$ 1 mAb. These results suggest that fibringen C-terminal domains have determinants for binding to  $\alpha v \beta 3$ , even though these domains do not contain the RGD motif.

### **DISCUSSION**

The present study provides direct evidence that  $\alpha v \beta 3$ specifically recognizes the fibrinogen C-terminal domains,  $\gamma C$  and  $\alpha_E C$ , even though these fragments lack RGD motifs. Unlike  $\alpha \text{IIb}\beta 3$ ,  $\alpha v\beta 3$ -mediated adhesion to  $\gamma C$  does not require the dodecapeptide HHLGGAKQAGDV400-411 sequence; this is consistent with the fact that  $\alpha_E C$ , which does not have the dodecapeptide-like sequence, still supports  $\alpha v \beta 3$ adhesion. These findings indicate that the  $\gamma C$  and  $\alpha_E C$ domains each have at least one major  $\alpha v \beta 3$  binding site, and that the  $\gamma C$  sequence required for  $\alpha v \beta 3$  binding is distinct from the sequence required by  $\alpha \text{IIb}\beta 3$ . Adhesion of  $\beta$ 3-CHO cells to the C-terminal domains is blocked by RGD peptides, even though the domains do not have RGD motifs. This suggests that the C-terminal domains may use binding sites in  $\alpha v\beta 3$  that are common to other RGD-containing  $\alpha v\beta 3$  ligands (e.g., vitronectin).

This study also provides the first demonstration of a possible biological function of  $\alpha_E C$ , which is unique to fibrinogen-420. Fibrinogen-420 represents only 1-2% of the fibrinogen in an adult human, and its physiological role is unknown. However, its levels in fetal human plasma are about 3 times higher than in adult human plasma (26). Additionally,  $\alpha_E C$  is conserved among vertebrates (27, 28). The present study suggests that fibrinogen-420 has two additional  $\alpha v \beta$ 3-binding sites situated in the  $\alpha_E C$  domains. It is possible that fibrinogen-420 may play a significant role in cell adhesion during development.

 $\alpha v \beta 3$  is critically involved in endothelial (or tumor) cellmediated fibrin clot retraction (13, 14), and interestingly this process does not require the  $\alpha$  chain RGD  $^{95-97}$  and RGD  $^{572-574}$ sequences or the  $\gamma$  chain AGDV<sup>408–411</sup> sequence (14, 15). These observations are consistent with the findings of the present study on the fibrinogen recognition and specificity of  $\alpha v \beta 3$ , which specifically binds to the fibringen Cterminal domains that lack RGD motifs.  $\alpha v \beta 3 - \gamma C$  interaction is retained when the dodecapeptide sequence of  $\gamma C$  is truncated. Taken together, these findings suggest that  $\gamma C$  and  $\alpha_E C$  are the most likely locations for the  $\alpha v \beta 3$  binding sites in  $\alpha v \beta 3$ -mediated clot retraction. The fact that these domains are well conserved among species, unlike the  $\boldsymbol{\alpha}$  chain RGD<sup>95-97</sup> and RGD<sup>572-574</sup> sequences, supports the idea that these domains may mediate the primary function of fibrinogen, clot retraction. It should be noted that in our preliminary experiments, partially purified recombinant  $\beta C$  (residues 209-461 of the  $\beta$  chain) supported  $\alpha v \beta$ 3-mediated cell adhesion, which is blocked by LM609 and RGD peptides (data not shown). These results suggest that  $\beta$ C might also be involved in  $\alpha v \beta 3$ -mediated cell adhesion.

It has been established that deletion of the  $\gamma$  chain AGDV sequence blocks  $\alpha \text{IIb}\beta 3$ —fibrinogen interaction (29, 30). In transgenic mice that have no QAGDV sequence in their fibrinogen  $\gamma$  chain, binding of fibrinogen to  $\alpha \text{IIb}\beta 3$  and platelet aggregation are highly defective, but clot retraction is normal (30). The retained clot retraction in these transgenic mice has not been fully explained. The present study suggests that the interaction between  $\alpha v\beta 3$  and  $\gamma C$  is retained when the HHLGGAKQAGDV<sup>400-411</sup> sequence of the  $\gamma$  chain is truncated, even though this truncation eliminates  $\alpha \text{IIb}\beta 3$ - $\gamma C$  interaction. It is likely that  $\alpha v\beta 3$ -mediated clot retraction partly compensates for the lack of  $\alpha \text{IIb}\beta 3$ -mediated clot retraction in QAGDV-motif-deleted mice. The retained  $\alpha v\beta 3$ -fibrinogen interaction possibly explains the normal fibrin clot retraction in the QAGDV-deficient mice.

It has been reported that a proteolytic fibrinogen fragment that lacks  $\alpha RGD^{572-574}$  (fragment X) cannot support  $\alpha \nu \beta 3$ -mediated adhesion of endothelial cells (9) and melanoma cells (31). Mutation of the  $\alpha RGD^{572-574}$  sequence to RGE has been reported to markedly reduce adhesion of endothelial cells to fibrinogen (12). The present study does not contradict these previous reports. One possible explanation is that the  $\alpha RGD^{572-574}$  sequence of human fibrinogen may play a dominant role, and possibly overshadow the contribution of the C-terminal domains, in  $\alpha \nu \beta 3$ -mediated cell adhesion. Consistent with this explanation, mutation of the  $\alpha RGD^{572-574}$  sequence to RGE significantly reduces, but does not completely eliminate,  $\alpha \nu \beta 3$ -mediated adhesion (12). However, the  $\alpha RGD^{572-574}$  sequence of human fibrinogen may not be critical for  $\alpha \nu \beta 3$ -mediated clot retraction.

We have shown that  $\gamma C$  and  $\alpha_E C$  contain determinants for fibrinogen's specificity to  $\alpha v \beta 3$ . We have previously reported that  $\alpha v \beta 1$  does not recognize whole fibrinogen, but  $\alpha v \beta 3$  and the  $\alpha v \beta 1$ -3-1 mutant do (20). These results suggest that the YDMKTT sequence of  $\beta 3$  is critical for fibrinogen

specificity. We have shown in this paper that fibrinogen's determinants for  $\alpha v\beta 3$  specificity are located in its  $\gamma C$  and  $\alpha_E C$  domains. This is consistent with the finding that  $\alpha v \beta 3$ specifically recognizes the fibrinogen C-terminal globular domains. There is one  $\alpha v \beta 3$  binding site in  $\gamma C$  that is probably located within residues 148-226 of  $\gamma$ C. The  $\gamma$ chain 148-226 fragment contains domain A (residues 148-191) and part of domain B (residues 192-226). According to its 3-dimensional structure, the latter portion is stabilized by several internal hydrogen bonds and side chain—side chain contacts and also forms hydrogen bonds and side chain contacts with domain A. Thus it may be that the ordered conformation of the fragment accounts for its resistance to proteolysis. In addition the fragment contains the region 190-202 (P1), which has been reported to interact with  $\alpha M\beta 2$  (32). The Asp199-Gly200 to Gly-Ala mutation did not interfere with that interaction (22). The putative  $\alpha v \beta 3$ binding sites in the C-terminal domains might be major targets for modulating this interaction.

The present study does not address whether  $\alpha IIb\beta 3$  recognizes  $\alpha_E C$  or  $\gamma C/399t$ . We found that  $\alpha IIb\beta 3$ -CHO cells adhered to  $\gamma C$ ,  $\alpha_E C$ , and  $\gamma C/399t$  in preliminary experiments (data not shown).  $\alpha IIb\beta 3$ -CHO cells express both human  $\alpha IIb\beta 3$  and hamster  $\alpha v$ /human  $\beta 3$  hybrid.  $\alpha IIb\beta 3$ -CHO cell adhesion to  $\gamma C$  and  $\alpha_E C$  is not completely inhibited by the anti- $\alpha v\beta 3$  antibody LM609, but is completely inhibited by adding both LM609 and the anti- $\alpha IIb\beta 3$  antibody OPG2.  $\alpha IIb\beta 3$ -CHO cell adhesion to the  $\gamma C/399t$  mutant is completely blocked by LM609. On the basis of these preliminary results, we suspect that  $\alpha IIb\beta 3$  binds to  $\gamma C$  and binds only weakly to  $\alpha_E C$ , but does not bind to  $\gamma C/399t$ . Further studies must be performed using the cells that express  $\alpha IIb\beta 3$  but not  $\alpha v\beta 3$  to clarify this point.

# **ACKNOWLEDGMENT**

We thank D. Cheresh, M. H. Ginsberg, M. Handa, Y. Ikeda, and K. Yamada for valuable reagents, and Z. Ruggeri and S. Shattil for critical reading of the manuscript. We also thank Sae Takada for contributing to the initial phase of this work and Anna Ewers for assistance with editing the manuscript.

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BI9827619