

## COMMENTARY

# Integrin cytoplasmic domain-binding proteins

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Published on WWW 4 October 2000

## SUMMARY

**Integrins are a large family of cell surface receptors that mediate cell adhesion and influence migration, signal transduction, and gene expression. The cytoplasmic domains of integrins play a pivotal role in these integrin-mediated cellular functions. Through interaction with the cytoskeleton, signaling molecules, and other cellular proteins, integrin cytoplasmic domains transduce signals from both the outside and inside of the cell and regulate integrin-mediated biological functions. Identification and functional analyses of integrin cytoplasmic domain-binding proteins have been pursued intensively. In recent years, more cellular proteins have been reported to directly**

**interact with integrin cytoplasmic domains and some of these interactions may play important roles in integrin-mediated biological responses. Integrin  $\beta$  chains, for example, interact with actin-binding proteins (e.g. talin and filamin), which form mechanical links to the cytoskeleton. These and other proteins (e.g. FAK, ILK and novel proteins such as TAP20) might also link integrins to signaling mechanisms and, in some cases (e.g. JAB1) mediate integrin-dependent gene regulation.**

Key words: Integrin, Cytoplasmic domain, Binding protein, Cellular function, Signaling

## INTRODUCTION

Integrin adhesion receptors are heterodimers of  $\alpha$  and  $\beta$  subunits that contain a large extracellular domain responsible for ligand binding, a single transmembrane domain and a cytoplasmic domain that in most cases consists of 20-70 amino acid residues (Hynes, 1992; Sastry and Horwitz, 1993). Integrins play central roles in cell adhesion, cell migration and control of cell differentiation, proliferation and programmed cell death. They mediate signal transduction through the cell membrane in both directions: binding of ligands to integrins transmits signals into the cell and results in cytoskeletal re-organization, gene expression and cellular differentiation (outside-in signaling); on the other side, signals from within the cell can also propagate through integrins and regulate integrin ligand-binding affinity and cell adhesion (inside-out signaling; Hynes, 1992; Schwartz et al., 1995). The cytoplasmic domains of integrins play a pivotal role in these bi-directional signaling processes and intensive efforts have focused on identifying cellular proteins that can directly interact with integrin cytoplasmic domains in order to elucidate molecular mechanisms by which integrin mediate bi-directional signal transduction (Dedhar and Hannigan, 1996; Hemler, 1998; Hughes and Pfaff, 1998). Here, we focus on the most recent advances in this field.

## INTEGRIN $\beta$ CYTOPLASMIC DOMAIN-BINDING PROTEINS

Extensive mutational analysis has demonstrated that integrin  $\beta$  cytoplasmic tails play a central role in integrin functions.  $\beta_1$ ,  $\beta_2$  and  $\beta_3$  integrins lacking  $\beta$  tails fail to localize to focal adhesions, and show reduced ligand-binding activity and impaired activation of downstream signaling molecules (Solowska et al., 1989; Hayashi et al., 1990; Marcantonio et al., 1990; O'Toole et al., 1994). Furthermore,  $\beta_{1A}$ ,  $\beta_{1D}$ ,  $\beta_3$ ,  $\beta_5$  and  $\beta_7$  tails expressed in isolation as transmembrane chimeras localize to pre-existing focal adhesions and exhibit a dominant negative effect on the ligand-binding activity of  $\beta_1$ ,  $\beta_3$  and  $\beta_5$  integrins (Akiyama et al., 1994; Chen et al., 1994; LaFlamme et al., 1992; Lukashev et al., 1994; Zent et al., 2000). Isolated  $\beta$  tails are also sufficient to activate downstream signaling molecules, such as FAK, and can regulate cell cycle progression and actin cytoskeleton assembly (Belkin and Retta, 1998; David et al., 1999; Tahiliani et al., 1997).  $\beta$  tails are thus necessary and sufficient for correct subcellular localization of integrins and for activation of signaling pathways, and regulate the affinity of integrins for their ligands.

The mechanisms by which integrin  $\beta$  tails function in both outside-in and inside-out signaling remain to be fully resolved. Nonetheless, these processes are probably mediated mainly through direct associations between integrin  $\beta$  tails and

signaling and structural proteins. A complete understanding of the molecular basis of integrin regulation will require identification of these integrin-binding proteins and characterization of their activities. At least 21 proteins are known to bind to one or more integrin  $\beta$  tails (Table 1). This diverse list of proteins includes actin-binding proteins, enzymes, adaptor proteins, a transcriptional co-activator and additional proteins of unknown function. As the list lengthens, the challenge becomes determination of which interactions are significant *in vivo* and the roles of these interactions in specific cellular activities.

### Actin-binding proteins

Correct localization of integrins, and their role in cell spreading, migration and matrix assembly require connection to the actin cytoskeleton. This connection is formed by the direct or indirect association of actin-binding proteins with integrin  $\beta$  tails (reviewed by Calderwood et al., 2000 and Critchley, 2000). These interactions represent some of the best-characterized integrin  $\beta$  tail associations, and their significance has been investigated in a variety of contexts.

The first cytoplasmic protein shown to bind to integrins directly was the actin-binding protein talin (Horwitz et al., 1986). Talin colocalizes with integrins at certain sites of cell-substratum contact, and Horwitz et al., proposed that the talin-integrin interaction provides the link between integrins and the actin cytoskeleton. Subsequent experiments revealed that the  $\beta$  cytoplasmic tail is responsible for binding to talin (Pfaff et al., 1998; Knezevic et al., 1996; Table 1), although one report

indicates that talin also binds to the  $\alpha_{IIb}$  tail (Knezevic et al., 1996). The integrin-binding site has been localized to the head domain of talin, and overexpression of a fragment of talin containing this binding site leads to increased binding of soluble ligand (activation) by  $\alpha_{IIb}\beta_3$  in CHO cells (Calderwood et al., 1999). These data, together with the observation that reduced expression of talin disrupts cell surface expression of integrins and export from the Golgi, and impairs focal adhesion formation and cell migration (Priddle et al., 1998; Martel et al., 2000), suggest that binding of talin to integrin  $\beta$  tails is important for a variety of integrin functions. However, proof of this hypothesis requires evidence that specific disruption of the talin-integrin interaction alters integrin-dependent functions.

To date no point mutants of talin that lack integrin-binding activity have been reported. However, fragments that lack the entire, integrin-binding, head domain cannot activate  $\alpha_{IIb}\beta_3$  in CHO cells. The exact location of the talin-binding site within the  $\beta$  tail remains to be determined (Calderwood et al., 2000); nonetheless, point and deletion mutants that inhibit talin binding have been identified (Calderwood et al., 1999; Kaapa et al., 1999). Integrin mutants that are unable to bind talin are unable to localize to focal adhesions and fail to accumulate F-actin following integrin clustering (Reszka et al., 1992; Ylanne et al., 1995; Lewis and Schwartz, 1995). These mutants are expressed at the cell surface, although whether their trafficking from the Golgi to plasma membrane is altered has not been investigated. Furthermore, one report indicates that in v-Src-transformed cells, which exhibit reduced cell adhesion and a

**Table 1**

Binding partner	Integrin tail	Detection	Reference
<b>Actin-binding protein</b>			
Talin	$\beta_{1A}, \beta_{1D}, \beta_2, \beta_3$	COIP, PEP, EQ, INT, SLS	Horwitz et al., 1986; Knezevic et al., 1996; Pfaff et al., 1998; Goldmann, 2000
Filamin	$\beta_{1A}, \beta_2, \beta_3, \beta_7$	COIP, PEP, 2HYB, SLS	Pavalko et al., 1989; Loo et al., 1998; Pfaff et al., 1998; Goldmann, 2000
$\alpha$ -actinin	$\beta_{1A}, \beta_2$	PEP, INT, COIP, SLS	Otey et al., 1990; Pavalko et al., 1991; Cattelino et al., 1999
F-actin	$\alpha_2$	PEP	Kieffer et al., 1995
Myosin	$\beta_3$	PEP, COIP	Jenkins et al., 1998; Sajid et al., 2000
Skelemin	$\beta_1, \beta_3$	2HYB, PEP	Reddy et al., 1998
<b>Signaling protein</b>			
ILK	$\beta_1, \beta_3$	2HYB, COIP	Hannigan et al., 1996
FAK	$\beta_1, \beta_2, \beta_3$	PEP, COIP	Schaller et al., 1995; Chen et al., 2000
Cytohesin-1	$\beta_2$	2HYB, COIP, PEP	Kolanus et al., 1996
Cytohesin-3	$\beta_2$	2HYB	Hmama et al., 1999
<b>Other protein</b>			
Paxillin	$\beta_1, \beta_3, \alpha_4$	PEP, COIP	Schaller et al., 1995; Chen et al., 2000; Liu et al., 1999
Grb2	$\beta_3$	PEP	Law et al., 1996
Shc	$\beta_3$	PEP	Law et al., 1996
$\beta_3$ -endonexin	$\beta_3$	2HYB, INT, PEP	Shattil et al., 1995; Eigenthaler et al., 1997
TAP-20	$\beta_5$	PEP	Tang et al., 1999
CIB	$\alpha_{IIb}$	2HYB, PEP, COIP	Naik et al., 1997; Shock et al., 1999; Valler et al., 1999
Calreticulin	$\alpha$	PEP, COIP	Rojiani et al., 1991; Leung-Hagesteijn et al., 1994; Coppolino et al., 1995
Caveolin-1	$\alpha$	COIP	Wary et al., 1998
Rack1	$\beta_1, \beta_2, \beta_5$	2HYB, PEP, COIP	Liliental et al., 1998
WAIT-1	$\beta_7$	2HYB, PEP	Rietzler et al., 1998
JAB1	$\beta_2$	2HYB, PEP, COIP	Bianchi et al., 1998
Melusin	$\beta_{1A}, \beta_{1B}, \beta_{1D}$	2HYB, INT	Brancaccio et al., 1999
MIBP	$\beta_{1A}, \beta_{1D}$	2HYB, PEP, COIP	Li et al., 1999
ICAP-1	$\beta_{1A}$	2HYB, PEP, INT	Chang et al., 1997; Zhang and Hemler, 1999
CD98	$\beta_{1A}, \beta_3$	PEP	Zent et al., 2000
DRAL/FHL2	$\alpha_{3A}, \alpha_{3B}, \alpha_{7A}, \beta$	2HYB, PEP	Wixler et al., 2000

COIP--Coimmunoprecipitation; PEP--Synthetic/recombinant peptide studies; 2HYB--Yeast two-hybrid screen; INT--Binding to purified integrins; SLS--Static light scattering; EQ--Equilibrium gel filtration.

disorganized cytoskeleton, the NPXY motif (this motif is highly conserved among different integrin  $\beta$  subunit cytoplasmic domains and may play important roles in integrin-mediated signal transduction) in the  $\beta_1$  tail is phosphorylated on tyrosine, and talin binding is inhibited (Tapley et al., 1989). These observations strongly support the hypothesis that binding of talin to integrin  $\beta$  tails plays a role in integrin-mediated processes by connecting integrins to the actin cytoskeleton. However, note that the integrin mutants tested might also exhibit impaired interactions with other integrin-binding proteins whose function is not appreciated. For this reason reconstitution experiments in talin-null cells, using wild-type and mutated talin, should provide an additional test of the role of integrin-talin interactions.

The binding of integrins to two other families of actin-binding proteins,  $\alpha$ -actinin and filamin, has also been well characterized (Table 1; Calderwood et al., 2000; Critchley, 2000). Static light scattering experiments, which can measure equilibrium binding constants between purified proteins, indicate that both filamin and  $\alpha$ -actinin bind less tightly to integrin  $\alpha_{IIb}\beta_3$  than does talin (Goldmann, 2000). Like talin,  $\alpha$ -actinin colocalizes with integrins in focal adhesions, and  $\alpha$ -actinin targets to focal adhesions in microinjected cells and in a cell-free system, apparently by interaction with  $\beta$  cytoplasmic tails (Otey et al., 1990; Pavalko and Burridge, 1991; Cattelino et al., 1999).  $\alpha$ -actinin is also localized along stress fibers. Expression of isolated integrin-binding fragments of  $\alpha$ -actinin disrupts stress fibers, focal adhesions and shear-induced mechanical signaling in fibroblasts and osteoblasts (Ezzell et al., 1997; Pavalko and Burridge, 1991; Pavalko et al., 1998). The  $\alpha$ -actinin-binding site has been localized to the membrane-proximal half of the  $\beta_1$  and  $\beta_2$  integrin tails (Fig. 1; Otey et al., 1990), and mutations in this region alter formation of focal adhesions and stress fibers. However, truncated integrin mutants that retain  $\alpha$ -actinin binding but cannot bind to talin still exhibit a disrupted phenotype (Retta et al., 1998; Lewis and Schwartz, 1995), which indicates that these two  $\beta$  tail-binding proteins have separate functions.

Filamin localizes to the cortical actin cytoskeleton and along the length of stress fibers, but is also found in some focal adhesions (Pavalko et al., 1989). Its recruitment to  $\beta_1$ -containing focal adhesions is stimulated by mechanical stress and leads to F-actin recruitment (Glogauer et al., 1998). In addition to providing a mechanical link between integrins and the cytoskeleton, filamin also acts as an adaptor protein for a number of signaling proteins (e.g. RalA) that can regulate cytoskeletal dynamics (Ohta et al., 1999). Loss of filamin-1 expression in cultured melanocytes causes impaired migration, altered morphology and defective expression of cell surface molecules (Cunningham et al., 1992; Meyer et al., 1998), and human neurons lacking filamin-1 fail to migrate in vitro, which causes the disease periventricular heterotopia (Fox et al., 1998). The filamin binding site lies in the C-terminal portion of the  $\beta_{1A}$  tail, and point mutations in this region disrupt filamin-binding (Loo et al., 1998). These mutations also lead to impaired localization of integrins to focal adhesions. Thus, both  $\alpha$ -actinin and filamin can bind to integrin  $\beta$  tails, colocalize with integrins, and are required for integrin-mediated processes. However, detailed analysis of which processes require direct  $\beta$ -tail binding awaits identification of

subtle mutations that modulate integrin-filamin or integrin- $\alpha$ -actinin interactions.

Additional cytoskeletal proteins have been identified as integrin- $\beta$ -tail-binding proteins; however, their significance is not yet clear. Jenkins et al. used ligand blotting to demonstrate association of platelet myosin with a peptide corresponding to the last 23 residues of the  $\beta_3$  tail (Jenkins et al., 1998). The interaction was dependent on phosphorylation of both tyrosine residues in this sequence and was inhibited by a loss of function mutation in this region. Following platelet aggregation, phosphorylation of both tyrosines in the  $\beta_3$  tail can be detected, which suggests that myosin is recruited to contribute to clot retraction. CHO cells expressing mutants that have Tyr $\rightarrow$ Phe mutations in the  $\beta_3$  tail are less efficient at clot retraction, and these mutations are associated with a mild bleeding phenotype in mice (Jenkins et al., 1998; Law et al., 1999). In addition, Sajid et al. recently showed that non-muscle myosin heavy chain A coimmunoprecipitates with  $\alpha_v\beta_3$  integrins following thrombospondin stimulation of smooth muscle cells (Sajid et al., 2000). It will be of interest to determine whether this stimulation leads to  $\beta_3$  tail tyrosine phosphorylation, which could account for myosin recruitment.

Binding of skelemin, a cytoskeletal M-band protein, to  $\beta_1$  and  $\beta_3$  but not  $\beta_2$  tails was also reported recently (Reddy et al., 1998). Skelemin has an unique N-terminal region followed by Ig superfamily C2 and fibronectin (FN) type II motifs. Reddy et al., localized the skelemin-binding site to the membrane proximal ten residues of  $\beta_1$ . Under some conditions, skelemin colocalizes with  $\alpha_{IIb}\beta_3$  expressed in CHO cells, and microinjection of the integrin-binding domain of skelemin causes myoblasts to round up (Reddy et al., 1998), conceivably by disrupting integrin-cytoskeleton interactions. Skelemin is encoded by an alternatively spliced version of the myomesin gene (Steiner et al., 1999), and the integrin-binding sequence is also present in myomesin, which suggests that this protein also binds  $\beta$  tails. Although skelemin expression is restricted to muscle cells, antibodies against skelemin crossreact with a protein of similar size from non-muscle cells, which raises the possibility that integrin binding to a skelemin-like protein is important in many cell types.

### Cell signaling proteins

In addition to providing a link to the actin cytoskeleton, integrin- $\beta$ -tail-binding proteins also regulate outside-in and inside-out signaling. The absence of any detectable enzymatic activity in integrin cytoplasmic tails suggests that integrin-mediated signaling requires direct binding of signaling proteins, such as non-receptor kinases, or of adaptor proteins that can recruit these molecules.

Two kinases, focal adhesion kinase (FAK) and integrin linked kinase (ILK), have been reported to bind to integrin  $\beta$  tails (Table 1). FAK colocalizes with integrins at cell-substratum contact sites, and its phosphorylation state and tyrosine kinase activity are regulated by binding of cells to the ECM (reviewed by Schlaepfer and Hunter, 1998). FAK phosphorylation can also be induced by clustering of isolated integrin  $\beta$  tails. FAK has been implicated as a central player in integrin-mediated signaling (Schlaepfer and Hunter, 1998). However, what, if any, role FAK binding to integrin  $\beta$  tails plays in the process is not clear. Schaller et al. demonstrated that FAK binds to synthetic peptides corresponding to the

membrane-proximal region of the  $\beta_1$ ,  $\beta_2$  and  $\beta_3$  tails, and that mutations in this region inhibit FAK binding to a full-length  $\beta_1$  tail peptide (Schaller et al., 1995). FAK has also been reported to co-immunoprecipitate with  $\beta_1$  integrins from co-cultures of Schwann cells and neurons (Chen et al., 2000). Under these conditions paxillin is also co-precipitated with both FAK and  $\beta_1$  integrins, which raises the possibility that FAK is linked indirectly to  $\beta_1$  integrins. FAK binding to talin (Borowsky and Hynes, 1998) provides yet another mechanism by which FAK might be indirectly linked to integrin. The integrin-binding site in FAK was localized to the region N-terminal to the kinase domain; however, this region is not required for localization of FAK to focal adhesions. Instead, a region C-terminal to the kinase domain, the focal-adhesion-targeting domain, is necessary and sufficient for localization to focal adhesions. Furthermore, the reported FAK-binding region within  $\beta_3$  tail (Schaller et al., 1995) is neither required nor sufficient for FAK activation following clustering of isolated  $\beta_3$  tails (Tahiliani et al., 1997).

ILK is the subject of several recent reviews (Dedhar, 2000; Dedhar et al., 1999; Wu, 1999) and was initially identified in a yeast two-hybrid screen for  $\beta_1$ -tail-binding protein. It localizes to focal adhesions in a manner dependent on both the C-terminal domain, which contains the integrin-binding site, and the most N-terminal ankyrin repeat (Wu, 1999). This repeat is responsible for binding the LIM domain protein PINCH. PINCH in turn binds to other adaptor proteins, which could regulate additional signaling pathways or actin polymerization (Calderwood et al., 2000). Null mutations in the gene that encodes *C. elegans* ILK, *pat-4*, have a phenotype similar to that of integrin- or PINCH-null mutants, providing additional evidence for a functional link between these molecules. However, although ILK has been implicated in regulation of cell adhesion, fibronectin (FN) matrix assembly, anchorage-dependent cell growth, and cell cycle progression, whether direct integrin-ILK binding is required for any of these processes awaits studies using mutants in which integrin binding is selectively disrupted.

Another class of signaling molecule capable of binding to integrin  $\beta$  tails is the cytohesins. Cytohesins have guanine nucleotide exchange activity for the ARF family of small GTPases (Ogasawara et al., 2000). Cytohesin-1 and subsequently, cytohesin-3 were identified as  $\beta_2$ -tail-binding proteins in yeast two-hybrid screens, and the integrin-binding site was localized to the Sec7 domain of the molecule (Kolanus et al., 1996; Korthauer et al., 2000). Cytohesin-1 also coprecipitated with  $\beta_2$ , but not  $\beta_1$ , integrins from Jurkat cell lysate, and recombinant cytohesin-1 bound to peptides corresponding to the  $\beta_2$  tail. Overexpression of cytohesin-1 or cytohesin-3, but not cytohesin-2, increased  $\beta_2$ -integrin-mediated adhesion of unstimulated Jurkat cells, and antisense cytohesin-1 oligonucleotides reduced LPS-induced adhesion of THP1 cells to  $\beta_2$  integrin ligands (Korthauer et al., 2000; Hmama et al., 1999).

Recent data from Geiger et al. (2000) have identified membrane-proximal residues in  $\beta_2$  that are required for cytohesin-1 binding. Mutation of these residues inhibits  $\alpha_L\beta_2$ -mediated cell adhesion, possibly by preventing cytohesin-1 binding. However, although overexpression of cytohesin-1 induces expression of an activation epitope on  $\alpha_L\beta_2$ , binding of soluble ligand is unaffected. Unfortunately, whether

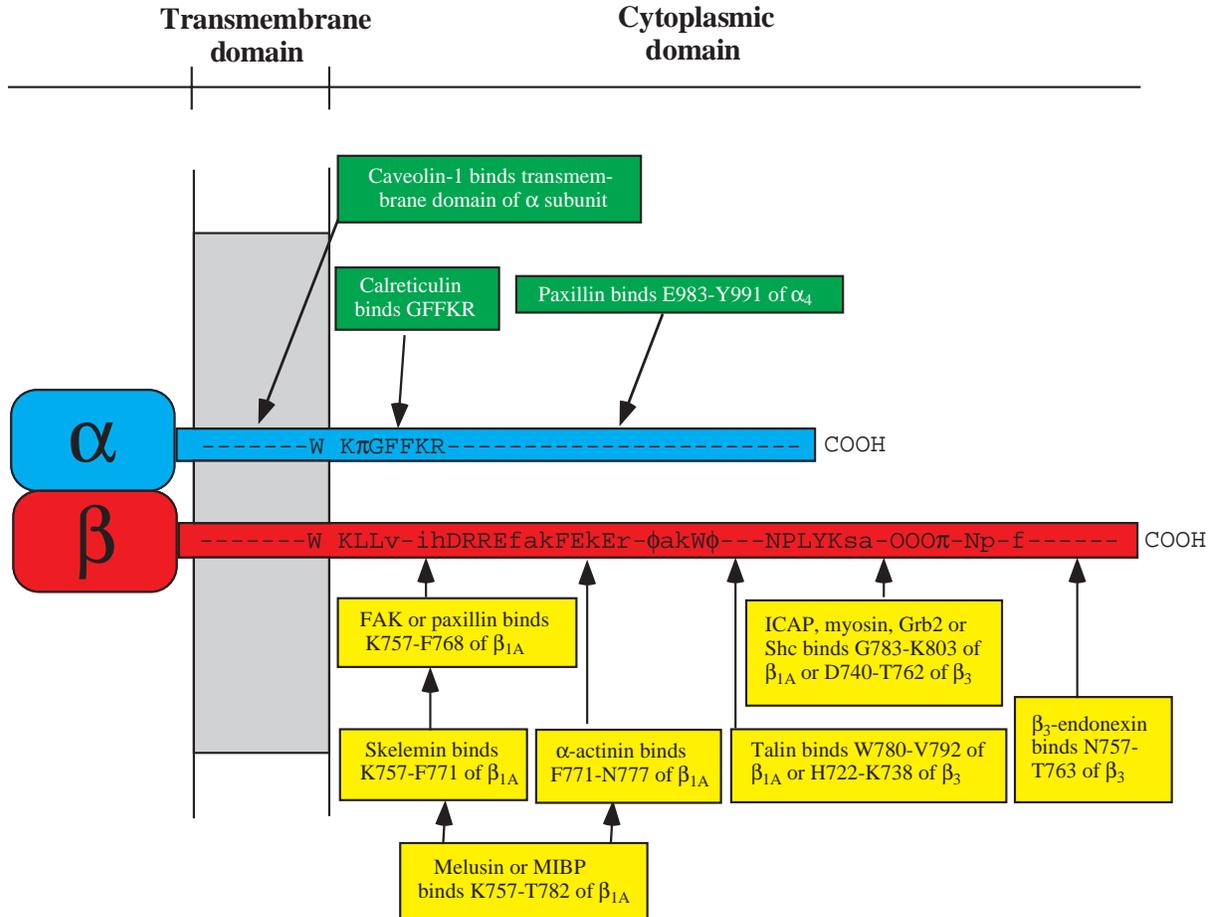
cytohesin-1 could induce this epitope on the mutated integrin was not tested. Geiger et al. (2000) did show that ARF-GEF activity was required for the effects on cell adhesion and spreading, but not for induction of the activation epitope, suggesting that a major role for cytohesin lies in regulation of cell shape, which may in turn affect the adhesive properties of the cell. Some controversy remains as to the localization of cytohesins within the cell (i.e. whether they reside in the cytoplasm, the plasma membrane or Golgi membranes). This probably reflects differences in cell type and cytohesin isoforms present, along with a signal-dependent regulation of cytohesin localization (Lee and Pohajdak, 2000; Korthauer et al., 2000; Venkateswarlu et al., 1999). The PH domain of cytohesins is capable of binding phosphatidylinositol phosphate, and this might regulate cytohesin localization and GAP activity, and thereby explain the effect of phosphatidylinositol phosphate levels on  $\beta_2$ -integrin-mediated adhesion (Hmama et al., 1999).

The actin-binding proteins and enzymes discussed above probably play additional roles as adaptor proteins (Calderwood et al., 2000), but three previously characterized adaptor proteins, paxillin, SHC and GRB2, also bind to peptides corresponding to integrin  $\beta$  tails (Schaller et al., 1995; Law et al., 1996). Paxillin also binds strongly to the  $\alpha_4$  tail (Liu et al., 1999) and is discussed in detail below. Binding of GRB2 and SHC required phosphorylation of the  $\beta_3$  tail peptide, a process dependent on platelet aggregation (Law et al., 1996). Further experiments will be necessary to determine whether  $\beta_3$  associates with GRB2 and SHC *in vivo*.

Several other proteins that have no clear enzymatic activity have been reported to bind  $\beta$  tails (Table 1). Most of these have been identified in yeast two-hybrid screens. The first  $\beta$ -tail-binding protein identified in this manner was  $\beta_3$ -endonexin.  $\beta_3$ -endonexin binds specifically to  $\beta_3$ , but not  $\beta_1$  or  $\beta_2$ , tails through both membrane proximal and distal motifs (Shattil et al., 1995; Eigenthaler et al., 1997). When expressed in CHO cells,  $\beta_3$ -endonexin increased the ligand-binding activity of  $\alpha_{IIb}\beta_3$  (Kashiwagi et al., 1997).  $\beta_3$  mutants incapable of binding  $\beta_3$ -endonexin are insensitive to  $\beta_3$ -endonexin transfection, which suggests that binding of  $\beta_3$ -endonexin to the  $\beta_3$  tail is important for integrin regulation.  $\beta_3$ -endonexin can also bind to cyclin A and inhibit the cyclin-A-Cdk2 kinase activity (Ohtoshi et al., 2000), which raises the possibility that it is involved in integrin-mediated regulation of cell cycle progression.

Interestingly, a novel 175-residue protein, TAP20, shares 55% amino acid sequence similarity with  $\beta_3$ -endonexin over the first 110 residues and appears to bind to and regulate  $\beta_5$  integrins (Tang et al., 1999). TAP20 expression in rat capillary endothelial cells is induced by protein kinase C $\theta$  (PKC $\theta$ ), which regulates  $\alpha_V\beta_5$  mediated endothelial cell migration. TAP20 overexpression in cultured endothelial cell lines reduces  $\alpha_V\beta_5$ -mediated adhesion and increases  $\alpha_V\beta_5$ -mediated migration on vitronectin. Recombinant TAP20 binds to  $\beta_5$ , but not  $\beta_1$ ,  $\beta_3$  or  $\alpha_V$ , tails. Thus, two related proteins that bind to and regulate  $\beta_3$  or  $\beta_5$  integrins have been identified. It remains to be seen whether TAP20 regulates the affinity state of  $\beta_5$  integrins, as  $\beta_3$ -endonexin does for  $\beta_3$  integrins, although it is noteworthy that  $\beta_3$ -endonexin leads to activation of  $\beta_3$  integrins whereas TAP20 appears to downregulate  $\beta_5$  function.

The WD repeat proteins Rack1 (receptor for activated



**Fig. 1.** Binding sites on integrin  $\alpha$  and  $\beta$  subunits for integrin cytoplasmic domain binding proteins. The reported interacting sites on integrin tails for integrin-tail-binding proteins are indicated by boxes and arrows. Conserved amino acid sequences among integrin  $\alpha$  and  $\beta$  cytoplasmic domains are illustrated: uppercase letters correspond to near-invariant residues; lowercase letters correspond to residues conserved in at least three subunits; O represents conserved hydroxylated residues;  $\pi$  and  $\phi$  represent conserved apolar and polar residues, respectively; and dashes represent unconserved residues and/or gaps.

protein kinase C) and WAIT-1 (WD protein associated with integrin tails) have also been identified in yeast two-hybrid screens for  $\beta$ -tail-binding proteins (Liliental and Chang, 1998; Zhang and Hemler, 1999). Rack1 is composed of seven WD repeats, and the integrin-binding site is localized to repeats 5-7. The binding site within the integrin  $\beta_1$ ,  $\beta_2$  and  $\beta_5$  tails lies in the membrane proximal region. Interaction of full-length Rack1 with integrins requires stimulation of the cell with phorbol esters, which indicates that the Rack1-integrin interaction is regulated. The significance of the interaction between Rack-1 and integrins has not been well defined and the specificity of this interaction has been questioned because Rack1 also interacts with  $\alpha_4$  and  $\alpha_v$  tails (Zhang and Hemler, 1999). The other  $\beta$ -tail-binding WD repeat protein, WAIT-1, also binds to both  $\alpha$  and  $\beta$  tails, specifically  $\beta_7$ ,  $\alpha_4$  and  $\alpha_E$ , but not  $\beta_2$ ,  $\beta_1$  or  $\alpha_L$  (Rietzler et al., 1998). WAIT-1 can therefore bind to both tails of the  $\alpha_4\beta_7$  and  $\alpha_E\beta_7$  integrins. However, whereas  $\beta_7$  expression is localized to leukocytes, *WAIT-1* mRNA appears to be expressed in a variety of cell types, which suggests that WAIT-1 has additional functions besides binding to  $\beta_7$  integrins. Like Rack1, WAIT-1 interacts with a membrane-proximal region of the  $\beta$  subunit. No functional data

suggesting a role for their interaction with  $\beta$  tails have been provided.

Similarly, the muscle-specific proteins Melusin and MIBP (muscle-specific  $\beta_1$ -integrin-binding protein) both bind to membrane-proximal regions of the  $\beta_1$  tail. However, the functional significance of this interaction has not been addressed (Brancaccio et al., 1999; Li et al., 1999). Binding of Melusin to the  $\beta_1$  tail appears to be regulated by calcium, which is consistent with the identification of potential calcium-binding motif at its C terminus. Melusin also contains putative binding sites for SH2 and SH3 domains at its N terminus, which raises the possibility that it functions as an adaptor protein to recruit additional signaling proteins to the  $\beta$  tail.

The most recently identified integrin-binding protein, JAB1 (Jun-activation-domain-binding protein), binds to the  $\beta_2$  but not to the  $\alpha_L$  tail in a yeast two-hybrid screen and in studies using recombinant proteins (Bianchi et al., 2000). JAB1 is found both in the nucleus and in the cytoplasm, and its shuttling between the two might be related to its transcriptional co-activator activity. Bianchi et al., observed some colocalization of JAB1 with  $\alpha_L\beta_2$  integrins at the cell membrane, and following integrin engagement the nuclear

pool of JAB1 increased. However, whether direct  $\beta_2$ -JAB1 interaction is involved in integrin regulation of gene expression or other JAB1-mediated effects awaits further study.

ICAP-1 (integrin-cytoplasmic-domain-associated protein 1) binds specifically to the membrane-distal 13 residues of the  $\beta_{1A}$  tail but not other  $\beta$  tails (Chang et al., 1997; Zhang and Hemler, 1999; Fig. 1). Point mutations within the C-terminal NPXY motif or between the two NPXY motifs inhibit ICAP-1 binding to the  $\beta_{1A}$  tail. ICAP-1 is rich in serine residues, contains consensus phosphorylation sites for PKC, cAMP- or cGMP-dependent kinases and calcium/calmodulin-dependent protein kinase II (CaMKII), and is phosphorylated in response to cell adhesion to FN. ICAP-1-overexpressing COS cells exhibit increased  $\beta_1$ -mediated migration on FN and in CHO cells expressing chimeric  $\beta_1/\beta_5$  integrins migration correlates with the ICAP-1 binding ability of the chimera. In addition, point mutations within the putative ICAP-1 CaMKII-phosphorylation site that mimic phosphorylation inhibit CHO cell spreading on FN, whereas mutations that prevent phosphorylation stimulate cell spreading to levels seen in cells that express wild-type ICAP-1 in the presence of a CaMKII inhibitor (Bouvard and Block, 1998). Thus, ICAP-1 binding to  $\beta$  tails might regulate cell spreading and migration in a manner dependent on CaMKII phosphorylation of ICAP-1. Further experiments are required to determine whether CaMKII does indeed phosphorylate ICAP-1, whether this alters its binding to the  $\beta_1$  tail and whether this phosphorylation is regulated by cell adhesion.

Finally, we have recently shown that CD98 can bind to recombinant models of  $\beta_{1A}$  and  $\beta_3$ , but not  $\beta_{1D}$  or  $\beta_7$ , tails (Zent et al., 2000). CD98 is a type II transmembrane protein first discovered as a T-cell activation antigen and is involved in regulation of amino acid transport, cell fusion and integrin activation. CD98 was identified in an expression cloning screen for proteins that reverse the dominant suppression of integrin activation by isolated  $\beta_{1A}$  tails (Fenczik et al., 1997). The binding of CD98 to different  $\beta$  tails correlates with its ability to reverse the suppression, which suggests that CD98-integrin binding is important for regulation of integrin activation (Zent et al., 2000). Antibody crosslinking of CD98 within the cell membrane stimulates  $\beta_1$ -integrin-dependent cell adhesion of small lung cancer cells, and, in combination with anti-CD3 antibodies, antibodies to CD98 cause proliferation of peripheral blood T lymphocytes (Fenczik et al., 1997; Warren et al., 2000). This co-stimulatory activity is inhibited in the presence of an anti- $\beta_1$ -integrin antibody. The ongoing characterization of regions within CD98 responsible for integrin  $\beta$  tail binding should facilitate investigation of which other CD98-mediated functions require  $\beta$  tail binding.

## INTEGRIN $\alpha$ CYTOPLASMIC DOMAIN BINDING PROTEINS

In contrast to  $\beta$  subunits, different  $\alpha$  subunit cytoplasmic domains share little sequence similarity, except for the membrane proximal KXGFFKR sequence (Fig. 1); this suggests that each tail plays a unique role in integrin function. However, each  $\alpha$  subunit is highly conserved among different species, which indicates that the  $\alpha$  cytoplasmic domains are important for integrin functions (Hynes, 1992; Sastry and

Horwitz, 1993). Indeed, different  $\alpha$  cytoplasmic domains differentially regulate integrin-mediated biological responses. A classical example of this is the  $\alpha_4$  integrins.  $\alpha_4$  integrins regulate cell migration, cytoskeletal organization and gene expression differently from other integrin  $\alpha$  subunits.  $\alpha_4$  integrins increase cell migration and oppose cell spreading and focal adhesion formation (Chan et al., 1992; Hemler et al., 1992; Kassner et al., 1995). These unusual biological properties depend on the  $\alpha_4$  cytoplasmic domain. Indeed, when joined to other integrin  $\alpha$  subunits, the  $\alpha_4$  tail markedly enhances cell migration and opposes cell spreading and focal adhesion formation (Kassner et al., 1995; Liu et al., 1999).

Parise and colleagues reported that R-Ras, a Ras-related GTPase, promotes migration of cells expressing integrin chimeras containing the  $\alpha_2$ , but not the  $\alpha_5$ , cytoplasmic domain (Keely et al., 1999). Furthermore,  $\alpha_2\beta_1$ -mediated migration is inhibited by the expression of excess  $\alpha_2$ - but not  $\alpha_5$ -cytoplasmic-domain-containing chimeras, which suggests that there are limiting factors that bind the  $\alpha_2$  tail (Keely et al., 1999). Weber et al. have shown that two  $\beta_2$  integrins expressed on lymphocytes,  $\alpha_M\beta_2$  (Mac-1) and  $\alpha_L\beta_2$  (LFA-1), display different kinetics of integrin activation upon chemokine stimulation. This difference appears to reside within the cytoplasmic domains of  $\alpha_M$  and  $\alpha_L$ , since exchange of the cytoplasmic tail conferred the  $\alpha$  tail-specific integrin activation (Weber et al., 1999). Therefore,  $\alpha_M$  and  $\alpha_L$  tails transduce distinct pathways for integrin activation possibly through interaction with different cellular components.

Sastry et al. reported that integrin-mediated cell cycle withdrawal and onset of terminal differentiation are controlled differently by the  $\alpha_5$  and  $\alpha_{6A}$  cytoplasmic domains (Sastry et al., 1999). However, both of the  $\alpha$  tails did not appear to initiate these signals but instead to regulate  $\beta_1$  signaling (Sastry et al., 1999). In another study, Shaw et al. reported that the  $\alpha_{6A}$  tail induced integrin-dependent paxillin phosphorylation more effectively than did the  $\alpha_{6B}$  tail (Shaw et al., 1995). These data suggest that each  $\alpha$  cytoplasmic tail uniquely regulates integrin functions either by directly initiating signaling events, by modulating  $\beta$  subunit signaling or by regulating  $\beta$  tail ligand binding (e.g. the  $\alpha_4$  tail partially inhibited filamin binding to the  $\beta_{1A}$  tail; Liu et al., 1999). Extensive efforts have focused on identifying cellular proteins that can directly associate with  $\alpha$  cytoplasmic domains. However, thus far, most of the key  $\alpha$  tail partners remain elusive.

Kieffer et al. have reported that F-actin binds directly to the  $\alpha_2$  cytoplasmic domain and removal of five amino acid residues from the C terminus of the tail disrupt the binding; this suggests that this region is responsible for F-actin binding (Kieffer et al., 1995). This F-actin- $\alpha_2$  association might play a role in the focal adhesion localization of  $\alpha_2$  integrins and the enhanced collagen gel contraction by the  $\alpha_2$  tail (Chan et al., 1992; Kassner et al., 1995). However, the molecular mechanism and effect of this interaction on  $\alpha_2$ -integrin-mediated biological properties have not been reported.

Calreticulin, a luminal endoplasmic reticulum calcium-binding protein directly interacts with the KXGFFKR motif, the highly conserved membrane-proximal sequence of  $\alpha$  cytoplasmic domains (Fig. 1; Rojiani et al., 1991). Calreticulin can directly bind to the synthetic KLGFFKR peptide, co-precipitates with different  $\alpha$  integrins and co-localizes with integrins (Leung-Hagesteijn et al., 1994; Coppolino et al.,

1995). Calreticulin-deficient cells have a severe defect in integrin-mediated cell adhesion; however, this defect can be rescued by expression of calreticulin. Furthermore, transient elevation of intracellular calcium concentration initiated by integrin-mediated adhesion is also absent in calreticulin-deficient cells (Coppolino et al., 1997). Thus, the  $\alpha$ -tail-calreticulin interaction might modulate integrin-mediated cell adhesion and signal transduction, although the mechanism by which calreticulin gains access to the cytoplasm is unclear.

CIB (calcium- and integrin-binding protein) is another calcium-binding protein that specifically binds to  $\alpha_{IIb}$ , but not  $\alpha_V$ ,  $\alpha_2$ ,  $\alpha_5$ ,  $\beta_1$  or  $\beta_3$ , tails in the yeast two-hybrid system (Naik et al., 1997). CIB also interacts with intact  $\alpha_{IIb}\beta_3$  integrin in an enzyme-linked immunosorbent assay and can be coimmunoprecipitated with intact  $\alpha_{IIb}\beta_3$  upon  $Mn^{2+}$  activation (Shock et al., 1999; Vallar et al., 1999). Thus, it is suggested that CIB is a candidate for a regulator of integrin  $\alpha_{IIb}\beta_3$  and might be involved in  $\alpha_{IIb}\beta_3$  post-receptor-occupancy events (Nail et al., 1997; Vallar et al., 1999).

Giancotti's group has reported that caveolin-1, a transmembrane adaptor, can interact with some integrins through the transmembrane domain of the  $\alpha$  subunit (Wary et al., 1998). They report that the association of caveolin-1- $\alpha$  subunit can physically and functionally link integrins to the tyrosine kinase, Fyn (or Yes), recruit the adaptor protein Shc and subsequently Grb2 and Sos and thereby regulate Ras-ERK signaling and cell cycle progression (Wary et al., 1998).

DRAL/FHL2, a LIM-only protein, has recently been reported to bind  $\alpha_{3A}$ ,  $\alpha_{3B}$  and  $\alpha_{7A}$ , as well as several  $\beta$  integrin cytoplasmic domains (Wixler et al., 2000). The amino acid residues C-terminal of the conserved GFFKR sequence among  $\alpha$  subunits are crucial for DRAL/FHL2 binding. DRAL/FHL2 is also localized to focal adhesion complexes; thus, it is suggested that DRAL/FHL2 is involved in integrin-mediated signal transduction (Wixler et al., 2000).

We have recently reported that paxillin, an intracellular adaptor protein, binds directly and tightly to the  $\alpha_4$  tail but not other  $\alpha$  tails (Liu et al., 1999). Direct association between paxillin and the  $\alpha_4$  tail was also confirmed by immunoprecipitation with intact  $\alpha_4$  or  $\alpha_{IIb}\alpha_4$  chimeric integrins. Binding of paxillin to the  $\alpha_4$  tail markedly enhanced the rates of  $\alpha_{IIb}\beta_3$ -dependent tyrosine phosphorylation of FAK and cell migration. It also reduced cell spreading, focal adhesion and stress fiber formation. We have identified a nine-residue (E983-Y991) region conserved among the  $\alpha_4$  cytoplasmic domains that is sufficient for paxillin binding (Liu and Ginsberg, 2000). A point mutation within this region (Y991A) reversed the  $\alpha_4$ -tail-specific effects (Liu et al., 1999; Liu and Ginsberg, 2000). Furthermore,  $\alpha_4\beta_1$ -dependent adhesion to VCAM-1 led to spreading of paxillin-null cells and reconstitution of paxillin inhibited spreading (Liu et al., 1999). Paxillin directly interacts with several intracellular signaling and adaptor molecules (Turner, 1998) and most paxillin-interacting proteins, such as FAK, Src, PTP-PEST, vinculin, Crk, p95PKL as well as PIX and PAK (Turner, 1998; Turner et al., 1999), have been implicated in regulation of cell migration, cytoskeletal organization and gene expression. Thus, the direct association of paxillin with the  $\alpha_4$  tail might facilitate the rapid recruitment and activation of these signaling molecules and therefore account for some of the unusual biological properties of  $\alpha_4$  integrins.

## CONCLUSIONS AND FUTURE DIRECTIONS

The list of reported integrin cytoplasmic domain binding proteins is relatively long and still expanding. Most of the interactions have been identified in vitro. This raises two major questions: which of these proteins interact with integrin cytoplasmic domains in vivo and are these interactions important for integrin functions? Addressing these concerns will be a major challenge in future studies. In evaluating these associations, several considerations apply. (1) Do mutations that prevent the interactions affect integrin-dependent functions? (2) Does absence of the integrin-binding protein affect integrin-dependent functions? (3) Does the protein associate with endogenous integrins when both proteins are present at physiological levels? (4) Is the protein in physical proximity to integrins in intact cells? (5) Ultimately the significance of the association should be validated in vivo; thus, what, if any, are the phenotypes of organisms bearing mutations in binding proteins that disrupt its interactions with integrins and are these phenotypes related to integrin functions?

The large number of integrin cytoplasmic domain binding partners suggests that cellular regulation of the interactions might be important. To date, little is known about post-translational modifications, such as phosphorylation or proteolytic cleavage of integrin tails and their binding partners and changes in their subcellular localization are likely to play roles in regulating integrin-dependent biological responses.

This work was supported in part by grants from the National Institutes of Health (to M.H.G.) and a Scientist Development Grant from American Heart Association (to S.L.). D.A.C. is the recipient of a fellowship from the Susan G. Komer Breast Cancer Foundation.

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