

## Review

# Integrin-actin interactions

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**Abstract.** The integrin family of extracellular matrix receptors regulates many aspects of cell life, in particular cell adhesion and migration. These two processes depend on organization of the actin cytoskeleton into adhesive and protrusive organelles in response to extracellular signals. Integrins are important switch points for the spatio-temporal control of actin-based motility in higher eu-

karyotes. Ligands of integrin cytoplasmic tails are central elements of signalling pathways involving small GTPases as well as protein and lipid kinases in the regulation of F-actin crosslinking, actin treadmilling and de novo nucleation of actin filaments. We present an overview of common pathways and discuss recent evidence for their differential use by individual integrin receptors.

**Key words.** Integrin; actin; motility; adhesion.

## Introduction

To maintain the integrity of multicellular organisms, cell shape and motile behaviour must be tightly controlled. To this end, higher eukaryotes have developed mechanisms that regulate cell adhesion and motility in response to extracellular signals. The analysis of these mechanisms is central to the understanding of many biologically and clinically important processes, such as the creation of new tissues and organs during embryogenesis, the coordinated movement of keratinocytes and fibroblasts during the closure of skin wounds and the extravasation of immune cells during inflammation. Over the last 10 years, enormous progress has been made towards understanding the molecular machinery that cells use to change their shape and move [1]. The combined use of genetic, biochemical and biophysical approaches has identified molecules and mechanisms which appear to be common to almost all animal cells. Basic building blocks of cell protrusions show remarkable evolutionary conser-

vation, in particular the actin cytoskeleton and key actin binding proteins such as the actin-nucleating Arp2/3 complex, the formins and their respective activators. Biochemical and biophysical models have been developed which can account quantitatively for many aspects of cell migration. Simultaneously, the Rho family of small molecular weight GTPases have emerged as pivotal control elements of protrusive and retractive cell movements. Motile cell behaviour is influenced by a complex interplay of signals induced by chemical messengers such as growth factors, by cell-matrix and cell-cell interactions, and by cell-autonomous regulation.

The integrin family of cell surface receptors plays a central role in the transduction of cell-matrix adhesion signals. Integrin signalling contributes not only to cell adhesion and migration, but also regulates cell proliferation, survival and differentiation. The actin cytoskeleton is one of the most important targets of integrin-mediated signalling. Many of the molecules that transmit signals from integrins to the actin cytoskeleton have been identified; we are now faced with the challenge of explaining how their manifold interactions with each other, with integrins, with effectors of the actin cytoskeleton and with

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other signalling pathways work together to achieve the astounding specificity of integrin-mediated signalling. This review focuses on common mechanisms of signal transduction from integrin cytoplasmic tails to the actin cytoskeleton and discusses recent evidence for differential use of these signalling pathways by different classes of integrin receptors.

Given the high tissue and cell type specificity of integrin signalling and its far-reaching consequences for cell fate, it is important to emphasize that the following description of integrin-actin interactions and regulatory mechanisms cannot claim to be universally valid. Much of the available data was obtained from experiments using fibroblastoid cells cultured on rigid two-dimensional (2D) matrices. Few of the derived model pathways have been thoroughly validated in vitro using other cell types and experimental approaches, or in vivo through gene deletions and modifications. The role of integrins in actin-based motility may therefore be somewhat misrepresented. Anchorage-independent growth and motility are increasingly perceived as phenomena that occur not only in transformed cells but also in various normal cell types. For example, T-lymphocytes do not require integrins for migration through three-dimensional (3D) collagen lattices [2]. To avoid confusion, in this review we will mainly focus on data obtained from cell types that display well-characterized anchorage-dependent growth.

## Integrins

Integrins are a family of heterodimeric receptors composed of non-covalently linked class I transmembrane  $\alpha$  and  $\beta$  subunits. Members of the integrin family have been identified in many diverse organisms from *Drosophila melanogaster* and *Caenorhabditis elegans* to sponges and corals [3–5]. Both vertebrate and invertebrate integrins show conserved structural and functional features. Through the globular head of their extracellular domains,

integrins bind components of the extracellular matrix (ECM). The short cytoplasmic tail domains of  $\alpha$  and  $\beta$  subunits have no catalytic function. Rather, they transduce signals by binding to a variety of effector proteins that may be either directly or indirectly associated with the actin cytoskeleton. Integrins and their cytoplasmic binding partners are organized into large, highly dynamic multiprotein complexes termed matrix adhesions.

In man, 18  $\alpha$ -integrin and 8  $\beta$ -integrin subunits have been described which can associate in a heterodimeric fashion to form at least 24 different receptors (table 1; [6–8]). A simplified classification system based on specificity for ECM ligands yields three classes of receptor: RGD receptors that bind to ECM components containing the Arg-Gly-Asp motif (fibronectin, vitronectin), laminin receptors and collagen receptors. Apart from ECM components, some integrins such as the  $\beta_2$  subgroup mediate cell-cell adhesion by binding to counter receptors on other cells. Many integrins also bind to soluble proteolytic fragments of vascular basement membranes such as endostatin [9], and a number of pathogens make use of integrins as receptors for cell entry [10].

Integrins display allosteric regulation in that binding of both extracellular, and intracellular ligands can trigger a transition between a low-affinity conformation (characterized by close association of the cytoplasmic tails and a bent extracellular domain) and a high-affinity conformation (dissociated tails, erect extracellular domain) [7, 11, 12]. The mechanisms underlying these conformational changes have become clearer in the past few years through high-resolution structural analysis of integrin heterodimers in complex with ligand fragments [13–15]. Integrin subunits undergo extensive posttranslational modification that affects their function. The regulation of integrin-ligand binding by phosphorylation, alternative splicing and proteolytic cleavage of integrin cytoplasmic tails is discussed below. Glycosylation of the extracellular domains of  $\alpha$  and  $\beta$  subunits is also likely to regulate function [16].

Table 1. The integrin receptor family in man.

$\beta_1$			$\beta_3$			$\beta_4$		
$\beta_1$			$\beta_7$	$\beta_2$		$\beta_3$	$\beta_{5,6,8}$	$\beta_4$
RGD	Laminin	Collagen	RGD	cell-cell	cell-cell	RGD	RGD	Laminin
$\alpha_5\beta_1$								
$\alpha_8\beta_1$		$\alpha_1\beta_1$			$\alpha_D\beta_2$			
	$\alpha_3\beta_1$						$\alpha_V\beta_5$	
$\alpha_V\beta_1$		$\alpha_2\beta_1$			$\alpha_L\beta_2$	$\alpha_V\beta_3$		
	$\alpha_6\beta_1$		$\alpha_4\beta_7$	$\alpha_E\beta_7$			$\alpha_V\beta_6$	$\alpha_6\beta_4$
$\alpha_4\beta_1$		$\alpha_{10}\beta_1$			$\alpha_M\beta_2$	$\alpha_{IIb}\beta_3$		
	$\alpha_7\beta_1$						$\alpha_V\beta_8$	
$\alpha_9\beta_1$		$\alpha_{11}\beta_1$			$\alpha_X\beta_2$			

The grouping is based on the probable evolutionary relationship of the  $\beta$  subunits and the main ligands of individual receptors.

### Biological functions of integrins

The most basic function of integrins, as that of other adhesion receptors, is to provide a mechanically strong connection between cells and the ECM. This function is particularly evident where integrins mediate attachment to basement membranes. For example, loss-of-function alleles of the *C. elegans*  $\beta$ -integrin subunit  $\beta$ pat-3, which localizes to the basement membrane connecting the body wall muscles to the cuticle, leads to a detachment of muscles from the cuticle following the first contraction [17]. Beyond cell-ECM attachment, matrix adhesions are also involved in the regulation of matrix deposition and degradation, and they are important signalling platforms that recruit proteins regulating small GTPase activity, protein and lipid kinases and adaptor proteins.

The transduction of mitogenic signals through integrins is closely coordinated with growth factor receptor activity (reviewed in [18, 19]). Activated integrins can cause transactivation of a number of receptor tyrosine kinases such as Met [20], platelet-derived growth factor receptor [21], vascular endothelial growth factor receptor [22] and epidermal growth factor receptor [23, 24]. In some cases this involves close physical proximity of growth factor receptors and integrins [25].

Additionally, activated integrins, through their cytoplasmic ligands, can activate a number of extracellular signal-related kinases (ERKs) and mitogen-activated protein kinases (MAPKs) [26–28]. Conversely, binding of integrins to soluble ligands [29] or integrin overexpression [30] can inhibit proliferation and lead to programmed cell death through both caspase-dependent [31] and caspase-independent mechanisms [32]. Dysfunctional integrin-mediated signalling can contribute to cancer progression by promoting invasion and metastasis of neoplastic cells, and tumor angiogenesis [33–35]. Thus, integrin-mediated signalling in response to ECM adhesion acts in concert with growth factor signalling to create a specific microenvironment for cells in a tissue context, and exerts a precise control over cell fate.

### The anatomy of matrix adhesions

Matrix adhesions are highly dynamic structures that organize around activated integrin clusters [36]. Many of their protein components (table 2) are essential in higher eukaryotes or lead to severe defects in cell motility when deleted. All subtypes of matrix adhesions are areas of very close contact between the plasma membrane and the

Table 2. Ligands of  $\beta$  integrin cytoplasmic tails.

Protein	Integrin	Function/phenotype	Binding partners	Isoforms
Talin	$\beta 1, \beta 2, \beta 3$ $\alpha 1 \text{Ib}$	integrin activation/F-actin binding KO: no MA formation	FAK, vinculin F-actin PIP(4,5)2, PIPKI $\gamma$	talin-1, talin-2 (H)
Paxillin	$\beta 1, \beta 2, \beta 3$ $\alpha 4, \alpha 9$	adaptor KO: reduced migration rates and MA turnover	FAK, ILK, vinculin, $\alpha$ -parvin PKL, PAK Git, PAG LIM kinase	paxillin $\alpha, \beta, \gamma$ (AS) Leupaxin (H) Hic-5 (H)
FAK	$\beta 1, \beta 2, \beta 3$	kinase, adaptor KO: reduced migration rates and MA turnover	paxillin, talin p130Cas, Src PI3K, PLC $\gamma$ GRAF, ASAP, p190RhoGEF N-WASP	FRNK (AS) Pyk2 (RAFTK/CAK $\beta$ ) (H)
ILK	$\beta 1, \beta 2, \beta 3$	kinase, adaptor KO: delayed MA formation	paxillin PINCH, parvin ILKAP PIP3	Ilk-1, Ilk2 (AS)
$\alpha$ -actinin	$\beta 1, \beta 2, \beta 3$	F-actin binding	vinculin, zyxin, $\beta$ -parvin F-actin Erk1/2	$\alpha$ -actinin 1-4 (H)
Filamin	$\beta 1, \beta 2, \beta 7$	F-actin binding	F-actin Trio migfilin	filamin A,B,C (H)
Tensin		F-actin binding KO: reduced migration		tensin 1,2,3; c-ten (H)
Myosin-X	$\beta 1, \beta 3, \beta 5$	motor		

MA, matrix adhesions; AS, alternative splicing; H, homologue(s); KO, targeted deletion in mouse.

substrate. The number of adhesions, their morphology and molecular composition vary widely between cell types and also between subcompartments within the same cell. Tremendous progress has been made in analyzing the molecular composition, dynamics and cell type specificity of matrix adhesions.

The current nomenclature differentiates between focal complexes, focal adhesions, fibrillar adhesions and podosomes. Focal complexes are small, dot-like matrix adhesions found within spreading or migrating cells and are usually concentrated in membrane protrusions (size around 100 nm). They are dynamic structures that either turn over or mature into larger, more elongated focal adhesions (alternatively named focal contacts; size around 1  $\mu$ m) within a few minutes. Focal adhesions are structures predominantly found in resting cells or areas of cells with low motility and display much slower turnover than focal complexes. They are usually the attachment points of actin stress fibres to the cell membrane. A variant of focal adhesions is the fibrillar adhesions formed by many cell types adhering to fibronectin via integrin  $\alpha 5 \beta 1$ . They differ from focal adhesions in that they arrange extracellular fibronectin fibrils in a parallel orientation with actin stress fibres, and they do not contain some common focal complex/adhesion components such as vinculin and paxillin [37]. Podosomes are found naturally in osteoclasts or cells of hematopoietic origin such as neutrophils, and represent the only matrix adhesion type found in these cells (recently reviewed in [38]). They compare with focal complexes in both size and half-life, but are composed of a ring-like assembly of matrix adhesion components surrounding an F-actin core. Podosomes are also prominent in v-Src transformed cells [39]. Recently, a related structure has been characterized in various epithelial cell types [40]. Epithelial podosomes are described as structures that are surrounded by a rosette of hemidesmosomes, and share many features with mesenchymal podosomes.

### Regulation of the actin cytoskeleton by integrin cytoplasmic tail binding proteins

Matrix adhesions are short-lived and difficult to study as isolated organelles. Therefore, immunofluorescence and video microscopy studies have been most beneficial to our understanding of the molecular mechanisms at work in these structures. We dispose today of several hypotheses to explain how focal complexes form in response to integrin activation, and how their fate bifurcates to signal either activation of actin-based protrusion mechanisms associated with focal complex turnover, or maturation of focal complexes into focal adhesions connected to the cytoskeleton by actomyosin stress fibres. Several proteins in the focal adhesion cytoplasmic plaque are implicated in regulation of the actin cytoskeleton.

### Talin and vinculin

Talin is a 270-kDa F-actin binding protein which plays a key role in integrin activation, the initiation of matrix adhesion formation and the linkage of integrin receptors to the actin cytoskeleton (reviewed by [41, 42]). Talin, which self-associates via the rod-shaped C-terminus to form a dimer, is one of the first proteins identified as a cytoplasmic integrin ligand [43]. The globular head of talin contains a four-point-one, ezrin, radixin, moiesin (FERM) domain which binds with high affinity to the cytoplasmic tails of integrin  $\beta 1$ ,  $\beta 2$ ,  $\beta 3$  and  $\beta 5$ , but only weakly to  $\beta 7$  [44]. This interaction involves a conserved NPxY motif in  $\beta$ -integrin tails [45]. The head region also contains binding sites for focal adhesion kinase (FAK) [46], phosphatidylinositol-4,5-bisphosphate (PIP<sub>2</sub>) [47], phosphatidylinositol-4-phosphate 5-kinase type I  $\gamma$  (PIPKI $\gamma$ ) [48, 49] and for the hyaluronan receptor layilin [50]. The tail region contains an additional low-affinity binding site for  $\beta$ -integrin tails [51] as well as two actin and vinculin binding sites [52]. Binding activity of this region for F-actin as well as G-actin has been demonstrated [53].

Talin plays a central role in the first steps of focal complex formation following initial integrin engagement, and talin degradation plays a critical role in focal adhesion turnover [54]. A first demonstration of this was that microinjection of anti-talin antibodies into chicken dermal fibroblasts led to matrix adhesion disassembly [55]. Since talin-deficient mice die at E8.5–9.5 [56], much of the biological function of talin has been elucidated from cell culture experiments. Talin-1-deficient undifferentiated embryonic stem (ES) cells fail to spread on collagen or laminin; however, these cells can spread on fibronectin but are unable to assemble vinculin- or paxillin-containing focal adhesions, or stress fibres [57]. Talin knock-down in CHO cells was shown to inhibit activation of integrin  $\alpha \text{IIb} \beta 3$ ,  $\alpha \text{V} \beta 3$  and  $\alpha 5 \beta 1$  [58]. Conversely, overexpression of the talin N-terminal head leads to a threefold increase in integrin  $\alpha \text{IIb} \beta 3$  activation in CHO cells [59]. By using optical tweezers to obtain force measurements, talin was identified as the important component for maintaining a 2 pN slip bond between fibronectin and the cytoskeleton [60, 61]. It has been suggested that the mechanistic basis for talin-mediated integrin activation is through disrupting a salt bridge between the  $\alpha$  and  $\beta$  cytoplasmic tails [62, 63].

The current model of integrin activation by talin includes a positive feedback loop through increased local PIP<sub>2</sub> production, possibly mediated by the PIP kinase isoform PIPKI $\gamma$ . PIPKI $\gamma$  is recruited to matrix adhesions in a complex with talin [49]. PIP<sub>2</sub> binding by talin increases the affinity of the FERM domain for integrin cytoplasmic tails [47]. Both PIP<sub>2</sub> and talin bind to and activate vinculin, an actin binding protein, by relieving autoinhibitory binding of the vinculin head domain (V<sub>H</sub>) with

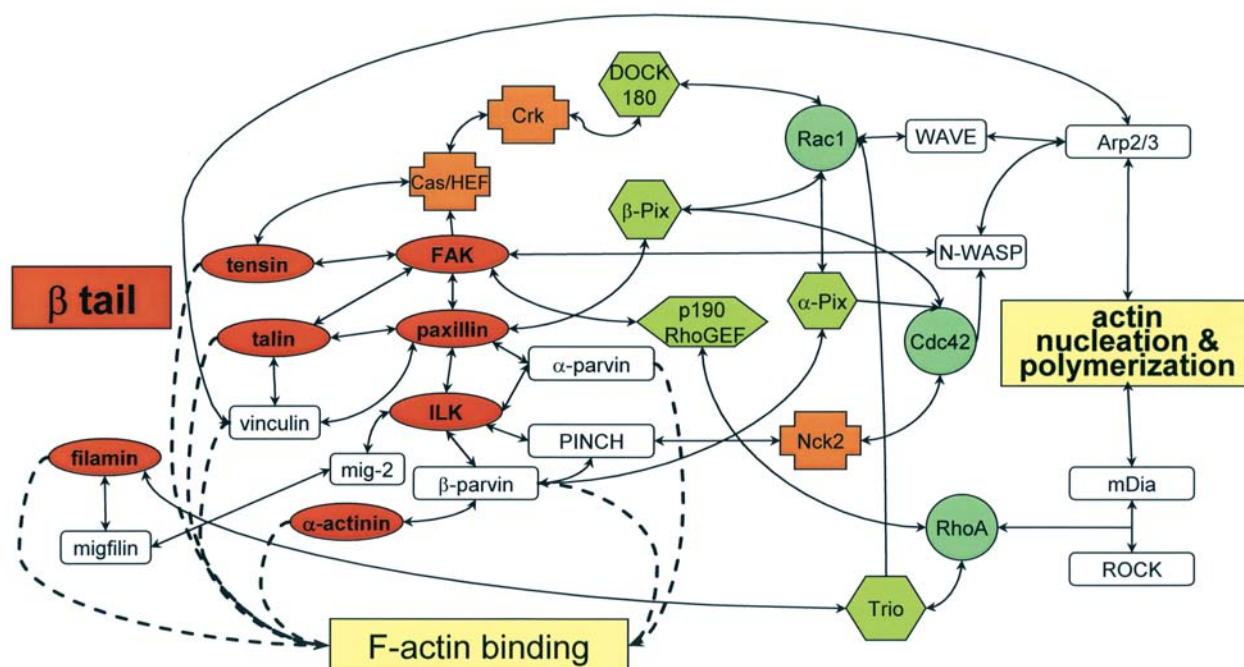


Figure 1. Schematic overview of the interaction between integrin-proximal cytoplasmic proteins. Integrin  $\beta$  cytoplasmic tail and direct ligands are depicted in red; GEFs, yellow-green; small GTPases, bright green; SH3/SH2 adaptors, orange.

the tail domain ( $V_T$ ) [64]. Vinculin may promote and stabilize initial integrin clustering mediated by talin dimer formation by providing additional F actin crosslinks to the nascent focal complex. A role for vinculin as a negative regulator of matrix adhesion turnover is suggested by reports showing that the migration velocity of vinculin  $-/-$  murine embryonic fibroblasts is two times faster than that of wild-type cells [65], and that vinculin localizes preferentially to mature focal adhesions [66]. Thus, the coordinated recruitment of talin, PIPKI $\gamma$  and vinculin to activated integrins may be considered as a minimal paradigm for how different protein classes work together to form focal complexes, link them to the cytoskeleton and promote their maturation into focal adhesions.

Talin-induced conformational changes of the  $\alpha\beta$ -tails as well as the presence of talin itself could provide an initial scaffold to assemble a more complex matrix adhesion. Interestingly, a talin homologue is also present in *Dicystostelium discoideum*, an organism which lacks integrins. In this organism talin functions in actin-based motility and adhesion-dependent cytokinesis [67, 68].

## FAK

FAK is a non-receptor protein tyrosine kinase that plays a central role in signalling through integrins and a variety of other receptors (reviewed in [69]). The kinase domain is situated in the central part of the molecule and is flanked by large non-catalytic domains. The N-terminus

contains a FERM homology domain which binds to peptides of the  $\beta 1$ -integrin cytoplasmic tail [70]. The functional relevance of direct FAK binding to integrin is unclear since the integrin-binding region of FAK is not required to target the molecule to focal adhesions [71]. Based on the observation that N-terminal deletion mutants of FAK display increased kinase activity under certain conditions [72], it has been proposed that, in analogy to other FERM domain-containing proteins, FAK is subject to autoinhibition by binding of its FERM domain to its carboxyl terminus, a hypothesis that has recently been strengthened by binding studies using recombinant fragments of FAK [73].

The carboxyl terminus of FAK contains the focal adhesion targeting (FAT) domain, a four-helix bundle bearing resemblance to similar domains found in Cas family members and vinculin [74]. The FAT contains binding sites for the integrin ligands paxillin [75] and talin [46], as well as for p190Rho-GEF [76]. The C-termini of FAK and its homologue Pyk2 are expressed as separate splice isoforms in certain tissues and have been ascribed inhibitory functions [77, 78].

Activation of FAK in response to integrin activation leads to autophosphorylation of Y397, creating a high-affinity binding site for Src family kinases (SFKs) [79, 80]. FAK and Src can in turn phosphorylate the linker protein p130 Cas, which binds via its SH3 domain to a proline-rich region in the C-terminal half of FAK [81, 82]. A second proline-rich site is bound by the Rho-GAP GRAF [83]. Other known ligands of FAK include phosphatidylinosi-



tol-3-kinase, phospholipase C-gamma and the adaptor protein Grb7 [84–86]. Additionally, FAK and SFKs can bind to and activate several proteins that regulate the actin cytoskeleton, discussed below.

Deletion of the FAK gene in mice leads to embryonic lethality before day E10.5 [87]; FAK-deficient cells show delayed spreading, increased number of focal adhesions and reduced adhesion turnover [88]. This phenotype can be reverted by transfection of the null cells with FAK, provided that it contains a functional autophosphorylation site; p130 Cas binding also contributes to the phenotype [89]. p130 Cas has emerged as a major transducer of FAK-mediated signalling affecting the regulation of focal adhesion turnover (see below).

### Integrin-linked kinase

Integrin-linked kinase (ILK) is a non-receptor serine/threonine kinase with an important adaptor protein function. The protein is composed of three N-terminal ankyrin repeats followed by a linker sequence bearing resemblance to a PH domain. The C-terminus contains the kinase domain and mediates direct ILK binding to  $\beta 1$  and  $\beta 3$  cytoplasmic tails [90, 91]. Many of the known interaction partners of ILK also bind to this region. Parvins, proteins composed of two calponin homology (CH) domains, bind to ILK as well as to paxillin,  $\alpha$ -actinin, PIX2 and F-actin. Of the three known parvin isoforms,  $\alpha$ -parvin/actopaxin and  $\beta$ -parvin/affixin have been shown to bind to ILK [92, 93]. In addition, paxillin binds directly to ILK, and the paxillin binding site of ILK is necessary but not sufficient for targeting ILK to focal adhesions [94]. The first ankyrin repeat of ILK binds Pinch-1 (particularly interesting new Cys-His rich protein) and its homologue Pinch-2 [95–97]. Both Pinch isoforms contain five LIM domains; the first of these mediates binding to ILK [95, 98] and the fourth to the SH2/SH3 adaptor protein Nck2 [99]. ILKAP, a serine/threonine phosphatase, also binds to the N-terminus of ILK [100].

ILK-dependent phosphorylation is debated as a regulatory mechanism for PKB/Akt and GSK3 $\beta$  function [101]. Matrix adhesion and cytoskeletal proteins phosphorylated by ILK include ILK itself [102],  $\beta$ -parvin [93] and  $\beta$ -integrin cytoplasmic tails [90, 91] (reviewed in [103]). Cooperativity between components of multiprotein complexes is a salient feature of ILK-mediated regulation of the actin cytoskeleton. It is known that ILK-PINCH-parvin complex formation protects the individual components from proteosomal degradation, and is essential for the localization of ILK, PINCH and parvin to matrix adhesions [96, 104]. A study addressing the kinetics of ILK-PINCH-parvin recruitment to matrix adhesions has shown that  $\beta$ -parvin and ILK are recruited to early membrane protrusions in CHO cells spreading on fibronectin,

as well as the leading edge of lamellipodia and along stress fibres [93]. Additionally, Yamaji and co-workers recently reported that  $\beta$ -parvin binds to  $\alpha$ -actinin, which localizes similarly to the leading edge as well as to matrix adhesions and stress fibres [105]. This interaction depends on ILK-dependent  $\beta$ -parvin phosphorylation. Quantitative studies on focal adhesion turnover in cells deficient for components of the ILK-PINCH-parvin complex are required to further elucidate how each individual component contributes to the properties of the complex.

Knockout studies have revealed decisive roles for ILK and PINCH in matrix adhesion formation and turnover, and in actin organization. Deletion of the *ilk* gene in mice leads to peri-implantation lethality, and ILK-deficient fibroblasts show severely impaired adhesion to fibronectin, vitronectin and laminin [106]. The formation of paxillin/vinculin-positive matrix adhesions and of stress fibres is extremely delayed, leading to impaired spreading. This phenotype can be compensated by expression of a mutant of ILK lacking kinase activity. Conditional ablation of ILK in chondrocytes results in reduced adhesion to collagen I and fibronectin and in fewer, more peripherally localized matrix adhesions [107, 108]. Likewise, PINCH-deficient fibroblasts show marked adhesion and migration spreading defects [F. Stanchi and R. F., unpublished].

### Paxillin

Paxillin is a modular adaptor protein with important functions in matrix adhesion assembly, turnover and signalling. It is an evolutionarily conserved protein with isoforms present in *D. melanogaster* [109] and *C. elegans* [110]. Paxillin contains five N-terminal LD repeats of 13 amino acids each and 4 C-terminal LIM domains that serve as sites for protein-protein interactions. There are three splice isoforms in mammals of which only paxillin  $\alpha$  shows broad expression [111]. Paxillin coimmunoprecipitates with  $\beta 1$  integrin and can bind synthetic peptides mimicking  $\beta 1$  cytoplasmic tails [70, 112], but it binds the  $\alpha 4$  cytoplasmic tail with much higher affinity [113]. Paxillin's non-integrin matrix adhesion binding partners all appear to bind through a consensus paxillin binding sequence to one or several LD repeats. Two F-actin binding proteins bind to paxillin, vinculin to LD1, LD2 and LD4 [114], and  $\alpha$ -parvin to LD1 and LD4 [115]. Paxillin also binds to the integrin-binding kinases FAK, via LD2 and LD4 [115], and ILK, via LD1 [94], and with the p21-activated kinase isoform PAK3 [116]. Other interactors include the Arf-GAP Glt1 [117] and the modular protein paxillin-kinase linker (PKL) [118]. Both of these proteins link paxillin to the Rac1/Cdc42-specific GEF  $\beta$ -PIX/Cool-1. Additionally, Foletta and co-workers recently showed that paxillin coimmunoprecipitates with LIM kinase 1, a regulator of ADF/cofilin [119].

Paxillin can be phosphorylated on four N-terminal tyrosines [120], and there is genetic evidence that the responsible kinases may be FAK [121] and Src family kinases [122]. Tyrosine phosphorylation creates high-affinity binding sites for the SH2 domains of the adaptor protein Crk and for Src [70].

Deletion of the paxillin gene in mice leads to death at E9.5 [123]. The protein appears to be one of the first to be recruited to nascent focal complexes, and its incorporation into  $\alpha\text{v}\beta 3$ -containing focal complexes appears to occur simultaneously with talin [66]. Laukaitis and co-workers have reported that paxillin recruitment is detectable in focal complexes before integrin  $\alpha 5\beta 1$  [124]. It is not clear, though, how paxillin is recruited into nascent focal complexes, although a C-terminal focal adhesion targeting sequence appears to be required [114]. The function or binding partners of this sequence, and of all the paxillin LIM domains, are thus far unidentified.

The complex of FAK, Cas and Src with paxillin is emerging as a molecular timer that regulates focal complex turnover. FAK $^{-/-}$  and paxillin $^{-/-}$  cells display a similar phenotype of reduced migration velocity and slow turnover of matrix adhesions [88, 123]. A systematic study has recently addressed matrix adhesion turnover in mouse embryonic fibroblasts (MEFs) null for Fak, Cas and Src [125]. While paxillin localization to focal adhesions does not require FAK, activated Y397-phosphorylated FAK and tyrosine-phosphorylated paxillin localize to dynamic matrix adhesions and are both required for high turnover rates. In the absence of either paxillin, FAK, Src or Cas, matrix adhesion turnover rates are reduced more than tenfold. Expression of constitutively active Rac or dominant-negative Rho in FAK $^{-/-}$  MEFs does not rescue this defect, arguing against a decisive role of Rho GTPases in the regulation of matrix adhesion turnover via this pathway. A possible mechanism may involve the recruitment of the protease calpain 2 by a Src/FAK/p42ERK complex [126, 127]. Calpain 2 cleaves several matrix adhesion components, including FAK, paxillin, tensin and talin, and calpain-2 knockdown in MEFs results in increased protrusive activity coupled to decreased protrusion persistence [128].

### $\alpha$ -Actinin

$\alpha$ -Actinins are proteins originally discovered in skeletal muscle extracts based on their ability to bind and crosslink F-actin. In mammals there are four isoforms encoded by separate genes. The non-muscle  $\alpha$ -actinin-1 binds to cytoplasmic tails of  $\beta 1$ ,  $\beta 2$  and  $\beta 3$  integrins [129–131].  $\alpha$ -Actinin is a modular protein composed of an N-terminal actin-binding domain and a C-terminal EF hand. The interaction between  $\alpha$ -actinin and actin is negatively regulated in vitro by FAK-mediated tyrosine phos-

phorylation on Y12 in the  $\alpha$ -actinin actin binding domain [132]. The protein homodimerizes in an antiparallel fashion, allowing for its F-actin crosslinking capacity.  $\alpha$ -Actinin has a considerable number of additional binding partners (reviewed in [133]), including the actin-binding proteins vinculin [134] and zyxin [135] as well as the p85 subunit of phosphatidylinositol-3-kinase (PI3K) [136]. Recently,  $\alpha$ -actinin-1 has also been shown to bind to  $\beta$ -parvin [105].  $\alpha$ -Actinin mouse knockouts have so far not been reported. 3T3 cells overexpressing  $\alpha$ -actinin demonstrate decreased locomotion; conversely, locomotion is increased upon reduction of  $\alpha$ -actinin expression by antisense RNA [137]. Chromophore-assisted laser inactivation of  $\alpha$ -actinin-GFP fusion protein has demonstrated that  $\alpha$ -actinin links actin stress fibres to focal adhesions [138].

### Filamin

Filamins are a small family of large (280 kDa) F-actin binding and crosslinking proteins (reviewed in [139]). The non-muscle filamins A and B also bind to  $\beta$ -integrin cytoplasmic tails. The interaction is strong with  $\beta 7$  and weaker with  $\beta 1A$  [44]. The actin-binding domain is located in the N-terminal region, while the remainder of the molecule comprises 24 immunoglobulin (Ig)-like repeats, separated by two hinge regions. These domains mediate protein-protein interactions with other binding partners, and the most C-terminal repeat mediates filamin homo- and heterodimerization [140]. Apart from integrins, filamins associate with other receptors and with many molecules affecting the actin cytoskeleton. These include the small GTPases RhoA, Rac1 and Cdc42 [141], Trio, a GEF for Rac1 and RhoA [142], Rho-associated kinase [143] and a LIM domain-containing protein, Migfilin, which in turn can bind Mig-2 that associates both with ILK and the  $\beta 1$ -integrin cytoplasmic tail [144]. Filamin A expression can be induced by applying mechanical force to cultured cells [145]. Like  $\alpha$ -actinin, filamin-integrin binding appears to negatively regulate cell migration, since CHO cells expressing integrin  $\beta 7$  tail fused to the  $\beta 3$  extracellular domain showed decreased migration when compared to constructs that were less competent to bind filamin [146]. In man, loss-of-function mutations of the X-linked filamin A gene causes periventricular heterotopia, a hereditary disease characterized by defective neuron migration into the cerebral cortex [147]. The disease leads to embryonic lethality in most male patients. Mouse knockouts of filamin genes have so far not been reported.

### Tensin

Tensin is a 220-kDa F-actin binding protein (reviewed in [148]). F-actin binding occurs through three actin binding

domains. Tensin binds to integrins  $\beta 3$ ,  $\beta 5$  and  $\beta 7$  and more weakly to  $\beta 1$  cytoplasmic tails [149]. A C-terminal SH2 domain can mediate binding to FAK, p130 Cas and PI3K [150, 151]. Tensin-null mice are viable but display skeletal muscle and kidney defects [152, 153]. Tensin-deficient fibroblasts display reduced transwell migration rates, while overexpression of GFP-tensin has the opposite effect [154].

### Other proteins

Src family kinases have recently been shown to bind directly to  $\beta$ -integrin cytoplasmic tails, adding another dimension to their important role in integrin-mediated signalling to the actin cytoskeleton [155]. Clustering of integrin  $\beta 3$  results in activation of c-Src by stimulating Src trans autophosphorylation.

RACK1 is an adaptor protein with high similarity to a small G protein  $\beta$  subunit originally described as an effector of various protein kinase C (PKC) isoforms (reviewed in [156]). RACK1 is reported to bind several  $\beta$  cytoplasmic tails [157]. It also binds to and inhibits Src family kinases [158]. Knockdown studies show that loss of RACK1 leads to impaired cell migration, perhaps through a failure to recruit PKC $\epsilon$  to focal adhesions [157]. Similar results have been obtained with a RACK1 mutant deficient in Src binding [159].

The unconventional myosin myosin-X has been described recently as an integrin ligand [160]. Myosin-X binds to cytoplasmic tails of integrin  $\beta 1$ ,  $\beta 3$  and  $\beta 5$  through a C-terminal FERM homology domain. It has been implicated in active transport of integrins to filopodial tips.

### The machinery of actin-based motility

The molecular machinery of actin-based motility is highly conserved throughout evolution, and arose before the branching of metazoans from fungi. Actin and many key actin-binding proteins are already present in *Saccharomyces cerevisiae*, where they function in organizing the cortical cytoskeleton and actin cables. A good deal of our current knowledge about the molecules and mechanisms of actin-based cell motility stems from research using unicellular organisms such as *Dictyostelium discoideum* and *Acanthamoeba castellanii*, which lack integrins and matrix adhesions. (*D. discoideum* does have adhesion receptors, which are members of the nine-transmembrane superfamily [161, 162]).

Cell motility requires generation of directed mechanical forces and control of cell body adhesion and tension. Actin filaments are the major building blocks of the membrane protrusions, and the system of matrix adhesions and connecting stress fibres mediate motility. Actin can be present in concentrations close to one millimolar

in these structures [163]. In membrane protrusions such as the lamellipodia and filopodia of migrating cells, a considerable forward thrust of some nN/ $\mu\text{m}^2$  [164, 165] is generated by directional treadmilling of a dense, branched actin network against the cell membrane. The key molecule in the generation of this network is the seven-polypeptide Arp2/3 complex [166]. Arp2/3 has the unique activity of inducing autocatalytic branching of actin filaments [167, 168]. A limited set of additional actin-binding proteins has been shown to be sufficient to reconstitute this aspect of actin-based motility in vitro, namely ADF/cofilin, profilin and a barbed-end capping protein such as CapG or gelsolin [169]. Arp2/3 and capping factors act in an antagonistic fashion by balancing barbed end production [168, 170], while ADF/cofilin and profilin can act in synergy with barbed end capping proteins to enhance actin treadmilling velocity [171].

Actin nucleation in the cytoplasm is tightly controlled. The isolated Arp2/3 complex has no endogenous actin-nucleating activity and must be activated by complex formation with activator proteins. The most extensively characterized Arp2/3 activator family are the WASp/Scar proteins, which all bind and activate Arp2/3 through a common C-terminal verprofilin-cofilin-acidic (VCA) domain [172, 173]. The family falls into two subfamilies with N-WASp and its haematopoietic isoform WASp on the one side and the three WAVE/Scar proteins 1, 2 and 3 on the other. All are modular proteins containing binding sites in their N-terminal domains for a variety of cofactors. Purified N-WASp and WASp are constitutively inactive due to intramolecular binding of the regulatory N-terminus to the catalytic VCA-domain [174, 175]. This autoinhibition is relieved through binding of both PIP<sub>2</sub> and the Rho family GTPase Cdc42 [174, 175]. In contrast, WAVE proteins are constitutively active and bind neither Rho family GTPases nor PIP<sub>2</sub> directly. Instead, WAVEs assemble into multimolecular complexes together with Nck-associated protein 1 (Nap1) [176], the Rac1-binding protein Sra-1/PIR121 and Abl-interacting protein 1 (Abi1) [177]. The localization of these complexes is regulated by the Rho family GTPase Rac1 [178]. Both N-WASp and the WAVE/Scar isoforms appear to have overlapping but non-identical roles in cell motility, and it is an accepted simplification to describe N-WASp as the main Arp2/3 activator in filopodia [179], while WAVE2 is the predominant Arp2/3 activator in lamellipodia [180]. The central in vivo role of these two family members is underscored by the finding that the disruption of either gene is embryonic lethal in mice [180, 181].

Stiffness of the cell body and retraction of the cell rear are regulated through a mechanism relying not on directed polymerization but on directed or isometric force generation by actomyosin cables (stress fibres) connected to matrix adhesions. The accumulation of these structures as well as the activation of myosin activity is under control



of the RhoA GTPase. RhoA controls stress fibre formation via its effectors Rho-associated kinase (ROCK) and diaphanous-related formins [182].

### Integrin effectors meet actin effectors

Integrin signalling has been linked to direct recruitment or activation of various activators of the Arp2/3 complex, thus complementing or perhaps even bypassing GTPase-mediated control mechanisms. Tyrosine phosphorylation of WASp and N-WASp at the residues Y291 and Y256, respectively, increases their potential to activate Arp2/3-mediated actin nucleation [183, 184]. These tyrosine residues lie within the GBD domain of WASp and N-WASp and can be phosphorylated by various Src family kinases. Thus, SFK recruitment by FAK or other members of the matrix adhesion protein complex may provide a docking site for WASp or N-WASp within matrix adhesions and account for the described requirement of WASp/N-WASp for podosome formation in macrophages and v-Src transformed cells, respectively [185, 186]. Additionally, direct interaction between N-WASp and FAK and tyrosine phosphorylation of N-WASp by FAK at Y256 has been reported recently [187]. An alternative mode for targeting N-WASp to matrix adhesions involves recruitment of N-WASp through the adaptor proteins Nck-2 and PINCH [188]. Cortactin is another example for a Src substrate that directly binds and activates the Arp2/3 complex [189]. Cortactin is considered as one of the characteristic protein components of podosomes [38].

Arp2/3 can also be localized to matrix adhesions via binding to vinculin [190]. Although Arp2/3 is not activated upon binding vinculin, vinculin binding may serve to concentrate the complex at the membrane. Individual Arp2/3 subunits may also be regulated through integrin-binding proteins. The regulatory p41-Arc subunit of Arp2/3 was recently reported to be phosphorylated by PAK1, a paxillin ligand, and this phosphorylation is important for promoting cell motility [191].

### Regulation of integrin-actin signalling by small molecular weight GTPases

The regulation of Rho family GTPases by matrix adhesion components is certainly an important axis of signalling. The global control of the actin cytoskeleton by the combined action of Rho family GTPases is universal in metazoans [192]. It is subject to control by specialized effector proteins. The transition between GDP-bound inactive Rho and GTP-bound active Rho, and subsequent GTP hydrolysis is controlled by guanine nucleotide exchange factors (GEFs) and GTPase-activating proteins

(GAPs), respectively. GEF/GAP activation by phosphorylation and GEF/GAP recruitment to matrix adhesions are important modes of integrin receptor signalling to the actin cytoskeleton.

Pioneering studies have demonstrated a global role for integrin-mediated adhesion in the regulation of small GTPase activity. Within the first 10 min following substrate adhesion, fibroblast spreading on fibronectin is accompanied by an initial increase in Rac and Cdc42 activity, as assayed by an increase in PAK kinase activity [193]. This is followed by an increase in Rho GTP loading [194].  $\beta$ -Integrin tails play an important role in Rac activation since mutation of the  $\beta$ 1 tail leads to impaired Rac signalling [195], and clustering of  $\beta$  tails in human primary fibroblasts is both necessary and sufficient for Rac activation [196].

So far Eps8, which forms part of a RacGEF complex with Abi-1 and Sos-1 [197], is the only GEF identified to target to matrix adhesions via a direct interaction with the  $\beta$ 1A cytoplasmic tail [149]. Instead, many GEFs are localized to matrix adhesions indirectly via binding to other integrin cytoplasmic ligands, perhaps reflecting the evolution of integrin control over this ancient system. Only some of the involved integrin-GEF-GTPase pathways have so far been studied in detail. Rac/Cdc42 activation appears to occur through several parallel pathways. Activated FAK can recruit the non-conventional Rac-GEF DOCK180, the SH2/SH3 adaptor protein Crk and p130Cas [198]. Paxillin can recruit the Rac/Cdc42-GEF  $\beta$ -PIX/Cool-1 in complex with PAK and PKL [199] or with Git1 [117]. Coimmunoprecipitation and GST pull-down assays have revealed that  $\beta$ -parvin binds to the related GEF  $\alpha$ -PIX/Cool-2 [200]. Trio, which possesses GEF activity both for Rac and RhoA, binds to and colocalizes with filamin [142]. The preponderance of GEFs found localized to matrix adhesions suggests that trafficking of actin cytoskeleton-regulating GTPases to matrix adhesions results in activation of these GTPases at sites of membrane-ECM attachment.

Integrin engagement also leads to translocation of inactive Rac and Cdc42 from the cytoplasm to the membrane and their activation by dissociating them from RhoGDI [201]. The authors have recently shown that Rac1 is targeted preferentially to lipid rafts and that integrin-mediated adhesion prevents the rapid internalization of lipid rafts that occurs when cells are in suspension [202].

The transient RhoA suppression associated with cell spreading has been ascribed to p190RhoGAP, which is activated upon early integrin signalling in a Src-dependent manner [203]. The current hypothesis to explain how this occurs states that p190RhoGAP is liberated from a complex with p120RasGAP upon recruitment of p120RasGAP to paxillin phosphorylated by FAK/Src on Y31/Y118 [204]. How RhoA activation is mediated is less clear. FAK binds to p190RhoGEF; overexpression of

FAK leads to increased p190RhoGEF phosphorylation and increased RhoA activity [76]. Rho targeting to the leading edge of cells is, like Rac, mediated by lipid rafts. Palazzo and co-workers have shown that lipid rafts are localized to the leading edge by an unknown mechanism that requires FAK, and that these lipid rafts are important for local coupling of Rho to mDia and that integrins localize such lipid rafts [205].

### Regulation of integrin-actin signalling by lipid kinases

Polyphosphoinositides (PPIs) have emerged as important regulators of focal adhesion and actin dynamics, particularly the PPIs PI(4,5)P<sub>2</sub>, synthesized by phosphatidylinositol phosphate (PIP) kinases, and PI(3,4,5)P<sub>3</sub>, synthesized by PI-3 kinases. As more becomes known about the biochemical roles of these PPIs, it appears as though PI(4,5)P<sub>2</sub> plays a role in mediating both cell adhesion and migration, whereas PI(3,4,5)P<sub>3</sub> plays a greater role in mediating cell migration.

Expression of constitutively active PI-3 kinase in cells leads to an increased level of activated Rac and increased lamellipodia and ruffle formation [206]. Conversely, treatment of several cell types with the PI-3 kinase inhibitor wortmannin results in decreased amounts of activated Rac and Cdc42 [207–209]. Although Rac and PI-3 kinase directly interact [210] and activated Rac and Cdc42 increase PI-3 kinase activity [211], PI(3,4,5)P<sub>3</sub> does not appear to influence these GTPases directly. Rather, several GEFs contain PH domains that bind PI(3,4,5)P<sub>3</sub> (reviewed in [212]). Binding of PI(3,4,5)P<sub>3</sub> to the PH domain is thought to induce a conformational change in these GEFs, thereby relieving autoinhibitory mechanisms.

The migration of chemotactic cells up a shallow chemical gradient is regulated by establishing a relatively steep intracellular gradient of PI(3,4,5)P<sub>3</sub>, by localizing PI-3 kinase at the leading edge and the phosphatase PTEN towards the rear of the cell [213]. Activation of PI-3 kinase under chemotactic conditions is dependent upon heterotrimeric G proteins which sense extracellular chemical gradients (reviewed in [214]). Integrin-mediated migration, on the other hand, depends on PI-3 kinase present within the matrix adhesion. PI-3 kinase binds via its 85-kDa regulatory subunit to a sequence including phosphotyrosine Y397 within FAK [84]. Mutation of D395 greatly diminishes PI-3 kinase binding to FAK, resulting in an inhibition of cell migration to an even greater extent than is achieved by treating cells with wortmannin or another PI-3 kinase inhibitor, LY294002 [215]. The strength of adhesion to the substrate was unaffected by these drugs, demonstrating that PI(3,4,5)P<sub>3</sub> is not important for anchoring cells to the substratum.

Recently another product of PI-3 kinase, PI(3,4)P<sub>2</sub>, was shown to bind lamellipodin, an Ena/VASP ligand present

at the edges of lamellipodia [216]. Treatment of cells with PDGF, which causes an increase in PI(3,4)P<sub>2</sub> synthesis [217], is sufficient to target a lamellipodin PH domain green fluorescent protein (GFP) fusion protein to the tips of lamellipodia, implicating PI(3,4)P<sub>2</sub> binding in correct targeting of lamellipodin to lamellipodial tips, and therefore Ena/VASP proteins to the leading edge of migrating cells.

Although the effects of PI(3,4,5)P<sub>3</sub> on influencing the architecture of matrix adhesions appear limited to  $\alpha$ -actinin [218], there are several lines of evidence implicating PI(4,5)P<sub>2</sub> in mediating protein-protein interactions between several matrix adhesion binding proteins. PI(4,5)P<sub>2</sub> binding has been demonstrated for talin [48], filamin [219], vinculin and  $\alpha$ -actinin [220]. PI(4,5)P<sub>2</sub> binding to talin causes the localization of talin to matrix adhesions, presumably by increasing the affinity between talin and the cytoplasmic tail of  $\beta$ 1 integrin [48]. Vinculin binding to PI(4,5)P<sub>2</sub> induces a conformational change in vinculin, unmasking domains responsible for binding talin and actin [64, 221]. However, actin binding is inhibited by PI(4,5)P<sub>2</sub>, suggesting that there are other regulatory steps downstream of PI(4,5)P<sub>2</sub> binding [222]. Filamin is inhibited in the presence of PI(4,5)P<sub>2</sub> [219], while  $\alpha$ -actinin actin cross-linking activity is either enhanced [223] or reduced [224] in the presence of PI(4,5)P<sub>2</sub>; the reason for the discrepancy is not known.

It is well established that adhesion of cells to ECM causes a transient increase in PI(4,5)P<sub>2</sub> concentration, and that at least some of this PI(4,5)P<sub>2</sub> is localized at matrix adhesions [225]. Local production of PI(4,5)P<sub>2</sub> at sites of matrix adhesions likely arises from the  $\gamma$  isoform of type I phosphatidylinositol phosphate kinase (PIPKI $\gamma$ ). PIPKI $\gamma$  targets to focal adhesions by binding to the FERM domain of talin [48, 49]. Tyrosine phosphorylation of the talin-binding sequence of PIPKI $\gamma$  by Src increases the affinity of PIPKI $\gamma$  for talin, in a FAK-dependent manner [49, 226]. It was also shown that the activity of PIPKI $\gamma$  increases upon tyrosine phosphorylation, but this may also arise from controlling the phosphorylation status of a serine residue (S214) which regulates the catalytic activity of PIPKI $\alpha$  [227, 228]. Furthermore, the PIPKI $\gamma$  binding site on talin overlaps with the  $\beta$ 1-integrin binding site, and binding of PIPKI $\gamma$  and  $\beta$ 1 integrin are mutually exclusive [226, 229]. Therefore, PIPKI $\gamma$  may also serve to regulate the turnover of matrix adhesions by blocking the interaction between talin and  $\beta$ 1 integrin.

On the actin side, WASP family proteins, cofilin, profilin, gelsolin and CapZ have all been shown to be regulated by PI(4,5)P<sub>2</sub> (see [230] and references therein). The control of PI(4,5)P<sub>2</sub> synthesis for this purpose may be achieved by Rho family GTPases. PIPKI activity is present in Rac1 immunoprecipitates, and a ternary complex between Rac1, RhoGDI and PIPKI has been identified [231, 232]. Furthermore, activation of PIPKI activity in vivo is en-

hanced by expression of RhoA, Rac1 and Cdc42 [233]; the RhoA-dependent activation is mediated by Rho-kinase [234, 235], but it is not known whether Rac1 and Cdc42 can activate PIPKI directly, or whether other proteins are responsible. In all cases, it is likely that activation of PIPKI occurs once it has been targeted to the plasma membrane [236]. In this way, PI(4,5)P<sub>2</sub> availability for actin binding proteins may be spatio-temporally controlled by Rho family GTPases.

### Differential integrin signalling to the cytoskeleton

Distinct *in vivo* roles for different integrin receptors have been amply demonstrated by gene ablation studies (reviewed in [237]). Considering that many of the proteins discussed above can bind to several different  $\beta$  cytoplasmic tails, how does signalling downstream of  $\alpha 3\beta 1$  differ from  $\alpha 5\beta 1$ , or  $\alpha V\beta 3$ ? First, signals may be directly transmitted by the extracellular and transmembrane domains of integrin receptors. Second, although most known cytoplasmic integrin ligands bind to  $\beta$  tails, there are examples of differential signalling through  $\alpha$  tail ligands. Third, some protein ligands are highly specific for only one  $\beta$  isoform or splice variant. Fourth, integrin  $\beta$  tails are posttranslationally modified by phosphorylation and proteolytic cleavage that affect ligand binding, and many  $\beta$  tail binding proteins have homologues or splice isoforms expressed in a cell type-specific fashion.

Table 1 proposes a classification of the human integrin receptors by the probable evolutionary relationship of the  $\beta$  chains [3, 5]. This subdivision yields three groups comprising  $\beta 1$ ,  $\beta 2$  and  $\beta 7$ ;  $\beta 3$ ,  $\beta 5$ ,  $\beta 6$  and  $\beta 8$ ; and  $\beta 4$ . The  $\beta 1$  group alone comprises two thirds of all integrin heterodimers. It comes as no surprise that  $\beta 1$ -integrin gene disruption shows the most severe phenotype of all  $\beta$  chains, leading to peri-implantation lethality [238, 239]. The  $\beta 2$  and  $\beta 7$  subgroups are hematopoietic cell-specific. Four  $\beta 1$  integrins ( $\alpha 1\beta 1$ ,  $\alpha 2\beta 1$ ,  $\alpha 10\beta 1$  and  $\alpha 11\beta 1$ ) form the collagen receptor subfamily [240], present only in chordates. The members of the  $\beta 3$  subfamily are all RGD receptors formed by association with  $\alpha V$ , with the notable exception of  $\alpha IIb\beta 3$ , the major integrin receptor in platelets.  $\beta 8$  appears to have diverged early from the rest of the group since the cytoplasmic domain shows low homology with  $\beta 3$ ,  $\beta 5$  and  $\beta 6$ , and it lacks the otherwise conserved NPxY motifs.  $\beta 3$ -deficient mice are viable and fertile and show normal retinal neovascularization, but they display bleeding disorders related to  $\alpha IIb\beta 3$  and increased tumor angiogenesis [241, 242]. In contrast, antibodies against  $\alpha V\beta 3$  integrin, intended to block the function of this integrin, inhibit angiogenesis [241–243]. Possible reasons for this discrepancy have been discussed [244–246].  $\beta 4$  associates exclusively with  $\alpha 6$  and defines a unique member of the integrin  $\beta$  chain family by virtue

of the size of its cytoplasmic domain (>1000 aa). It is well established that  $\alpha 6\beta 4$  is a laminin receptor which also binds to intermediate filaments and is a key component of hemidesmosomes in epithelial cells. Mechanisms of  $\beta 4$ -mediated signalling in adhesion and motility are currently under investigation (reviewed in [247]) but so far do not appear to involve the integrin-binding ligands discussed above. We will therefore limit the following discussion to the  $\beta 1$  and  $\beta 3$  groups.

Differential regulation of cell adhesion and small GTPase activity by fibronectin receptors has been demonstrated by ectopic expression of  $\beta 1$  or  $\beta 3$  in  $\beta 1$ -deficient fibroblasts [248]. While Rac1 GTP loading was equally high in both cell lines, RhoA signalling was markedly different. Both cell lines showed decreased RhoA activity immediately following binding to fibronectin, but only cells expressing  $\beta 1$  integrin subsequently displayed increased RhoA GTP loading. Cells expressing only  $\beta 3$  integrin showed high RhoA GTP loading in suspension but no subsequent increase upon binding to fibronectin. Tyrosine phosphorylation of p190RhoGAP was comparable in both lines, arguing against differential regulation of RhoA activity through phosphorylation of 190RhoGAP by FAK and/or Src. In a similar study, Miao and co-authors investigated the effects of  $\beta 1$  and  $\beta 3$  overexpression in CHO cells, which do not express endogenous  $\beta 3$  integrin [249]. Rac activity was higher in  $\beta 1$ -expressing cells while only  $\beta 3$ -expressing cells showed an increase in RhoA GTP loading during late spreading. Both groups also used mutation constructs in which the extracellular domain of  $\beta 1$  was fused to the  $\beta 3$  cytoplasmic tail or the extracellular domain of  $\beta 1$  was mutated to acquire  $\beta 3$  specificity, respectively. Strikingly, cells expressing these constructs gave results similar to  $\beta 1$  or  $\beta 3$  expression, respectively. These results demonstrate that the extracellular domain of  $\beta$  subunits can play a decisive role in integrin signalling specificity, possibly through integrin-integrin or integrin-RTK crosstalk.

Paxillin binding to  $\alpha 4$  integrin is arguably the best-characterized example for differential signalling through an  $\alpha$ -integrin cytoplasmic tail.  $\alpha 4\beta 1$  differs from other RGD-binding integrin receptors in that it enhances the velocity and persistence of cell migration when expressed endogenously or ectopically [250].  $\alpha 4$  binds tightly to paxillin [113]; this interaction is disrupted by PKA-mediated phosphorylation of  $\alpha 4$  on S988 [251, 252]. In CHO cells transfected with wild-type  $\alpha 4$ , phospho- $\alpha 4$  localizes to the leading edge, while the non-phosphorylated, paxillin-bound  $\alpha 4$  localizes to the lateral and trailing edges. Expression of a S998A mutant or of an  $\alpha 4$ -paxillin chimera results in impaired migration.

Both  $\beta 1$ - and  $\beta 3$ -integrin genes can undergo alternative splicing to generate different C-termini adjacent to the membrane-proximal part of the cytoplasmic domain, termed  $\beta 1A$ -D and  $\beta 3A$ -C. The ubiquitous  $\beta 1A$  and the

muscle-specific  $\beta 1D$  variants share high homology and localize to focal adhesions when expressed in non-muscle cells [253, 254]. In contrast,  $\beta 1B$  and  $\beta 1C$ , which are human-specific, are deficient in binding to a number of ligands, including talin [44]. Consistent with a possible inhibitory role of some of these splice variants in malignant cell progression, Moro and co-workers have recently detected that expression of  $\beta 1C$  is posttranscriptionally downregulated in a prostate carcinoma cell line, when compared to a non-cancerous control cell line [255].

Tyrosine phosphorylation of  $\beta$  tails by SFKs appears to be relevant for a number of physiological processes. Inducible tyrosine phosphorylation of the  $\beta 3$  cytoplasmic tail on Y747 has been implicated in regulating the avidity of  $\alpha v \beta 3$  [256, 257]. Tyrosine phosphorylation of the  $\beta 3$  tail is also important for normal platelet function in vivo as demonstrated by the expression of  $\beta 3$  tails in which this residue was mutated [258] as well as the observation that binding of the adaptor proteins Grb2 and Shc to  $\beta 3$  cytoplasmic tails is dependent on tyrosine phosphorylation of the cytoplasmic tail [259]. The recently reported recruitment of Arp2/3 into matrix adhesions is also dependent on phosphorylation of  $\beta 3$  on Y747 [260].

Serine/threonine phosphorylation of  $\beta 2$ -integrin cytoplasmic tails correlates with increased association with cytoskeletal cell fractions [261]. PKC $\delta$  and PKC $\beta$  were shown to be the main kinases in leukocyte extracts that phosphorylate  $\beta 2$  peptides [262].

Proteolytic cleavage of integrin cytoplasmic tails may provide another mechanism to regulate ligand binding to integrin cytoplasmic tails. Calpain cleavage was first demonstrated for the  $\beta 3$  cytoplasmic domain in vivo [263]; subsequently, calpain cleavage sites were identified in several other  $\beta$  tails [264]. Several components of focal adhesions including talin, FAK, paxillin, vinculin and  $\alpha$ -actinin are also cleaved by calpain in vivo [54, 128, 265]; therefore protease cleavage likely plays an important role in regulating matrix adhesion turnover. Differential cleavage of  $\beta$  tails could also be implicated in regulating integrin signalling.

Finally, isoforms of  $\beta$ -integrin tail binding proteins (summarized in table 2) are likely to be involved in differential regulation of integrin-actin signalling by cell type-specific expression and unique binding properties. For example, the FAK isoform Pyk2 (alternatively named CAK $\beta$ , RAFTK or CADTK), which is highly expressed in brain and hematopoietic cells [266], appears to have additional or even antagonistic functions in comparison to FAK. A recent study [267] reported positive and negative correlation between Pyk2 and FAK expression, respectively, with cell migration rates in glioblastoma cell lines. Cells that do not express FAK but express Pyk2 also express the paxillin isoform leupaxin. It has been suggested that Pyk2 and leupaxin may form a hematopoietic cell-specific signalling complex [268]. An impressive il-

lustration of the tissue specificity of integrin-mediated signalling in mammals is given by the phenotype of mice with a targeted deletion of the  $\alpha 8$  subunit. 50% of these  $\alpha 8^{-/-}$  mice are born without kidneys, but without major defects in other inner organs [269].

## Conclusions and perspectives

We dispose today of a solid base to qualitatively explain many aspects of integrin-mediated signalling to the actin cytoskeleton. However, our current framework of model pathways is still very preliminary. While new downstream effectors and crosstalk partners of integrin signalling are constantly being discovered, there is still scarce data on the affinities and especially on the topology of binding of the identified  $\beta$  tail ligands to  $\beta$  tails and among each other. Many of these interactions are likely to be mutually exclusive, while others may be cooperative. To understand which subset(s) of integrin-proximal protein complexes actually mediate integrin-actin signalling in a specific cell type, careful biochemical and structural analyses will have to be combined with experiments on cells or animals expressing mutant forms of matrix adhesion proteins. As in the study of actin-based motility, reconstituted model systems would certainly be of great benefit to gain a quantitative understanding of the molecular mechanisms of integrin-actin signalling. The 'matrix adhesion on a chip' is not reality yet, but biophysical methods are increasingly being used to analyze and manipulate matrix adhesions in living cells. Finally, much uncharted territory remains to be explored beyond matrix adhesions. Integrins are localized to many actin-containing structures such as the lamellipodial leading edge, filopodial tips and the actomyosin contractile ring. Their contribution to the proper function of these structures, let alone the implicated signalling pathways, is unknown.

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