### Focal adhesion kinase: structure and signalling



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#### **SUMMARY**

Studies on the attachment and spreading of cells in culture have provided valuable insights into the mechanisms by which cells transmit information from the outside to the inside of the cell. This brief review considers recent information on the role of focal adhesion-associated protein tyrosine kinases in integrin-regulated cell signalling.

Key words: integrin, paxillin, focal adhesion kinase

#### INTRODUCTION

Cell adhesion and motility play a central role in a diverse array of cellular events, including cellular differentiation, development and cancer (Albelda and Buck, 1990; Hynes, 1991). An experimental entry into the study of the molecular events triggering cell adhesion comes from the analysis of cell attachment an vereading, a process that is driven by the for tion of molecular structures called focal adhesions. Focal adhesions (also referred to as focal contacts) are points of close apposition between the cell membrane and the extracellular matrix (ECM), which is comprised of proteins ch as collagen, fibronectin or vitronectin (Burridge et al., 1988; Luna and Hitt, 1992). The structural organization of focal adhesions is complex. Integrins, heterodimeric transmembrane receptors comprised of φ and β subunits (A slda and Buck, 1990; Hynes, 1992) by ge cell membrane, the extracellular ligand-binding domains engaging the ECM on the outside of the cell and the short cytoplasmic tails interacting with the cytoplasmic cytoskeleton. Thus, interior physically link the ECM to the cytoplasmic actin cytoskeletal network and may function to transmit signals from the extra-<u>cellular</u> matrix to the cytoplasm (Turner and Burridge, Schwartz, 1992). The actual linkage between integrin cytoplasmic tails and actin bundles or stress fibers appears mediated by an intricate structure comprised of focal adhesion-associated proteins. Considerable evidence suggests that at least two of these focal adhesion-associated proteins, talin and α-actinin, interact directly with the cytoplasmic domain of β integrin subunits (Tapley et al., 1989a; Otey et al., 1990). The talin and oxactinin have also been shown to bind to the actin-binding pein vinculin, supporting the idea that protein-protein interactions are responsible in large part for the ordered structure of the focal adhesion (Burridge et al., 1988).

Several lines of evidence point to the importance of tyrosine phosphorylation in the formation and organization of focal

adhesions. In cells transformed by the tyrosine kinase oncogene pp60src, two focal adhesion-associated proteins, tensin and axillin, are highly phosphorylated on tyrosine (Turner et al., 1990; Davis et al., 1991). In addition, in Srctransformed cells, other focal adhesion proteins, talin, vinculin and  $\beta_{l}$  integrin subunits have been reported to be tyrosine phos prylated, albeit at low stoichiometry (Sefton and Hunter, 1981; DeClue and Martin, 1987; Tapley et al., 1989b). Thus the dramatic alterations in cytoskeletal structure induced by Src transformation may be due in part to the tyrosine phosphorylation of focal adhesion-associated proteins. In no al cells, immunofluorescence analysis with antibodies to phosphotyrosine reveals prominent staining of focal adhe indicating the presence of significant levels of tyrosine phosphorylated proteins (Maher et al., 1985; Burridge et al., 1/8). The attachment and spreading of rodent fibroblasts in culture leads to the increased tyrosine phosphorylation of both paxillin and tensin (Burridge et al., 1992; Bockholt and Burridge, 1993), while treatment of cells with inhibitors of protein tyrosine kinases blocks spreading of fibroblasts in culture (Burridge et al., 1992).

Studies from our own laboratory have led to the identification of a major pp60src substrate, of  $M_r$  125,000 (pp12 which localizes to for adhesions of normal adhort chicken embryo cells (Schaller et al., 1992). The isolation and characterization of cDNA clones encoding pp.125 revealed that 125 was a novel protein tyrosine kinase, the we designated cal adhesion kinase, or pp125FAK. Clues to the function of pp125FAK come from tumerous studies showing that the tyrosine phosphorylation of pm125FAK is increased as a consequence of either the engage nt of integrins with the racellular matrix, for example the attachment and spread of embryo fibroblasts onto a fibronectin matrix (Guan et al., 1991; Burridge et al., 1992; Schaller et al., 1993) or the cross-linking of surface integrins with integrin-specific antibodies (Kornberg l., 1991, 1992). In addition, activation of fibrinogen-<u>dependent</u> platelet aggregation also induces tyrosig hospho-

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rylation of pp125<sup>FAK</sup> in vivo and an increase in pp125<sup>FAK</sup> tyrosine kin activity in vitro (Lipfert et al., 1992) hus, the increased tyrosine phosphorylation of pp125<sup>FAK</sup> appears to be closely coupled with binding and action of cell surface integrin receptors. In this brief review, we consider recent experimental data indicating that pp125<sup>FAK</sup> plays a role in regulating cellular events leading the assembly of final adhesions. In addition, we speculate on the possible role of pp125<sup>FAK</sup> in cellular signalling via pathways that modulate or control cellular gene expression.

### THE BASIC FAKS: FUNCTIONAL DOMAINS OF pp125<sup>FAK</sup>

To date, pp125<sup>FAK</sup> homologues have been identified in mouse, human a Xenopus (Hanks et al., 1992; Andre and Becker-Andre, 1993; Whitney et al., 1993; M. Hens and D. Det one, personal communication. The structure of pp125<sup>FAK</sup> in each of these species is highly conserved and is tinct from all other known protein tyrosine kinases. The catalytic domain exhibits most of the structural hallmarks of a typical tyrosine kinase, however, in the case of pn125<sup>FAK</sup> the catalytic domain is flanked by two non-catalyt domains that exhibit little sequence similarity to other proteins (or gene products) present in the existing data bases (Fig. 1). FAK is expressed in most cell lines and tissues examined to date (Hanks et al., 1992; Andre and Becker-Andre, 1993; Turner et al., 1993). In some cells the carboxyl-terminal domain of pp125FAK is expressed autonomously as a 41,000  $M_r$  protein led FRNK - <u>FAK</u>related non-kinase; Schaller et al., 1993). In avian cell and tissues, FRNK is encoded by an alternatively processed  $\overline{2.4}$  kb mRNA (Schaller et al., 1993). A similar sized mRNA has been detected in human tissues, but it remains to be determined if this mRNA encodes pa 1 FRNK. A notable feature of pa 125 FAK structure is the absert of SH2 and SH3 domains mains present in the Src family of kinases and other cytoplasmic protein tyrosine kinases, as all as many protein components of receptor-directed signalling pathways (reviewed by Pawson and kish, 1992). In most SH2-containing proteins, the SH2 dom s appear to direct protein-protein interactions, promoting stable interactions with unique phosphotyrosinecontaining peptide sequence motifs (Pawsor ad Gish, 1992;

FAK kinase (p125)
Focal Adhesion Kinase

FRNK (p41)
Fak Related Non-Kinase

Src kinases

Src kinases

(p41)

Fig. 1. A comparison of the structure of pp125<sup>FAK</sup> and the Src family kinase, pp60<sup>src</sup>. See text for detail.

Songyang et al., 1993). SH3 domains also appear to mediate protein-protein interactions, directing binding to proteins with proline-rich peptide sequence motifs (Ren et al., 1993). The lack of SH2 and SH3 domains in pp125 FAK suggests that FAK may play a role in cell signalling funct from previously characterized non-receptor protein tyrosine kinases. In additions we will discuss below, it is likely that the non-catalytic domains of pp125 FAK participate in directing the protein-protein function.

# THE 'INS AND OUTS' OF THE FOCAL ADHESION: SEQUENCES THAT TARGET po125FAK TO FOCAL ADHESIONS

Little information is available as to how focal adhesion-asso-<u>ciated</u> proteins are directed to the existing or wly formed focal adhesions. The first clues as to how pp125<sup>FAK</sup> is targeted to focal adhesions came from the analytical as series of deletion mutations within the amino- and boxylterminal non-catalytic domains (Hildebrand et al., 1993). Deletion of sequences between residues 853 and 1012 greatly diminished the translocation of retrovirally expressed FAK protein to the focal adhesions chicken embryo cells grown in culture. In contrast, delego of sequences within the amino-terminal non-catalytic domain or small deletions within a region of the C-terminal domain proximal to the kinase domain by no effect on the efficient localization of pp125FAK to focal adhesions. These data indicate that residues 853 to 1012 comprise a targeting sequence (termed the 'focal adhesion targeting' or 'FAT' sequence) necessary for the efficient localization of pol25FAK to focal adhesions (Fig. 2). Further evidence for importance of the FAT sequence comes from studies analyzing hybrid proteins comprised of unmyristylated, cytosolic pp60<sup>src</sup> fused to a polypeptide ontaining residues 853 to 22 of pp125<sup>FAK</sup>. Immunofluorescence staining of chicken bryo cells infected with a retrovirus en ling the Src-FAT fusion protein showed officient leading to the state of the state protein showed efficient localization of Src-FAT protein to focal contacts, providing additional evidence that FAT sequences direct the translocation of pp125FAK to focal adhesions.

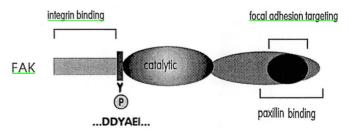


Fig. 2. Functional domains of the focal adhesion kinase, pn125<sup>FAK</sup>. Genetic and biochemical styles described in the text have do to the identification of domains within pn125<sup>FAK</sup>. Integrin binding is localized to the mino terminal described in the text have do to the identification of domains within pn125<sup>FAK</sup>. Integrin binding is localized to the mino terminal described in the text have do to the identification of domains within pn125<sup>FAK</sup>. Integrin binding is localized to the focal adhesion-associated protein, paxillin, and targeting to the focal adhesion is mediated by sequences present in the carboxylterminal domain.

# MORE THAN FAT: THE CARBOXYL-TERMINAL NON-CATALYTIC DOMAIN DIRECTS THE BINDLY OF po125<sup>FAK</sup> TO THE FOCAL ADHESION PROTEIN PAY LIN

Recent evidence indicates that within the cell there is a direct interaction between pp125FAK and the focal adhesion-associated protein paxillin numunoprecipitation of 125<sup>FAK</sup> from extracts of cells exprang wild-type pp125<sup>FA</sup> lemonstrates the efficient co-immunoprecipitation (M. Schaller, J. Hildebrand and J. Zosons, unpublished observations). The stable association of these two proteins was not observed when cells expressing FAK mutants lacking the FAT sequence or mutants lacking the C-terminal 11 residues of pp125<sup>FAK</sup> were subjected to a similar analysis. Parallel in vity experiments using glutathione S-transferase fused to FAK peptides containing sequences present in residues 687 to 1052 confirmed that paxillin could efficiently bind to sequences present in the carboxyl-terminal non-catalytic domain of pp125FAK (J. Hildebrand, M. Schaller and J. T. Parsons, unput hed observations). Furthermore, the binding to paxillin appears to be direct, since isotopically labelled GST-FAK bound to paxillin immobilized on a filter matrix (a 'sthwestern' blot). A careful analysis of a series GST from proteins containing deletions of residues within the carboxyl-torminal demains shows that against him the series of the carboxyl-torminal demains shows that against him the series of the carboxyl-torminal demains shows that against him the series of the carboxyl-torminal demains shows that against him the series of the carboxyl-torminal demains shows that against him the series of the carboxyl-torminal demains a se terminal domains shows that paxillin binding was fur onally distinct from sequences necessary for focal adhesion targeting, although sequences required for paxillin binding appear to overlap, in part, the sequences required for focal adhesion targeting (Fig. 2). These results provide evidence for a role for the carboxyl-terminal non-catalytic domain of po125FAK in both the localization of pp $125^{FAK}$  to focal adhesis as well as directing the binding of  $125^{FAK}$  to a potential cellular substrate.

### HOW DO INTEGRINS SIGNAL FAK: THE AMINO-TERMINAL NON-CATALYTIC DOMAIN DY CTS THE BINDING OF DO125FAK TO THE CYTOPLASMIC DOMAINS OF NTEGRINS

The cell adhesion-dependent activation of pp125<sup>FAK</sup> tyrosine phosphorylation suggests that integrins may rectly regulate, in some fashion, the activation of pp125<sup>FAK</sup> kinase activity. Previous experiments by Otey et a 1990) showed that the

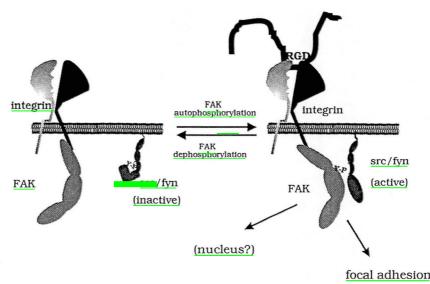
interactions of focal adhesion proteins and integrin cytoplasmic domains can be analyzed in vitro. The focal adhes -associated protein, α-actinin, binds in vitro to synthetic pept mimicking the 47 amino acid cytoplasmic domain of the β<sub>k</sub> integrins. A similar experimental approach reverse the pp125<sup>FAK</sup> also binds efficiently to peptides mimicking the complete cytoplasmic domain of  $\beta_1$  and  $\beta_3$  integrins (M. Schaller, C. Otey and J. T. Parsons, unpublis observations). Schaller, C. Otey and J. 1. Parsons, unpuony coscivations). Further, analysis of pol25<sup>FAK</sup> binding to a set of four overlapping peptides coverising the total cytoplacic down sequence of β<sub>1</sub> shows that pol25<sup>FAK</sup> interacts preferentially with a peptide sequence report native of the first 13 residues adjacent to the transmembrane domain of β<sub>2</sub> (Fig. 3). Binding of pol25<sup>FAK</sup> to peptide-containing beads to be blocked by production with excess soluble peptide and pol25<sup>FAK</sup> does pre ubation with excess soluble peptide and pp125FAK does not bind to beads containing a 'scrambled' shy peptide. To determine where in pp125 FAK the integrin peptide-binding sequences resides, i vidual domains of pp125 FAK were expressed in *Escherichia coli* and used in the vitro binding assay. Significant binding activity was observed with peptides derived from the amino-terminal non-catalytic domain, whereas no binding activity was observed with peptides derived from the carboxyl-terminal region of pp125FAK. These data argue convincingly that pol25<sup>FAK</sup> is calle of directly binding to integrin cytoplast domain sequences in vitro. Interestingly a comparison of the sequences of individual \( \beta \) cytoplasmic domains shows a a high degree of sequence cor servation within sequences corresponding to the β<sub>A</sub> pp125<sup>FAK</sup>binding of pp125<sup>FAK</sup> and integrins in vivo, whether pp125<sup>FAK</sup> interacts ith different B integrins via a conserved quence motif, and how such in actions regulate pp125FAK activity are issues under current investigation.

# WHERE'S THE PHOSPHOTYROSINE? THE MAJOR AUTOPHOSPHORYLATION SITE OF po125<sup>FAK</sup> IS TYR<sup>397</sup>, A HIGH AFFINITY BINDING SEF FOR pp60<sup>src</sup> AND p59<sup>fyn</sup>

In Src-transformed cells the tyrosine phosphorylation of pp125<sup>FAK</sup> is increased several fold, an observation that lead to its cinal identification as a Src-substrate (Kanner et al., 1990). In these cells the majority (>80%) of pp125<sup>FAK</sup> is stably associated with pp60<sup>src</sup> (Cobb et al., 1994).

	pp125FAK binding	
P1 KLLMIIH <b>D</b> RR <b>E</b> FA	+++	
P2 FAKFEKEKMNAKW	_	
NWDTGENPIYKSA	=	
AVTTVV-NPKYEGK	=	
KLLMIIH <b>D</b> RR <b>E</b> FAKFEKEKMNAKWDTGENPIYKSAVTTVV-NPKYEGK	+++	
KALIHLS <b>D</b> LR <b>E</b> YRRFEKEKLKSQWNN-DNPIFKSATTTVM-NPKFAES	NT	
KLLITIH <b>D</b> RK <b>E</b> FAKFEEERARAKWDTANNPIYKEATSTFT-NITYRGT	+++	
KLLVTIH <b>d</b> rr <b>e</b> fakfqsersraryemasnpiyrkpisthtvdftfnksyngtvd	NT	
KLLVSFH <b>D</b> RK <b>E</b> VAKFEAERSKAKWQTGTNPLYRGSTSTFK-NVTYKHREKQKVDLSTDC	NT	
RLSVEIY <b>D</b> RR <b>E</b> YSRFEKEQQQLNWKQDSNPIYKSAITTTINPRFQEADSPTL	NT	
S   S   S   S   S   S   S   S   S   S	FAKFEKEKMNAKW  KWDTGENPIYKSA  AVTTVV-NPKYEGK  KLLMIIHDRREFAKFEKEKMNAKWDTGENPIYKSAVTTVV-NPKYEGK  KALIHLSDLREYRRFEKEKLKSQWNN-DNPIFKSATTTVM-NPKFAES  KLLITIHDRKEFAKFEEERARAKWDTANNPIYKEATSTFT-NITYRGT  KLLVTIHDRREFAKFQSERSRARYEMASNPIYRKPISTHTVDFTFNKSYNGTVD  KLLVSFHDRKEVAKFEAERSKAKWQTGTNPLYRGSTSTFK-NVTYKHREKQKVDLSTDC	KLLMIIHDRREFA

Fig. 3. Comparison of the sequences of the cytoplasmic domains of  $\beta$  integrins. SP1-4 denote the sequences of four short peptides that together comprise the complete sequence of  $\beta_1$  cytoplasmic domain. (+++) denotes significant binding of pp125<sup>FAK</sup>, (–) denotes little detectable binding; NT, not tested.



**Fig. 4.** Model for the integrin-dependent activation of pp125<sup>FAK</sup> and Src family kinases. See text for discussion.

ments using retroviruses expressing mutants of Src, as well as in vitro analysis of pp60<sup>src</sup>-pp125<sup>FAK</sup> complex formation, clearly indicate that the sembly of stable FAK-Src complexes requires both the SH2 domain of po60<sup>src</sup> do the autophosphorylation site of pp125FAK. Pepy mapping exp ments, coupled with site-directed mutagenesis of potential phosphorylation sites have identified the major site of 25<sup>FAK</sup> autophosphorylation as Tyr<sup>397</sup> (Fig. 2) (Schaller et 1994). Mutation of Tyr<sup>397</sup> to Pt fficiently blocks pp60<sup>src</sup>-pp125<sup>FAK</sup> interactions it is on an in vitro. Several feat so of the Tyr<sup>397</sup> autophosphorylation site are of interest. The position of within pp125FAK distinguishes it from other receptor and recepto vrosine kinases. In most instances tyrosine ki autophosphorylation occurs at a highly conserved tyrosine within the catalytic domain (equivalent to  $Tyr^{576}$  in pp.125<sup>FAK</sup>;  $Tyr^{416}$  in pp.60<sup>src</sup>), within a kinase insert main, ich is a nonconser insert found within the catalytic domains of some receptor protein tyrosine kinases (but not in pp125FAK) or distal to the catalytic domain at sites near the C to ginus (a region found in many growth factor protein tyrosine kinases). Tyr<sup>397</sup> resides immediately amino-terminal to the catalytic domain, in relative proximity to the ATP-binding site. In addition Tyr<sup>397</sup> is embedded in the sequence DDYAEI, a sequence ry similar to the consensus of a high-affinity Src SH2-binding peptide, YEEI (Songyang et al., 1993). These observations pose the possibility that in normal cells, integrin engagement may trigger autophosphorylation of po125FAK, which may, in turn, direct the translocation and comitant activation of Src or other Src-like tyrosine kinases. Experimental support for such a model comes from the identity ation of pp125FAK-p59fyn complexes in extracts of normal adherent cultury of chicken embryo cells (Cobb et 1994).

## SPECULATIONS, SPECULATIONS: A MODEL FOR 25FAK SIGNALLING

One important function of the integrins is to translate extracellular cues into cytoplasmic signals, a function that items.

sumably important for the biological activities of integrins. On the basis of the data summarized above we are led to speculate that integrin engagement with the extracellular matrix may result in either the direct clustering of po125FAK, allosteric changes in pp125<sup>FAK</sup> or the stimular of a regulator protein(s) the triggers pp125<sup>FAK</sup> activation. A direct consequence of such an active on step is the autophosphoryla of pp125<sup>FAK</sup> and generation of a high affinity binding site for Src and Src-family kinases. In armal cells the enzymatic activity of pp60src and pp59fyn is repressed through the action of a ve regular phosphorylation site at the C termin these kinases (Fig. 4). Phosphorylation of a highly conserved tyrosine within this region by a regulatory protein tyrosine kinase (Csk) is critical for down-regulation of catalytic activity (reviewed by Cooper and Howell, 1993). Trent models for Src regulation suggest that the tyrosine phosphorylated Gterminal sequence binds in an intramolecular interaction to own SH2 domain (Cantley et al., 1991; Cooper and Howell, 1993). The amino acid sequence flanking this C-terminal tyrosine does not resemble the consensus high affinity binding site and while a tyrosine phosphorylated C-terminal peptide can bind to the SH2 domain of po60src, it does so poorly (Songyang et al., 1993). In vitro, particles of poorly activated by incubation with a syletic phosphopeptide containing the consensus, high affinity, Src SH2-binding site sumably by binding more efficiently to the SH2 domain the regulatory C-terminal peptide (Liu et al., 1993). It is intriguing to speculate that phosphorylation of <u>Tyr<sup>397</sup></u> of pp125<sup>FAK</sup> may create a high affinity binding site for pp59<sup>fyn</sup> and that these kinases may bind to pp59<sup>FAK</sup> result g in the displacement of their C-termini from gir SH2 domains. Thus, binding to pp125FAK may be a mechanism by which pp60src and pp59fy are enzymatically activated in addition a mechan for the recruitment of these kinases to a highly localized site within the cell.

proteins

What might be the consequences the activation of pp125<sup>FAK</sup> or the translocation-dependent activation of Src or Fyn? The adhesion-dependent increase in tyrosine phosphorylation of paxillin and tensin suggests that either or by of these

focal adhesion proteins may be direct substrates for pp125FAK or the np125 FAK -Src/Fyn complex. The associon of pp125F and paxillin is interesting in this context and is consistent with the idea that pp125FAK may play a direct roll of bringing paxillin into the sine kinase complex. It is interesting to speculate that activation of both pp125FAK ad Src/Fyn may be necessary for catalyzing the for tion of focal adhesion assembly and for initiating signals that may direct the activation of other cellular signalling pathways. For example it is well established that cell adhesion and spreading can trigger the expression of cellular genes (Damsky and Werb, 1992). The association of pp125FAK with either Src or Fyn may be sufficient to activate cellular signatory pathways that in turn lead to the activation of cellular genes. What these pathways are and how they function to regulate adhesion-dependent phenomena remain to be elucidated.

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