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1. ABSTRACT

Cancer cell metastasis involves a series of changes in cell behaviour, driven by oncogenic transformation, that leads to local tissue invasion, migration through extracellular matrix, entry into the vascular or lymphatic system and colonisation of distant sites. It is well established that the Rho family GTPases Rho, Rac and Cdc42 orchestrate many of the processes required during metastasis. The Rho family GTPases regulate cellular behaviour through their interaction with downstream effector proteins. The p-21 activated kinases (PAKs), effector proteins for Rac and Cdc42, are known to be important regulators of cell migration and invasion. There are six mammalian PAKs which can be divided into two groups: group I PAKs (PAK1-3) and group II PAKs (PAK4-6). Although the two PAK groups are architecturally similar there are differences in their mode of regulation suggesting their cellular functions are likely to be different. This review will focus on the latest evidence relating to the role of PAK family kinases in the cell signalling pathways that drive cancer cell migration and invasion.

2. INTRODUCTION

2.1. Cancer cell invasion

A localised primary tumour can often be treated with radical surgery or radiotherapy, but once it has spread to other sites in the body it is almost impossible to eradicate. This facet of cancer progression highlights the need to improve knowledge regarding the mechanisms underlying metastasis with a view to identifying new therapeutic targets and prognostic tools. Cancer cell metastasis involves a series of changes in cell behaviour, driven by oncogenic transformation, that leads to local tissue invasion, migration through tissue, entry into the vascular or lymphatic system and colonisation of distant sites (Figure 1). Invasion of the surrounding stromal tissue requires the co-ordinated regulation of both actin cytoskeletal rearrangement and cell substratum adhesion turnover (1). To successfully migrate through the stromal microenvironment, cells must be able to extend processes (lamellipodia/filopodia/invadopodia), anchor those nascent protrusions to the underlying matrix (cell adhesions), generate the force required for forward movement and ultimately dissolve adhesions at the rear of the cell. It is well established that the Rho family GTPases Rho, Rac and

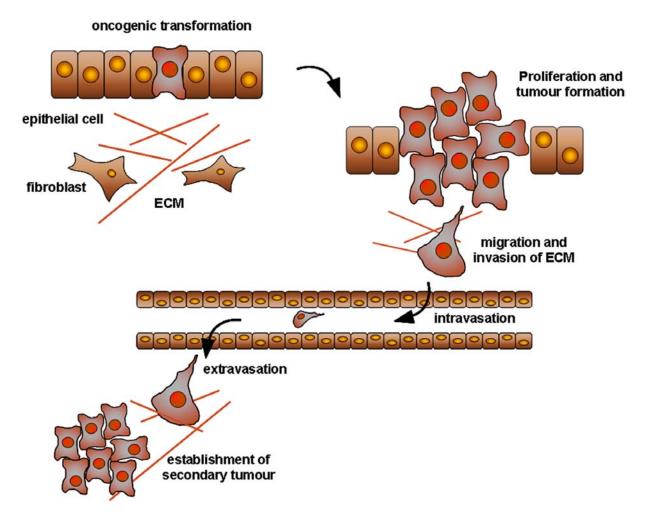


Figure 1. Progression of metastatic cancer. Schematic representation of epithelial carcinoma as a multistage process beginning with oncogenic transformation of cells, aberrant growth and proliferation to form a primary tumour. Tumour cells eventually acquire a migratory phenotype and invade their surrounding extracellular matrix (ECM) in a process possibly involving interplay with non-tumour cells such as fibroblasts. Cells metastasise, entering blood or lymphatic vessels by intravasation. At some point, metastatic cancer cells will attach and extravasate, establishing a secondary site. Non-tumour fibroblast and endothelial cells are shaded brown, and cancerous cells are depicted with red nuclei and highlighted blue.

Cdc42 orchestrate these processes (1). Rho, Rac and Cdc42 are the most studied Rho family GTPases, these proteins act as molecular switches existing in two conformational states, GDP and GTP bound. It is only in the activated GTP bound state that they interact with downstream effector molecules to elicit their cellular response. The intrinsic exchange of GDP for GTP within the Rho family is relatively slow and is accelerated by their association with guanine nucleotide exchanges factors (GEFs). Of the many effector proteins that bind to active Rac and Cdc42, the p-21 activated kinases (PAKs) are amongst the best characterised. This review will focus on the role of PAK family proteins in mediating cytoskeletal signalling events that contribute to cancer cell invasion, but will not detail PAK associated neuronal biology (recently reviewed (2)). We will address current knowledge of upstream regulation, evidence for involvement in tumour progression, contribution to cytoskeletal signalling pathways and relevance to cancer cell invasion.

2.2. PAK family kinases

p21-activated kinase 1 (PAK1) was the first PAK family member to be identified (3) as a serine threonine protein kinase activated by the small GTPases Cdc42 and Rac, followed by the closely related protein kinases, PAK2 and PAK3 (4). More recently three more family members were discovered (PAK4-6) and the six proteins are now divided into two groups (Figure 2) based upon sequence and structural homology (5). PAKs are highly conserved in evolution and have many known substrates whose phosphorylation affects numerous cellular processes, including cytoskeletal organisation, cell cycle progression, and cell survival (6, 7)as well as significant non-kinase related effects (7, 8)

2.2.1. Domain structure

Group I PAKs possess a distinctive N – terminal region that encompasses a p-21 GTPase binding domain (GBD), an overlapping autoinhibitory domain (AID) (9)

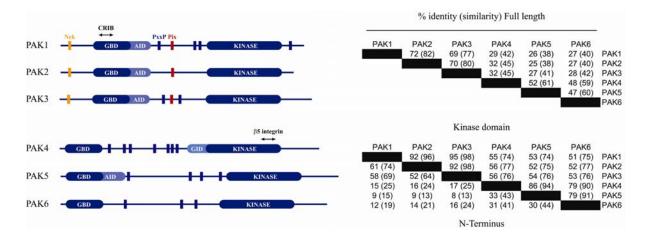


Figure 2. Domain structure of p21-activated kinases. All Pak family members share a common domain structure: an N-Terminal p21/GTPase binding domain (GBD) and a C-Terminal serine/threonine kinase domain. The GBD of Group I PAKs consists of a Cdc42/Rac interactive binding region (CRIB) and overlaps with an autoinhibitory domain (AID). PAK5 is the only member of the Group II PAKs that appear to contain an AID. All PAK proteins harbor variable numbers of core PxxP motifs, putative ligands for SH3 domains, although specific interacting partners are mostly unidentified. The N-Terminus of the Group I PAKs bind directly to the SH3 domains of Nck1/2 via a consensus binding motif (PxxPxRxxS) indicated in orange. The Group I PAKs also harbor a Pix binding site (indicated in red). Neither motif is present in any of the Group II PAKs. In addition PAK4 contains a unique GEF-H1 and Gab-1 interaction domain (GID) adjacent to the kinase domain. The kinase domain also contains a beta-5 integrin binding region. Percentage identity (similarity in parentheses) based on alignments using sequence alignment software (www.ebi.org/tools) for the full length, N-terminal and kinase domain sequences are indicated on the right.

and a C-terminal kinase domain (Figure 2). PAK3 has two alternatively spliced exons in the GBD/AID region that yield four splice variants, three of which have constitutive kinase activity (10). These splice variants have not been identified in PAK1/2. For group I PAKs the AID of one protein interacts with the kinase domain of a second. forming an autoinhibited dimer, and is important in the regulation of basal kinase activity (5, 9, 11). Active Cdc42 and Rac bind to the GBD (6, 8) releasing autoinhibition and enhancing kinase activity. Early reports suggest that binding of Cdc42 to Group II PAKs does not enhance kinase activity (12-14) and it is not clear whether these family members exist in an auto-inhibited state, are monomeric, dimeric or reside as part of a larger complex of proteins in vivo. However, an inhibitory region has recently been reported in PAK5 (at a region not conserved in the other group II PAKs) and this study indicated that GTP-Cdc42 was able to stimulate the autophosphorylation of purified PAK5 (15). Moreover, recombinant PAK4 proteins lacking either the N-terminal GBD (16, 17) or the ability to interact with Cdc42 (18) appear to have elevated kinase activity suggesting the GBD may interfere with kinase function. An alternative view is that interaction with active Cdc42 may influence group II PAK localisation. In support of this proposal, expression of constitutively active Cdc42 mediates PAK4 localisation to the Golgi (18). PAK4 uniquely contains an integrin binding site within the kinase domain (19), whilst both PAK5 and PAK6 possess a NLS (nuclear localisation signal) located in a region N-terminal to the GBD (20). PAK5 also possesses mitochondrial targeting signals whilst PAK6 uniquely contains a FXXMF motif which binds directly with the androgen receptor (AR) ligand-binding domain (LBD) (21).

2.2.2. Expression and localisation

PAK1 is expressed in muscle, spleen and basal expression has been reported in several tissues, including the mammary gland (3). All three group I PAKs are highly expressed in the brain, and PAK1 and PAK2 are both highly expressed in most cells of hematopoietic origin (Table 1). PAK1 is associated with cortical actin structures in PDGF-stimulated fibroblasts, whereas PAK2 localizes to the endoplasmic reticulum (ER) in COS-7 and 293T cells (22, 23). PAK1 localises to the leading edge of motile neutrophils (24), to pinocytic/phagocytic vesicles (22, 24) and to the mitotic spindle and centrosomes (25-28), as well as to the nucleus and nuclear membrane (29-31). PAK1 has also been localised to cell: substratum adhesions (32). PAK2 is uniquely cleaved by caspases and the catalytic fragment thus generated translocates to the nucleus or to the endoplasmic reticulum, where it is essential for the induction of growth arrest (23). In neuronal cells PAK3 is found in lamellipodia and membrane ruffles (33).

Amongst Group II PAKs, PAK4 is expressed in a wide range of tissue types (12) and is considered to be ubiquitously expressed. PAK5 is predominantly expressed in the brain (13) but has also been detected in the adrenal gland, ovary and pancreas(8). PAK6 is expressed in the prostate, testis, breast, kidney, placenta and brain (7, 34, 35). Within individual cells, PAK4 has been localised to a number of different subcellular compartments. PAK4 is predominantly found in the perinuclear region, but is relocalised to Golgi when co-expressed with active Cdc42 (12) and can also be found at the cell periphery downstream of growth factor and integrin mediated signalling (17, 19, 36). This variation in localisation suggests that PAK4 may shuttle between cytoplasmic compartments depending on

Table 1. Normal tissue distribution and alterations in expression of PAK during cancer

Pak isoform	Normal tissue expression	Alteration	Cancer	Ref
PAK1	Widespread inc. Brain, muscle, spleen	Increased pak1 phosphorylation	Glioblastoma	(132)
		Protein overexpression	Liver	(133)
			Kidney	(134)
			Colon	(135)
		Amplification of genetic locus	Ovarian	(147)
			Bladder	(148)
PAK2	Ubiquitous	Increased pak2 phosphorylation	Ovarian	(136)
PAK3	Brain, spleen, testis	Potential cancer 'driver' mutations identified		(50)
PAK4	Ubiquitous	Protein overexpression	Lung, ovarian, prostate, cns, leukaemia, renal, melanoma, breast	(18)
		Amplification of genetic locus	Pancreas	(99)
			Oral squamous cell carcinoma	(101)
		Somatic mutation	Colon	(102)
PAK5	Brain, ovary, pancreas, testis	Protein overexpression	Colon	(106)
		Likely cancer 'driver' mutations identified		(50)
PAK6	Brain, breast, kidney, prostate, placenta, testis	Protein overexpression	Prostate	(35)

the nature of the physiological input. Recent studies have confirmed that PAK5 shuttles between the mitochondria and the nucleus (20) whereas PAK6 was reported to be predominantly localised in the mitochondria of Chinese-hamster ovary cells but is present in both the cytoplasm (9) and nucleus of prostate cells (14).

2.2.3. Mouse knockout studies

Deletion of the PAK1 gene in mice has no adverse effects on viability or fertility but there are subtle defects in neuronal function, defects in mast-cell degranulation and macrophage function. Genetic deletion of PAK2 results in embryonic lethality at day E8 due to multiple developmental abnormalities (8) whilst deletion of the PAK3 gene is implicated in mental retardation; PAK3 knockout mice are viable but display cognitive impairment (37). Genetic deletion of *PAK4* in mice is embryonically lethal. PAK4-deficient embryos exhibit extensive and dramatic defects of heart and neuronal development and spinal cord motor neurons fail to differentiate and efficiently migrate into position (38). No abnormalities were detected in either PAK5 or PAK6 knockout mice, and PAK5/PAK6-double-knockout mice are viable and fertile (39). However these double-knockout mice do exhibit defects in learning and memory functions (39).

3. GROUP I PAKS

3.1 Group I PAKs and cancer

PAK1 kinase activity is required for the Rasinduced transformation (40) and PAK1 overexpression has been reported in colon, ovarian, bladder transitional cell carcinoma, T-cell lymphoma, and glioblastomas (41, 42) (Table 2). Indeed, glioblastoma patient survival time is significantly correlated with the presence of phosphorylated (active) PAK1 in the cytoplasm (43). More specifically, PAK1 expression is widely upregulated in human breast tumours and correlates with breast cancer invasiveness as well as tumour cyclin D1 expression (44). Furthermore, PAK1 activity has been linked to estrogen (tamoxifen) resistance in estrogen receptor-positive breast cancers (31, 45). These effects appear to involve the phosphorylation of the estrogen receptor on Ser 305 by PAK1, and correlate with PAK1 nuclear translocation. Moreover, inducible

expression of a constitutively active form of PAK1 rapidly induces breast cancer cell proliferation and aggressive cell phenotypes, which included anchorage-independent growth and mitotic defects (46). PAK1 has also been shown to have a central role in the Schwann-cell tumours of neurofibromatosis type 1 (NF1), which is caused by the loss of a Ras GAP protein, through a Ras-dependent pathway (47). Both PAK1 and PAK2 have been associated with neurofibromatosis type 2 (NF2), as PAKs phosphorylate the *NF2* tumour-suppressor gene product, Merlin, on serine 518 and block its activity (48, 49). Very little is known about PAK3 function outside of neuronal cells (reviewed in(2)) however a recent screen of somatic mutations in human cancer identified PAK3 mutations as a possible driver of cancer progression (50).

3.2. Group I PAKs - Upstream regulators

Several growth factors including epidermal growth factor, heregulin, platelet-derived growth factor, and hepatocyte growth factor activate PAK1 (51-53) (Figure 3). PAK1 receptor recruitment can be mediated through binding to Grb2 (54) and localisation of PAK1 at the membrane is a critical step during PAK activation. However regulation of PAK1 activity is a complex process involving protein-protein interactions, phosphorylation/ dephosphorylation and sphingolipid binding (55, 56). The binding of Rac/Cdc42 to the PAK1 regulatory domain induces the phosphorylation of important sites throughout the protein, both by PAK1 itself (56) and/or by exogenous kinases such as JAK2, PDK1 and PKA (57-59). Indeed, phosphorylation of PAK1 serine 144 in the kinase autoinhibitory domain contributes significantly to kinase domain activation (56). PAK2 is also activated by binding to Rac/Cdc42 and is likely that the same mechanism that regulates PAK1 also regulates PAK2 catalytic activity. Like PAK1, Rac/Cdc42 interaction stimulates PAK2 autophosphorylation (Thr 402 in the activation loop (60)), a requirement for kinase activity (61).

The adapter protein Nck (62) and PIX (PAK-interacting exchange factor (63)) are key regulators of the group I PAKs, binding directly to PAK1-3 near the N-terminal GBD domain. Nck1/2 (referred to hereafter collectively as Nck) are small adapter proteins primarily

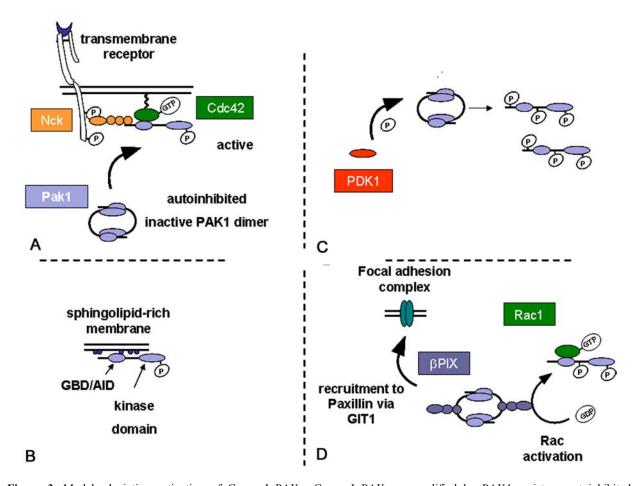


Figure 3. Models depicting activation of Group I PAKs. Group I PAKs, exemplified by PAK1, exist as autoinhibited homodimers, in which the kinase domain of one PAK molecule is inhibited by interactions from the GBD/AID domain of a second PAK molecule. Upon binding to Nck bound to activated transmembrane receptor (A), sphingolipids (C) or Rho family GTPases Cdc42 or Rac (A and D) autoinhibitory interactions are relieved enabling the kinase domain to undergo conformational change and autophosphorylation to become active. PAK1, 2 and 3 are also activated by phosphorylation by additional kinases, for example PDK1 (B), which inhibit AID-kinase and PIX interaction. Note that, despite their depiction, these mechanisms may not be mutually exclusive.

recruited via an SH2 domain to the cytoplasmic tail of activated tyrosine phosphorylated cell surface receptors and/or sites of cell: substratum adhesion. Initially it was thought that Nck recruitment alone was sufficient to induce PAK kinase activity (64), though it later emerged that activation of PAK by membrane clustered Nck is dependent on Rho family GTPases (65). Thus Nck serves to recruit PAK to areas of the cell where active Rac/Cdc42 are likely to be localised. Nck is also able to recruit a PAK1:PIX complex to sites of cell adhesion (66). PIX is a GEF for Rac/Cdc42 (67) which can complex with paxillin (a major component of cell: substratum adhesions) and the interaction between PIX and PAK1 is thought to mediate adhesion dynamics by localising both active Rac/Cdc42 and PAK1 at sites of cell adhesion (68)(Figure 3). Autophosphorylation of PAK1, an early event in PAK1 activation, drives the dissociation of PIX and Nck (69) suggesting that there is a complex feedback mechanism; moreover the interaction between Nck and PAK can also be disrupted by phosphorylation of PAK on serine 21 by

kinases such as Akt (70). In neuronal cells, PAK2 interacts with beta-PIX (71) leading to the formation of a PAK2-beta-PIX-Erk1/2 complex, which is essential for neurite outgrowth (72). Intriguingly, in this instance PAK2 inhibition blocks Rac activation, suggesting that PAK2 may also function upstream of Rac by regulating beta-PIX activity (73).

PAK2 is unique among the PAK isoforms because it can also be activated through proteolytic cleavage by caspases or caspase-like proteases to release an amino (N)-terminal fragment (PAK2p27) and a proapoptotic catalytic fragment (PAK2p34). Activation of full length PAK2 stimulates cell survival, whereas proteolytic activation of PAK2p34 is involved in programmed cell death. PAK2p34 exerts its pro-apoptotic effects via the activation of Jun N-terminal kinase (JNK) (74, 75).

Much less is known about the inactivation of PAKs; however the protein phosphatases POPX1 and

POPX2 can bind to the PIX/PAK complex and contribute to the deactivation of PAK. In addition to dephosphorylation, group I PAKs are also subject to inhibition by interaction with various proteins, including hPIP1, CRIPak, Nischarin, p110C, and Merlin (8), as well as down regulation by ubiquitin-mediated proteosomal degradation following binding to the small GTPase Chp (Cdc42 homologous protein) (2).

3.3. Group I PAKs signalling to the cytoskeleton

Although the substrate preferences among group I PAKs have never been directly or systematically compared, PAK1, PAK2 and PAK3 share 92-95% identity within their kinase domains (Figure 2), suggesting that they may phosphorylate common substrates (8). Indeed, PAK1 and PAK2 have been reported to have many identical substrate in vitro (76). It is therefore likely that isoformspecific functions of the group 1 PAKs are mediated by their participation in distinct molecular complexes and their localization to distinct subcellular structures. To date, more than 30 direct substrates of group I PAKs have been identified, proteins involved in the regulation of cytoskeletal dynamics, cell motility, cell death and survival signalling pathways (6). This review will focus on those interactions most closely related to cell migration and invasion (Table 1).

It has been known for some time that changing the activity level of PAK1 in cells leads to membrane ruffling as a result of actin cytoskeletal rearrangement (77) and that inhibition of PAK activity can block cell migration (78). We are now beginning to understand how PAKs orchestrate these effects on the actin cytoskeleton and cell migration.

Both PAK1 and PAK2 are thought to modulate the activity of myosin II (an actin interacting motor protein that can drive cell contractility) during cell migration. Myosin II is activated by myosin light chain kinase (MLCK) phosphorylation. Whilst PAK1 phosphorylates MLCK leading to a reduction in its catalytic activity (79) PAK2 can directly phosphorylate myosin II regulatory light chain inducing an activation of myosin II and increased cell contractility (80). PAK1 is also known to form a complex with, and phosphorylate, LIM-kinase (LIMK). LIMK is involved in reorganization of actin cytoskeleton through inactivating phosphorylation of ADF/ cofilin family proteins (81). ADF/cofilins are actin binding proteins that can promote actin polymerization by severing actin filaments to increase the concentration of free barbed ends (reviewed by(82). LIMK1 inactivates ADF/cofilin by phosphorylating cofilin at Ser3, inhibiting its ability to bind to F-actin (81). PAK1 regulation of actin dynamics at the leading edge of motile cells may also be mediated by phosphorylation of filamin A, a large actin binding protein which activates PAK1 and is required for PAK1 induced membrane ruffling (83). Evidence has now emerged that PAK1 may also regulate cross talk between Rac/Cdc42 signalling pathways and RhoA. GEF-H1 (guanine-nucleotide-exchange factor H1) is an exchange factor for RhoA whose activity is regulated through a cycle of microtubule binding and release. PAK1 phosphorylation of GEF-H1 induces microtubule binding resulting in suppression of RhoA activation (84).

PAK1 also binds to and phosphorylates p41-Arc, a subunit of the Arp2/3 complex. Arp2/3 drives the de novo nucleation of actin filaments during cell migration. Phosphorylation of p41-Arc by PAK1 promotes the formation of the Arp2/3 complex and PAK1 mediated phosphorylation of p41-Arc is required for breast cancer cell migration (85). These studies are the first to identify kinase regulation of Arp2/3 function and may place PAK activity at the centre of actin cytoskeletal dynamics.

In addition to actin cytoskeletal regulation PAK1 has also been implicated in the regulation of cell adhesion through its interaction with the PIX: paxillin complex (66). PAK1 activation has been shown to promote the interaction between PIX and Rac1 (86) at sites of nascent cell adhesion and a PAK/PIX/GIT complex has been implicated in adhesion regulation during migration (87). It should be noted however, that PAK1 kinase activity is not always required for cytoskeletal remodelling. Overexpression of PAK1 kinase dead mutants have been shown to induce the formation of lamellipodia, cell spreading and increased cell substratum adhesions (88, 89).

3.4. Group I PAKs and cancer cell invasion

Group 1 PAKs have been implicated in cell migration through their ability to phosphorylate multiple cytoskeletal regulators. In fibroblasts, PAK1 regulates lamellipodial extension and directionality (90, 91) and the formation and disassembly of focal adhesions (32, 87). In contrast, in endothelial cells both kinase-dead and constitutively active PAK1 inhibited migration (78), indicating that the role of PAKs in cell migration is likely to be cell-type specific. In prostate cancer cells, knockdown of PAK1 inhibits hepatocyte growth factor (HGF) induced loss of cell-cell junctions and subsequent migration whilst knockdown of PAK2 increases lamellipodium extension but does not affect migration speed (92). However, expression of either kinase-dead or constitutively active PAK1 has been shown to increase migration towards HGF in Boyden chambers (93). siRNAmediated knockdown of PAK1 in breast epithelial cells leads to decreased myosin light chain phosphorylation and smaller focal adhesions whilst dominant negative PAK1 blocks the invasiveness of breast tumour cells (88). In contrast, knockdown of PAK2 has the opposite effects (94). Interestingly, PAK1 has also been shown to co-ordinate extracellular matrix proteolysis in a three-dimensional (3D) breast cancer model (95). Moreover, a recent study reported that PAK1 and PAK2 are involved in promoting cell migration and invasion in ovarian cancer cells (96). Cancer cell dissemination may require a loss of cell: cell contact and PAK1 kinase mutants can induce a loss of cell-cell junctions (93). Moreover, active Rac acts via PAK1 to induce disassembly of E-cadherin-based adhesions (97). A process that may depend on an interaction between PAK1 and E-cadherin associated protein beta-catenin (98).

Table 2. PAK kinase substrates implicated in (metastatic) cell migration

Substrate	Cellular function	PAK	Ref
Caldesmon	Inhibitor of myosin ATPase activity	PAK1 & 3	(137)
CPI17	Inhibitor of myosin phosphatase	PAK1	(138)
Desmin	Intermediate filament protein	PAK1	(139)
Filamin A	Actin cross linking and adhesion protein	PAK1	(83)
GIT1	GTPase regulation Arf GAP	PAK1	(140)
GEF-H1	Rho GTPase regulation, RhoA GEF	PAK1 & 4	(84, 119)
LIMK1	Actin cytoskeleton dynamics; cofilin kinase	PAK1, 2 & 4	(113, 125)
MLCK	Regulation of myosin activity and actin cytoskeleton dynamics	PAK1 & 2	(79, 80)
Merlin	ERM binding protein	PAK2	(49)
p41-ARC	Subunit of Arp2/3 complex, actin nucleation	PAK1	(85)
Paxillin	Focal adhesion scaffold	PAK4	(36)
PDZ-RhoGEF	Rho GTPase regulation, RhoA GEF	PAK4	(141)
αΡΙΧ	Rho GTPase regulation, Rac GEF	PAK1 & 2	(56)
□PIX	Rho GTPase regulation, Rac GEF	PAK1 & 2	(72, 86)
Raf-1	MEK kinase	PAK1 & 3	(142, 143)
Rho-GDI	Inhibitor of Rho GTPase activity	PAK1	(144)
R-MLC	Regulatory chain of myosin motor	PAK2	(145)
SSH-1	Actin cytoskeleton dynamics; cofilin phosphatase	PAK4	(126)
Vimentin	Intermediate filament protein	PAK1	(146)

4. GROUP II PAKS

4.1. Group II PAKs and cancer

PAK4 has been found to be overexpressed or genetically amplified in numerous cancer cell lines and tumours including those derived from breast, lung and prostate (18) as well as pancreas (99, 100) squamous cell carcinoma (101) and colon cancer (102) (Table 2). Overexpression of PAK4 in a range of cell lines has revealed several phenotypes suggestive of a role in cancer. Overexpression of constitutively active PAK4 confers anchorage independent growth to cultured fibroblasts in soft agar assays independently of Ras transformation (18, 103) and kinase inactive PAK4 can inhibit either Dbl (103) or Ras (18) mediated oncogenic transformation of fibroblasts. Further, expression of kinase-dead PAK4 inhibits anchorage independent growth of a human colon cancer cell line (18). In addition to the role PAK4 plays in oncogenic transformation, overexpressed PAK4 is associated with protection from apoptosis (104). Finally, overexpression of both wild-type and constitutively active PAK4 in a nude mice model leads to an increased incidence of tumours, strongly implicating PAK4 as a driving force in cancer (105).

Little is known about PAK5 function outside of neuronal cells but PAK5 overexpression was recently detected in numerous colorectal carcinoma cell lines where increased expression correlated with cancer progression and invasive potential (106). Furthermore, PAK5 somatic mutations were also identified in the same cancer genetic screen as PAK3 (50).

PAK6 was identified in a screen to identify proteins that interact with the Androgen Receptor (AR) which mediates the development and differentiation of androgen-sensitive tissues and it is also important in the manifestation of prostate cancer (107). PAK6 binds to the ligand binding domain (LBD) of the AR (also to the estrogen receptor) and leads to the suppression of AR signalling (107). The aptitude of PAK6 to bind to steroid hormone receptors suggests that it may contribute to the hormonal independence that is characteristic of many aggressive tumours (76, 107). In support of this hypothesis,

increased PAK6 expression has been detected in both prostate cancer cells and breast tumours (7, 35). Moreover, a recent study demonstrated that reduced PAK6 expression, combined with irradiation, decreased prostate cancer cell viability (108). In contrast, the *PAK6* gene is hypermethylated in some prostate cancer cells; hypermethylated genes are often linked with tumour growth inhibition (109).

4.2. Group II PAKs - Upstream regulators

PAK4 kinase activity is specifically stimulated in response to hepatocyte growth factor (HGF) in a phosphatidylinositol 3-kinase (PI3K) dependent manner (17). HGF is a multifunctional cytokine and signals via it's oncogenic receptor c-Met/HGF receptor. HGF signalling plays a critical role in chemotaxis, cell growth, morphogenesis and metastatic migration and invasion (recently reviewed (110, 111). PAK4 recruitment to activated c-Met /HGFR is mediated by the large adaptor protein Gab-1. PAK4 binds directly to Gab-1 via a GEF-H1 interaction domain (GID) adjacent to the kinase domain(112) (Figure 4). PAK4: Gab-1 interaction is required for HGF-dependent scattering of MDCK cells and PAK4 and Gab-1 act synergistically to enhance cell scattering in 2D and invasion into matrigel (112). Unlike the Group I PAKs, PAK4 does not contain a prototypical Nck SH3 binding site, and reportedly does not bind Nck (113). In mice, PAK4 interacts with Grb2 downstream of KGFR (114), suggesting Grb2 and Gab-1 rather than Nck may regulate PAK4 recruitment to transmembrane receptors. PAK4 has also been implicated in signal transduction downstream of a number of transmembrane receptors, for example in C2C12 muscle precursor cells, PAK4 is activated downstream of BMP2, which induces cell migration (115).

Upstream regulators of PAK5/PAK6 have not be clearly identified however kinase activity is elevated by coexpression with the active form of MKK 6 (MAPK kinase 6)(116). At least for PAK6, MKK6 stimulates activity by interacting with serine – 165 (a p38 MAP kinase site) and tyrosine 566 located in the activation loop within the PAK6 kinase domain (116). Although the activity of group I PAKs can be regulated by the binding of Rac/Cdc42, it has

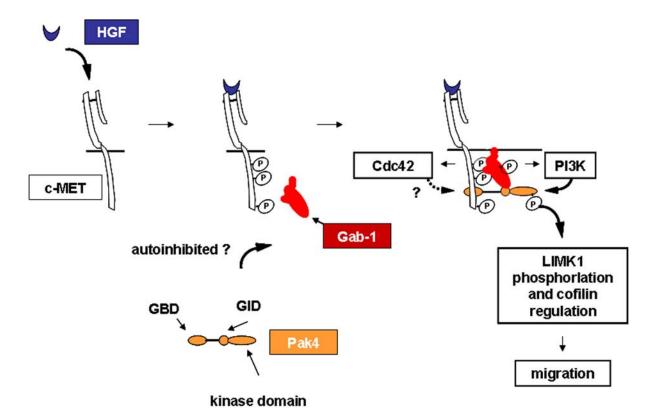


Figure 4. Activation of PAK4 in response to hepatocyte growth factor (HGF) signaling. HGF-induced activation of c-MET/HGFR results in activation of the intracellular portion of c-Met that consists of a kinase domain and tyrosine residues. Once phosphorylated, these tyrosines serve as docking sites for the recruitment of a number of adaptor/scaffold proteins (not shown for clarity), including Gab-1. Subsequently, Gab1 itself becomes phosphorylated recruiting a host of signalling molecules, including PAK4, which in turn is activated possible from an inactive inhibited state. HGF signalling involves activation of both Rho family GTPases including Cdc42 and PI3K. PAK4 activation in response to HGF is PI3K-dependent; though the mechanism remains illusive as does the role of Cdc42. Active PAK4 regulates the activity of cofilin via LIMK1, promoting cytoskeletal rearrangements and cell migration.

not yet been resolved whether Cdc42 is also an upstream regulator of Group II PAK activity even though these family members bind specifically to Cdc42 (see section 1.2.1).

4.3. Group II signalling to the cytoskeleton

To date, no kinase independent functions of PAK4 have been identified, thus the primary mechanism by which PAK4 regulates the activity of downstream effectors is via phosphorylation. PAK4 phosphorylates two RhoA GEFs, PDZ RhoGEF and GEF-H1, the adhesion associated protein paxillin, LIMK1 and slingshot homologue (SSH-1) both regulators of actin dynamics mediated through cofilin (117). Many of these substrates, at least in vitro, are shared with PAK1 (Table 2). GEF-H1, a RhoA exchange factor, is a key orchestrator of cell migration, mediating localised regulation of RhoA activity at the cell leading edge during migration; depletion of GEF-H1 leads to decreased cell migration due to the loss of the Rho exchange activity of GEF-H1 (118). GEF-H1 binds directly to PAK4 via a GEF-H1 interaction domain (GID) and PAK4 phosphorylates GEF-H1 on serine 885 (119), which inactivates RhoA exchange activity (120). The PAK4-GEF-H1 complex subsequently interacts with microtubules (MT) and the

release of this MT bound GEF-H1 into the cytoplasm results in a dissolution of stress fibres and the formation of actin-rich lamellipodia in murine NIH3T3 fibroblast cells (119). In DU145 prostate carcinoma cells, co-expression of active PAK4 and GEF-H1 significantly reduces GEF-H1mediated increases in active GTP-bound RhoA. Conversely, knockdown of PAK4 by RNAi increases the level of active RhoA, suggesting that PAK4 regulates RhoA via regulation of GEFH1 activity (36). The loss of GEF-H1 is also associated with decreased rates of focal adhesion turnover (118). Interestingly, reduction of PAK4 expression in DU145 prostate cancer cells not only triggers the formation of prominent actin stress fibres but also leads to an increase in the size and number of focal adhesions that exhibit reduced turnover rates (36). Paxillin is a central scaffold protein of focal-adhesion complexes, coordinating both complex assembly and disassembly (121). It has recently been reported that paxillin is serine phosphorylated on serine 272 which leads to increased turnover of cell adhesions (87). Initially PAK1 was identified as the kinase but subsequent reports have disputed this finding (122). The kinase domain of PAK4 binds paxillin and phosphorylates paxillin on serine 272 in vitro, suggesting a mechanism by which PAK4 regulates focal adhesion

turnover and therefore cell migration (36). In a separate study PAK4 has also been shown to interact directly with alpha-v beta-5 Integrins (19). A beta-5 Integrin Binding Domain (IBD) within the C-terminus of the PAK4 kinase domain binds directly to a SERS motif in the cytoplasmic tail of \beta 5 and phosphorylates both serine residues of this motif in vitro (123). Overexpression of either full length PAK4 or the kinase domain alone in MCF-7 breast cancer cells is sufficient to induce haptotactic cell migration towards the alpha-v beta-5 ligand vitronectin (19, 123). Although initially reported to be a kinase-independent process, in vitro binding of PAK4 to beta-5 integrin and concomitant haptotactic migration appears to require PAK4 kinase activity (19, 123). Interestingly, the IBD is well conserved amongst other PAK family members and mutation of several key residues within the IBD abolishes both kinase activity and beta-5 interaction(123). The SERS sequence motif is only partially conserved between integrin isoforms, so it will be interesting to see if PAK4 can bind other integrins (for example beta-6, which is highly upregulated during cancer progression), likewise it will be interesting to see if other PAK family members can interact with any of the integrin cytoplasmic tails.

In some cells PAK4 acts predominantly via LIMK1 and cofilin downstream of HGF rather than via GEF-H1 and paxillin (36, 124). Like PAK 1/2, PAK4 influences actin polymerisation by activating LIMK1 via phosphorylation of the LIMK1 active site threonine 508 (125) and (113) leading to serine 3 phosphorylation of cofilin as described above. PAK4 further regulates cofilin activity by phosphorylating and inactivating the cofilin phosphatase slingshot homologue 1 (SSH-1L) (126). SSH-1L both dephosphorylates and inactivates LIMK1 through dephosphorylation of Thr508 and dephosphorylates and activates ADF/cofilin on Ser3, resulting in a net increase in ADF/cofilin activity and actin filament turnover. PAK4 also has recently been shown to bind to GDCR6L, the product of a gene deleted in the rare genetic disorder Digeorge syndrome, DGCR6L colocalises with PAK4 in human gastric cancer cells and enhances the phosphorylation level of both LIMK1 and cofilin (127). Both LIMK1 and SSH have been implicated in coordinated chemotactic cell migration (Nishita et al., 2005) and deregulation of the PAK4-LIMK1 pathway by cooverexpression of PAK4 and LIMK1 or knockdown of PAK4 in PC3 cells leads to increased chemotaxis towards HGF and decreased cell motility, respectively (124).

PAK5 is a key component in the signaling pathway by which Rho GTPases regulate cytoskeletal changes required for promoting neurite outgrowth (128), PAK5 is yet to be extensively studied, however it is known that PAK5 triggers neurite outgrowth in a mouse neuroblastoma cell line via down regulation of RhoA activity (128). Still less is known about signalling between PAK6 and the actin cytoskeleton. PAK6 interacts with IQdomain GTPase-activating protein 1 (IQGAP1) (129). IQGAP1 overexpression has been observed in a number of tumours (129), although the precise role of IQGAP in cancer progression remains unresolved and is the focus of much current research.

4.4. Group II PAKs and cancer cell invasion

Several reports implicate PAK4 in regulation of cancer cell migration and metastasis. PAK4-null fibroblasts migrate slower than wild-type fibroblasts in response to an electric field (galvanotatic migration) (130), and knockdown of PAK4 by RNAi reduces both the mean speed of migration of prostate carcinoma cell migration (124) the ability of pancreatic ductal adenocarcinoma cells to invade matrigel (100) and inhibits HGF-induced cell (36, responses 112) Reciprocally, scattering overexpression of PAK4 enhances the migration speed of fibroblasts during galvanotaxis (130) and promotes the invasiveness of pancreatic cancer cells (100).

Very little is known about how PAK5 might contribute to tumour progression but colorectal carcinoma cells overexpressing PAK5 exhibited decreased cell adhesion concomitant with increased cell motility on collagen I substratum whilst siRNA knockdown of PAK5 expression in the same cells lead to enhanced cell adhesion and reduced cell migration. This study at least implies that PAK5 may play a role in colorectal carcinoma cell migration (106). The role of PAK6 in cancer cell invasion has not been extensively studied however it has been recently reported that a loss of PAK6 expression significantly reduces the invasive ability of prostate cancer cells (131).

5. PERSPECTIVE

PAKs are pluripotent kinases involved in many cellular functions including cell motility, regulation of neuronal outgrowth, hormone signalling, gene transcription and cell survival. Their role in these processes makes this family of kinases attractive therapeutic targets. Since the discovery of p-21 activated kinases in the early 1990s we have learnt much about the regulation and activity of Group I PAKs. Much less is known about group II PAKs, particularly PAK5 and PAK6. It is currently the case that much of our knowledge of their biology (as reviewed here) is derived from one or two publications. The future challenge is to validate these data and further elucidate their biological function *in vivo*.

Many cell types express multiple PAK family members and it will be important to understand how PAK activity is coordinated at the subcellular level to mediate the cytoskeletal events that orchestrate cell migration and invasion. Indeed, many of the original PAK1 studies were conducted before Group II PAKs were even discovered and recent work suggests that PAK1 and PAK4, at least in vitro, share many common substrates. There is also evidence to suggest that different PAK family members can play antagonistic roles in the same cell (94). Moreover, substrate specificity in vivo remains to be elucidated. Evidence from knockout mice studies points to both unique and overlapping functions and it is likely that spatial and temporal regulation of activity is required to elicit specific cellular responses. It is also likely that the activity of individual family members may differ between cells types.

Overexpression and amplification of PAK family members is reported in many tumour types and it is

important to note that PAKs originally thought to be neuronally restricted in expression (PAK3 and PAK5) are both implicated in tumour progression. It will be interesting to establish whether these family members also play a role in cancer cell migration and invasion.

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