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Perspective

HEF1-Aurora A Interactions

Points of Dialog Between the Cell Cycle and Cell Attachment Signaling Networks

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ABSTRACT

Regulated timing of cell division cycles, and geometrical precision in the planar orientation of cell division, are critical during organismal development and remain important for the maintenance of polarized structures in adults. Mounting evidence suggests that these processes are coordinated at the centrosome through the action of proteins that mediate both cell cycle and cell attachment. Our recent work identifying HEF1 as an activator of the Aurora A kinase suggests a novel hub for such integrated signaling. We suggest that defects in components of the machinery specifying the temporal and spatial integration of cell division may induce cancer and other diseases through pleiotropic effects on cell migration, proliferation, apoptosis, and genomic stability.

INTRODUCTION

During metazoan development, cell division is regulated by diffusible and localized extracellular factors that promote or inhibit proliferation, specify mitotic division orientation and symmetry, regulate differentiation into distinct cell types, and in some cases promote directed migration or apoptosis of dividing cells. These cues are essential during the conversion of a single fertilized egg into a complex multicellular organism. They remain important in adults, coordinating the limited cell division required for maintenance of organs. Because of these critical regulatory roles, mutated forms of the proteins comprising the machinery to transmit extracellular information to the cell division apparatus are frequently identified as oncogenes and tumor suppressors, or as cancer-predisposing factors. As summarized below, work by many groups has begun to outline a network of signaling proteins that operate to connect these processes, many of which utilize the centrosome as a central communication point for transmission of information. Aurora-A (AurA) kinase^{1,2} is now appreciated as an important transducer of signals at centrosomes; our recent studies describing interactions between HEF1 and AurA required for AurA activation³ illuminate a new branch of this signaling network. In this article, we will first summarize the diverse signaling functions that have been identified for centrosomes, then describe how the association of AurA and HEF1 may impact these functions.

ROLES OF THE CENTROSOME

The centrosome is composed of two paired orthogonal centrioles surrounded by "pericentriolar material" (PCM) that varies in abundance and content during cell cycle, and comprises hundreds of structural and signaling proteins. The centrosome has its own duplication cycle (reviewed in refs. 4–7), and was for a long time thought of predominantly as an organizing structure for cellular microtubules (a microtubule organizing center, MTOC). As such, its actions in physically nucleating the two ends of the mitotic spindle were a major focus of study. Through studies over the past decade, this view of the centrosome has been significantly revised. It has now been shown that the centrosome provides a contained platform to coordinate signaling related to polarity and cell cycle coordination. Several excellent reviews summarize centrosomal biology at length.⁷⁻¹⁰ In brief (see also Fig. 1), important centrosome-associated functions to consider include:

(1) **Orientation of the mitotic spindle in asymmetric cell divisions.** Cells growing in a plane (for example, as a sheet of epithelial cells) may divide in different directions. Symmetric planar division can extend the size of the sheet, with two daughter cells assuming the same fate as their mother. Asymmetric cell divisions orthogonal to the direction of the plane allow a mother cell to spawn two daughter cells with different cell fates, and can

cause cell propagation into a new dimension. *Drosophila* has been a productive model system for demonstrating the importance of the centrosome in these processes. Recent studies have addressed asymmetrically dividing neuroepithelial cells giving rise to neuroblasts,^{11,12} male germline stem cells producing gonialblasts after an apical-basal division away from a germline stem cell “hub”¹³ (Fig. 1A), and the syncytial divisions of early embryos.¹⁴ In these works, centrosomes have been shown to be the target for proteins that directly orient the mitotic spindle by forming physical bridges with polarity cues associated with the cell surface and cortical actin. Planar (lateral) divisions are specified based on signals from the adenomatous polyposis coli (APC) tumor suppressor protein, and Armadillo/beta-catenin. In the absence of these dominant signals, basal signals provided by Bazooka/Par3, a component of the cell polarity machinery,^{15,16} can direct cell divisions along the apical-basal axis.¹¹

There is mounting evidence that this signaling machinery is conserved through evolution. APC is distantly related to Kar9p, an *S. cerevisiae* protein that acts as a cue for orientation of the mitotic spindle to the bud, and associates with both the spindle pole body (the yeast “centrosome”) and the actin cortex within the tip of a forming bud.^{17,18} Excitingly, recent studies by Lechler and Fuchs have provided evidence for a similar process occurring during the stratification and differentiation steps of epidermal development in mammals.¹⁹ In this case, both integrins and cadherins provided essential signals regulating the polarity complex (Par3 /Pins/aPKC), and additionally influence NuMA and dynactin activity, thus controlling the orientation of the centrosome and spindle.

(2) **Specification of the site of process extension (neurites and cilia).** Centrosomes also influence the polarization of external cell processes. In a recent study of neurite formation that utilized both mammalian hippocampal neurons and *Drosophila* third instar neurons,²⁰ it was shown that formation of a neurite projection from an apparently undifferentiated, rounded cell body occurred at the site where the centrosome and associated Golgi apparatus abut the cell cortex (Fig. 1B). This site is specified based on the prior mitotic division, such that the new neurite forms on the opposite side of the cell from the previous cleavage plane. After cytokinesis, the cortex proximal to the centrosome undergoes transient lamellipodial extension. This is followed by formation of what becomes the dominant neurite at the same site. The observation that an actin polymerization inhibitor (cytochalasin D) can suppress neurite extension implies that initial reorganization of the actin cytoskeleton precedes the organization of microtubules and secretory machinery at the time of neurite extension.

As a separate example of centrosome-based polarization of non-mitotic structures, in nonproliferating (G_0 , stationary) eukaryotic cells, one of the centrioles within a centrosome undergoes a differentiation to form the ciliary basal body (ref. 21 and refs. therein), which then recruits microtubules and the vesicular trafficking machinery to create a cilium (Fig. 1C). These cilia are non-motile, share many (although not all) proteins with centrosomes, and are typically

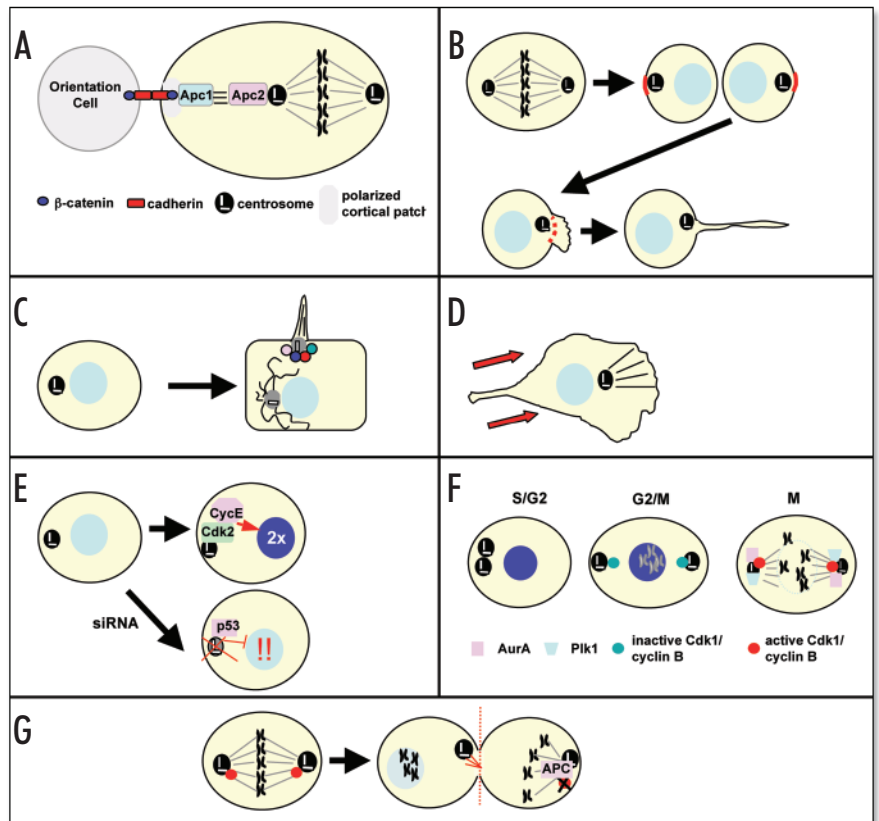


Figure 1. The centrosome coordinates diverse cellular processes. These include (A) orientation of the mitotic spindle in asymmetric cell divisions, (B) specification of the site of neurite process extension (neurites), (C) nucleation of cilia and flagella, (D) orientation of cell migration, (E) and regulation of cell cycle progression through G_1 (checkpoints), (F) mitotic entry, and (G) mitotic exit. See text for details.

reabsorbed if cells return to proliferation. Mutations in a number of the proteins associated with basal body (for example, inversin and others) are associated with diseases involving abnormal planar cell polarity, and in some cases, abnormal cell growth (refs. 10, 22 and others). Simons et al. have shown that inversin, a cilia-basal body-centrosome protein, directly interacts with Disheveled, which associates in turn with β -catenin,²³ previously shown to orient the spindle in *Drosophila* studies.¹³ Increasing evidence suggests that in stationary cells, receptors for external signals are specifically localized to the cilia.²⁴ It has been proposed that the cilia may also coordinate signals determining whether cells remain in or emerge from stationary phase, through communication with the cell cycle.²⁵ In this context, the Nek kinase family may play an important role, as many of the members of this family of kinases are distributed between basal body and centrosome, and some (e.g., Nek2) are known to regulate centrosome dynamics and possibly affect spindle checkpoints, by influencing centriolar cohesion.^{21,26}

(3) **Centrosomes and cell migration.** The studies of centrosomes in neurites suggesting a role for the centrosome in regulation of both actin and tubulin cytoskeletons is of additional interest because of reports suggesting a role for the centrosome in orienting cell migration (Fig. 1D). An initial study in *Dictyostelium* observed that positioning of the centrosome in front of the nucleus, behind the leading edge of a migrating cell, was important for the stabilization of the direction of cell migration, perhaps by orienting the microtubule network in support of the actin-based motility machinery.²⁷ Subsequent work by others in some cases supported,²⁸ and in others contradicted this

observation,²⁹ while additional work has suggested that the contribution of the centrosome may be to increase the efficiency rather than directionality of migration, through regulation of microtubule dynamics.³⁰ In one model, of fibroblast migration, it has been demonstrated that a signal dependent on the Cdc42 GTPase is required to orient the centrosome to face the direction of migration, while microtubules emanating from the centrosome interact at their plus ends with EB1 and APC, making contact with the cell cortex at sites involving Discs-large (Dlg), and once again specified by the polarity complex (aPKC and other proteins).³¹⁻³³ At present, it seems likely that the phenomenon of centrosomal contribution to migration is cell type specific,³⁴ which may reflect the abundance of differing polarization-associated proteins in diverse cell types. It is only now becoming widely appreciated that cells migrate by a variety of different strategies, and that as cancer cells become metastatic, they can serially adapt different strategies.^{35,36} hence, the importance of these observations in human disease remains to be established.

(4) Requirement for progression through G₁ (checkpoints). Centrosomal integrity is important for a number of different cell cycle transitions. Cells with centrosomes ablated by multiple approaches (ref. 9, and Refs. therein) undergo G₁ arrest (Fig. 1E). One mechanism proposed for this arrest is based on the observation that the cyclin E/Cdk2 and cyclin A/Cdk2 complexes that promote entry into S phase have an obligate association with centrosomes,^{37,38} such that cyclin E mutated to eliminate a centrosome localization domain is unable to promote entry into S phase.³⁷ Conversely, Cdk2/cyclin E also is required for the centrosome duplication cycle,^{38,39} and overexpression of cyclin E can promote centrosome overduplication.³⁷ A second mechanism of centrosome control of cell cycle may involve the activation at the centrosome of a p53-dependent cell cycle checkpoint, as cells with defective centrosomes (due to depletion of components by siRNA) do not undergo G₁ arrest in p53-deficient cells (and discussed in refs. 9 and 40).

(5) Roles in entering and exiting mitosis. The best-studied aspects of centrosomes are their roles in relation to G₂/M processes (Fig. 1F; reviewed in depth in refs. 5, 7-9 and 41). Prior to G₂/M transition, a series of interactions between Cdk1 and inhibitors such as Chk1 and Cdc25B at the centrosome restrain Cdk1 activity. At mitotic entry, the AurA and Plk1 kinases act at the centrosome to activate Cdk1/cyclin B and perform other actions necessary to initiate the intracellular organization accompanying karyo- and cyto-kinesis.^{42,43} Gamma-tubulin and other proteins associate with PCM components such as pericentrin, promoting formation of astral microtubules.⁴⁴ Later in mitosis (Fig. 1G), centrosomes are centers for ubiquitination activity, governing the action of the anaphase promoting complex/cyclosome (APC/C) in causing the degradation of substrates such as cyclin B.⁴⁵⁻⁴⁷ Separate studies indicate that the centrosome may also nucleate cellular degradation and proteasome activation at other phases in the cell cycle as well.⁴⁸ In 2001, Piel et al. made the intriguing observation that the mother centriole must undergo an excursion to the region of the midbody to allow completion of cytokinesis, suggesting delivery of some final signal to promote excision.⁴⁹ Although the nature of this signal remains to be established in detail, Cep55, which interacts with ERK kinases as well as Cdk1 and Plk1, has recently been shown to migrate from centrosome to midbody at cytokinesis, and play an important role in abscission and return to G₁.⁵⁰

INTRODUCTION TO AurA

The AurA kinase is also known as STK15, STK6, BTAK, ARK1, HsAirk1, and Aik; it is a member of the Ipl family of kinases (reviewed in ref. 1). AurA is abundant at the centrosome in G₂ to M phase, degraded upon completion of cytokinesis, and present at very low levels in G₁ and S phases, in part because of efficient post-translational degradation by the ubiquitination machinery.⁵¹ Although present at the centrosome from early G₂, AurA only becomes active around the time of prophase. This activation process is not completely understood, but requires AurA interactions with the proteins Ajuba,⁴² TPX2,^{52,53} and (as we have recently described, ref. 3) HEF1. Upon activation, AurA phosphorylates substrates that promote progression through the stages of mitosis: these include Cdc25B, TPX2, Eg5, Lats2, histone H3, D-Tacc, Brca1 and others, with the list continuing to expand (reviewed in ref. 1). Among its defined activities, one of the most important is in promoting the activation of cyclin B/Cdk1,⁴² which occurs physically at the centrosome, and may be mediated through phosphorylation and inactivation of Cdc25B.⁵⁴ Failure of AurA activation results in G₂ arrest or a defective entry into mitosis, marked by failure of centrosomes to separate and associated monopolar mitotic spindles, and consequent defects in chromosome alignment: failure to complete cytokinesis may arise from this, or also involve additional defects.^{55,56}

In the past several years, AurA has attracted increasing attention because it has been found to be overexpressed in many tumors arising from breast, colon, ovary, and other tissues,⁵⁷⁻⁶¹ and because it has been shown to function as an oncogene when exogenously expressed in various cell line models.⁶²⁻⁶⁵ AurA overexpression, whether in naturally occurring tumors or following deliberate overexpression, is associated with increased numbers of centrosomes and multipolar spindles, which arise as a consequence of failed cytokinesis. As the overexpressed AurA is not limited to expression in G₂ and M phases at the centrosome, but is also detected throughout the cytoplasm in cells in all cell cycle compartments, it is not clear at present whether the transforming activity of AurA arises from hyperactivated AurA targeting its normal substrates, or through anomalous targeting by AurA of additional substrates (as in the refs. 61 and 66). Unexpectedly, even overexpression of a kinase-inactive form of AurA can induce supernumerary centrosomes (although it cannot transform cells),⁶² supporting the idea that the protein has at least two different functions in regulating centrosome numbers. At least one set of important functions of the overexpressed active AurA is to override the spindle checkpoint, which causes resistance to spindle targeting agents such as taxol⁶³ and may arise in part through abrogation of the function of the Chfr mitotic checkpoint protein.⁶⁷ Separately, numerous reports have now documented a physical association between AurA and p53, most likely occurring directly at the centrosome (e.g., refs. 68-70). Although the functional consequences of these interactions are currently controversial, based on conflicting studies using varying assay conditions,^{62-64,68,69} it appears that AurA is able to influence and in some cases override the post-mitotic checkpoint. Based on these various properties, AurA is now being actively exploited as a target for development of new anti-cancer agents (reviewed in ref. 2).

INTRODUCTION TO HEF1

The newcomer to the discussion of AurA and centrosome functions is HEF1 (ref. 71 also known as Nedd9 and Cas-L).⁷² HEF1 and two related proteins, Efs/Sin,^{73,74} and p130Cas/Bear1,⁷⁵ comprise

the Cas protein family.^{76,77} These proteins are multidomain scaffolding proteins, with an amino-terminal SH3 domain followed by a large number of potential SH2 binding sites in a “substrate domain”; the carboxy-termini of the proteins, although well conserved within the family, are less well functionally characterized, lacking significant sequence homology outside the group. The first established and best-studied role for this group of proteins is as components of the integrin-dependent attachment signaling cascade, localized to focal complexes and focal adhesions on the basal cell surface. Upon receipt of attachment signals from the extracellular matrix through integrins at the focal adhesion, Cas proteins associate with focal adhesion kinase (FAK) and a Src family kinase. As a result of these interactions, the activity of Src is elevated,^{78,79} and Src phosphorylates Cas extensively in the Cas substrate domain, creating active SH2 binding sites.⁸⁰ These sites bind the adaptor protein Crk/CrkII, subsequently recruiting DOCK180 and C3G; these associations cause signals to propagate further, through DOCK180 to Rac and Pak, and through C3G to the Ras-related GTPase Rap1, in each case promoting lamellipodia formation and cell migration.^{81,82} HEF1, p130Cas, and Efs each increase cell migration when overexpressed.^{76,77}

Extending out from this set of functions, members of the Cas family have also been shown to influence additional cell processes. Through the C3G-Rac signaling axis, p130Cas is important for phagocytosis.^{83,84} In normal epithelial cells, detachment of a cell from external supports triggers a suicide program termed “anoikis”, which acts as a surveillance mechanism against cancer.^{85,86} Cas proteins are components of the attachment-dependent cell survival signaling cascade, with both HEF1 and p130Cas influencing cell viability under different attachment conditions.^{87,88} Elevated Cas levels activate Ras-dependent pathways,⁸⁹ enhancing Raf>MEK>ERK proliferation signaling, and also stimulating PI-3-K.⁹⁰ P130Cas overexpression has been shown to confer tamoxifen resistance on cells, and elevated expression of Cas proteins has been shown to associate with poor prognosis in breast cancer, although the mechanism for Cas action in these cases is not well defined.⁹¹⁻⁹⁵

Although the Cas proteins have many overlapping functions, some features distinguish HEF1. The most well-studied member of the Cas family, p130Cas, is near ubiquitously expressed. In contrast, HEF1 expression varies considerably between different cell types and tissues.^{71,72,96,97} It is most abundant *in vivo* in tissues with polarized cell populations, including epithelial cells, neuronal and glial cells, and lymphoid cells, and its signaling action may be particularly important in these cell lineages.^{97,98} p130Cas is abundant at all phases of cell cycle. In contrast, HEF1 is very low in G₀/G₁ phase cells, with abundance peaking in G₂ and M phase.^{3,99} HEF1 expression is induced by various pro-growth or pro-migratory stimuli, including all-trans retinoic acid, which induces polarized neurite extension in brain development,¹⁰⁰ and TGF-β, which induces epithelial-mesenchymal transition in development and metastasis.^{105,106} recently, HEF1(Nedd9) elevation was described as part of the lung metastasis transcriptional signature.¹⁰⁷ Besides being transcriptionally regulated by TGF-β, HEF1 physically associates with downstream effectors of TGF-β, the SMAD proteins: this causes post-translational regulation of HEF1 via the ubiquitination-proteasome machinery,¹⁰²⁻¹⁰⁴ and raises the possibility that interaction with HEF1 may target other proteins for proteasomal degradation. Finally, we have now shown that HEF1 localizes to the centrosome, where it associates with and positively regulates the activity of AurA kinase, through a mechanism yet to be defined.³

AurA, HEF1, AND EXPANDED ROLES IN CENTROSOME-ASSOCIATED SIGNALING

In our recent study,³ we demonstrated that like AurA, HEF1 accumulated at the centrosome predominantly between G₂ and M phase in normal and cancerous breast cell lines. Depletion of HEF1 by siRNA did not affect AurA accumulation at the centrosome, but blocked the activation of AurA at mitotic entry, and led to accumulation of cells with monopolar spindles. Conversely, overexpression of HEF1 induced AurA hyperactivation, and produced cells with multipolar spindles and supernumerary centrosomes. HEF1 also activated AurA kinase activity with both proteins in a purified *in vitro* system, indicating a direct mode of action. Further, *in vitro* and *in vivo* domain mapping experiments demonstrated that the sequences of HEF1 required for AurA activation differed from those required for HEF1-dependent regulation of cell spreading, ruling out the possibility that the HEF1-dependent effects seen at the centrosome were secondary consequences of changes in cell attachment. Finally, the phenotype of HEF1 differed in one important way from that of AurA depletion: in HEF1-depleted cells, premature splitting of the centrosomal pairs was observed, such that in an asynchronous population with similar profiles ~70% of cells had separated centrosomes, rather than ~27% in control siRNA-depleted cells.³ This implied that HEF1 might have a second action at centrosomes, in regulation of centrosomal cohesion. Indeed, we showed that HEF1 negatively regulated the action of Nek2, such that this kinase, which promotes centrosome splitting,^{26,108-110} had enhanced activity in HEF1-depleted cells. At present, it is not clear whether this reflects a direct or indirect consequence of loss of HEF1.

Upon initial inspection, the association of HEF1 and AurA, and the implicit potential for cross-signaling between the focal adhesion attachment machinery and centrosome-based cell division machinery, may seem surprising. However, returning to the list of centrosomal signaling roles summarized above, there are a number of reasons why the establishment of HEF1-AurA association is relevant to current models for development and cancer (Fig. 2).

First, as noted above, the orientation of cell division plane depends in part on both planar (cadherin-associated) and basal (integrin-associated) external adhesion cues. Focusing on basal signals, HEF1 and Pak, both of which are downstream integrin effectors in cell migration, are now known to associate with and activate AurA at the centrosome,^{3,111} discussed in.¹¹² Pak centrosomal localization requires association with another centrosomal protein, GIT1, which also binds the focal adhesion protein paxillin.¹¹³ These are not isolated instances of focal adhesion proteins finding a new use in mitosis. For example, the mitotic kinase WARTS/Lats has been shown to interact with the focal adhesion protein zyxin, with both proteins proximal to the centrosome at the astral microtubules in early mitosis, and collaborating in mitotic initiation (e.g., ref. 114). In their recent work describing extracellular matrix control of the cell division axis, They et al. have proposed that one factor contributing to spindle orientation is cell shape anisotropy arising from greater membrane retraction on non-adhesive surfaces.¹¹⁵ Interestingly, Cas and associated proteins CrkII and C3G have been implicated as an integrin-associated stretch-sensing machinery, with application of mechanical force activating downstream signaling.¹¹⁶ The numerous connections between focal adhesions and centrosomes now being identified make it plausible that reuse of the existing basal attachment machinery in the G₂ and M phase of cell cycle may offer an economical means to coordinate mitotic division polarity.

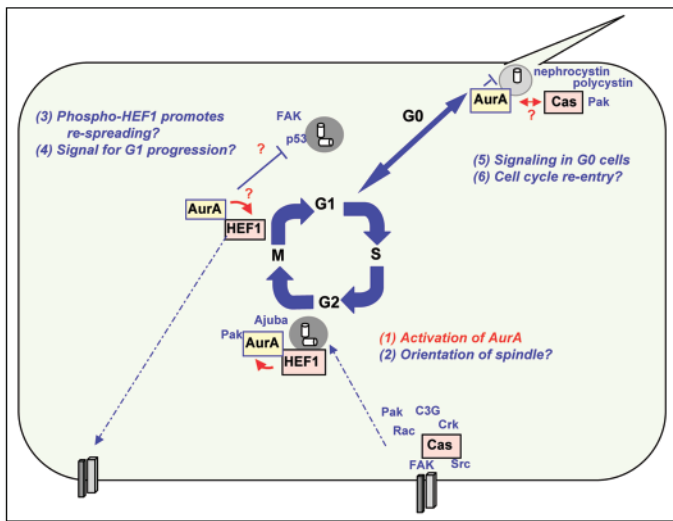


Figure 2. Demonstrated and speculative models for HEF1 and AurA interactions. We have shown (1) that HEF1 promotes AurA activation at the centrosome. Based on the biology summarized herein, and demonstrated protein-protein interactions placing AurA and HEF1 or p130Cas at specific intracellular locales, we speculate that HEF1 and/or p130Cas (2) may be a component of the integrin-dependent machinery orienting the mitotic spindle. We hypothesize that phosphorylation of HEF1 by AurA (3) may promote HEF1 localization to reestablishing focal adhesions at the end of mitosis, contributing to cell spreading: impairment of the HEF1-AurA interaction, or defective post-mitotic spreading, may contribute to activation of p53 and a post-mitotic checkpoint (4). Separately, HEF1 or p130Cas at cilia may coordinate signaling complexes in G₀ cells (5), or in response to external signals (growth reentry, or shearing force, given the hypothetical role of Cas proteins as stretch sensors, may trigger AurA activity, leading to ciliary disassembly (6). Proteins with which Cas or AurA have been shown to functionally associate relevant to these models are noted in blue.

Reciprocally, the plane and symmetry of mitotic division leads to the segregation of proteins that reinforce and extend polarity signals. AurA has been shown to be required for this latter process. In *C. elegans*, depletion of AurA (*air-1*) causes defective segregation of P-granules and the protein Pie-1, indicating loss of mitotic asymmetry.¹¹⁷ In *Drosophila*, flies with mutated AurA are unable to properly segregate the cell fate determinant Numb, with Numb distributed around the cell cortex instead of polarized in one daughter cell.¹¹⁸ The polarity machinery (Dlg, Pins, Bazooka/Par3, and aPKC) also specifies asymmetric Numb localization; how AurA signals might interact with this machinery is not clear. A possible role for AurA in governing localization of proteins to focal adhesions or adherens junctions in higher eukaryotes has never been investigated to our knowledge, although intriguingly, our data suggest that mutation of the AurA phosphorylation site on HEF1 influences the ability of HEF1 to return to focal adhesions at the end of mitosis (results not shown).

As noted above, centrosomes give rise to basal bodies in non-proliferating cells, and a number of proteins are shared between centrosome, basal body, and cilia (or flagella, in lower eukaryotes). Bolstering the idea of focal adhesion/centrosome cross-signaling, some recent studies have established relationships between Aurora, Cas proteins, Pak and these additional structures. In the algae *Chlamydomonas*, the AurA ortholog (CALK) is essential for the regulation of flagellar disassembly.¹¹⁹ CALK itself is phosphorylated (presumably affecting its activity) in response to an array of stimuli normally promoting flagellar

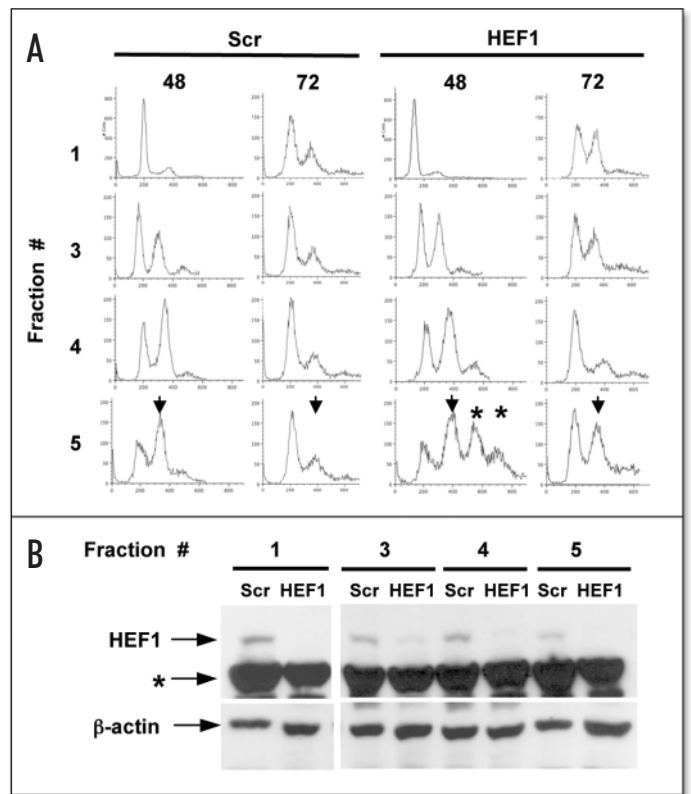


Figure 3. Depletion of HEF1 causes transient aneuploidy. (A) 10⁹ MCF7 cells treated with control nonspecific siRNA duplex (Scr) or HEF1-specific siRNA for 48 h were elutriated to separate cell cycle fractions using a Beckman J elutriating centrifuge. The FACS profiles of representative fractions across the gradient are shown (48 hours): in parallel, an aliquot of each fraction of the elutriated cells was replated, grown for an additional 24 hours, and then reassayed by FACS (72 hours). Arrows in fraction 5 indicate 4N DNA peaks; asterisks represent peaks of >4N DNA content, present at 48 hours but absent at 72 hours after siRNA treatment. (B) Western blot analysis of fractions shown in A after elutriation (time 48 hours). siRNA to HEF1 depletes HEF1 by 75-90% versus Scr control (based on NIH Image analysis of scanned films). Asterisk marks a nonspecific cross-reacting band, which serves as one loading control: additionally, blots were stripped and reprobed with antibody to β -actin.

resorption. The identity of the proteins transmitting resorption signals to CALK is not known.¹¹⁹ Nephrocystin and polycystins are proteins that are evolutionarily conserved, cilia-associated proteins that are abundant in renal cells in mammals. Mutations in these proteins are associated with a variety of polycystic kidney disorders;^{120,121} studies of their orthologs in lower eukaryotes such as *C. elegans* indicate the defects may involve sensing or response of external chemical or physical signals.^{121,122} p130Cas has been identified as an interactor for cilia-associated proteins, including nephrocystin^{121,122} and polycystin-1,¹²³ providing functional coupling between the cilium and proteins including FAK, paxillin, and other focal adhesion components.^{122,123} HEF1 mRNA is particularly abundant in kidney tissue:⁷¹ specific localization of HEF1 to cilia, and in renal cells, is currently under investigation. An exciting recent study has also implicated specific Pak kinase activity at the cilium in quiescent cells, where it has been proposed to contribute to environmental sensing and tissue homeostasis.²⁴ The fact that these recent studies have established relationships between Aurora, Cas proteins,

and Pak and these additional centrosome-related structures further buttresses the idea of focal adhesion to centrosome (to cilia?) cross-signaling,

It has long been known that loss of cell attachment induces defective cytokinesis, and arrest in early G_1 .^{124,125} As described above, AurA hyperactivation or overexpression promotes defective cytokinesis, and influences the activity of p53, with some studies finding that inactivation of the p53 checkpoint is necessary to promote AurA-dependent cell transformation. Like AurA, HEF1 overexpression and depletion induce M phase defects.³ We have begun to investigate interactions between HEF1 and the post-mitotic checkpoint machinery. As shown in Figure 3, elutriation of populations of p53-positive MCF7 cells with HEF1 depleted for 48 hours initially reveals a significant fraction of cells have $>4N$ DNA content. However, when these cells are collected, replated, and cell cycle compartmentalization reassayed after 24 hours, the majority of the $>4N$ cells are lost. This implies loss of HEF1 is not able to overcome the post-mitotic checkpoint, and places HEF1 on a signaling pathway relevant to detachment-induced cell cycle arrest or apoptosis. Intriguingly, the HEF1-interacting protein FAK has been shown both to localize to the centrosome,¹²⁶ and to interact directly with p53.¹²⁷ Both HEF1^{3,99} and FAK¹²⁸ are subject to substantial changes in phosphorylation during mitosis. These phosphorylations influence the ability of these proteins to associate with different partners.

Speculatively, HEF1 and associated proteins such as FAK and Pak may act in part as attachment-sensing checkpoint proteins at mitotic entry and exit. Movement of these proteins from the basal cell surface to the centrosome at G_2/M may provide a signal that cells have successfully disassembled focal adhesions, and are ready for mitotic rounding. Later in M phase, the destruction or phosphorylation of these proteins to remove them from the mitotic machinery, and their reinstatement at focal adhesions at cytokinesis may be a licensing event for cell reattachment and progression through G_1 phase. On the other hand, it is also well-established that Cas proteins and FAK influence G_1 progression by other means, exclusive of dialog with the checkpoint machinery: for example, FAK regulates cyclin D1 expression,¹²⁹ as do small GTPases and Cas effectors such as Rac;^{130,131} while Cas proteins positively regulate serum response proliferation signals.⁸⁹ Separating the various threads connecting AurA and Cas proteins to the control of cell division will take some time.

CONCLUSIONS AND FUTURE QUESTIONS

Characterization of proteins at the intersection of attachment, mitotic, and checkpoint signaling might be expected to offer important insights into cancer development, given that the deregulation of such proteins might simultaneously promote not only metastasis and tumor cell survival, but also genomic instability. Intriguingly, a recent study mutating genes associated with asymmetric cell division in *Drosophila* neuroblasts demonstrated that loss of Pins, Numb, and others resulted in the creation of tumors with some properties of stem cells, characterized by genome instability and centrosome alterations.¹³² In higher eukaryotes, it is difficult to track the genetic and epigenetic changes associated with tumor cell initiation, because by the time tumors have become large enough to detect, additional changes may have occurred. At present, the relationship of the status of AurA and human cancer initiation is complicated, with some studies identifying overexpression of AurA in large tumors, and others showing it as an event in early tumors, subsequently selected against

(also see discussion in ref. 133): for AurA and other proteins such as p130Cas, HEF1, and associated factors, more investigation is required.

A fundamental question arising from these many converging studies is the relationship between the cell asymmetry control machinery and the etiology of most human cancers. Suggestively, a significant number of the asymmetry control proteins are almost by definition exclusively or predominantly expressed in polarized cell types, such as epithelial or neuronal cells. This may contribute to the predisposition of such cells (rather than nonpolarized fibroblast or stromal cells) to form solid tumors, based on their possession of an apparatus that connects more vital cell processes. In the past several years, studies of the growth of cultured cells in more natural three-dimensional matrix environments has begun to reveal unexpected convergence between polarization cues and many cancer-related signaling processes, that differ from previous findings made in cells grown by traditional culture in two-dimensions.¹³⁴⁻¹³⁶ Extension of these studies to include analysis of mitotic processes is likely to tie together the sequence and interdependence of events leading to tumorigenesis.

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