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Cell cycle kinases in cancer

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Cell division in mammalian cells is driven by protein kinases that regulate progression through the various phases of the cell cycle. Cyclin-dependent kinases (Cdks) regulate cell cycle commitment, DNA synthesis and the onset of mitosis. Kinases of the Aurora, Polo and Nek families participate in the centrosome cycle and modulate spindle function. Additional kinases such as Bub1, BubR1 and Mps1 regulate the spindle assembly checkpoint. It has been well established that misregulation of Cdks is one of the most frequent alterations in human cancer. Recent evidence indicates that mutations involving mitotic kinases are also linked to tumor development. These findings suggest novel strategies to use cell cycle kinases as targets for therapeutic intervention.

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Introduction

To date, about 300 genes have been found to be mutated in at least one type of human cancer [1]. Many additional genes are likely to participate in tumor development by mechanisms that involve changes in expression levels (e.g. epigenetic silencing, transcriptional activation and microRNAs) or in their pattern of expression (e.g. ectopic expression and developmental misregulation). Unfortunately, only a limited number of ‘cancer genes’ encode drugable targets — targets for which suitable drugs can be generated. Among them, protein and lipid kinases provide some of the most suitable targets for small molecule inhibitors. The success of the breakpoint cluster region–Abelson (BCR–ABL) kinase inhibitor imatinib (known as Gleevec[®]) in the treatment of chronic myelogenous leukemia has provided the necessary ‘proof of principle’ for the use of kinase inhibitors in a clinical setting. Although kinases are implicated in most ‘cancer pathways’, the cell cycle has attracted special attention, given

the direct relevance of cell proliferation to tumor development [2,3]. Accumulated evidence indicates that misregulation of cell cycle kinases might result in at least two cancer-associated defects: unscheduled proliferation and aberrant cell division leading to genomic instability. Here, we review recent findings on the involvement of several cell cycle kinases in these cancer pathways, along with current efforts aimed at designing novel therapeutic strategies to combat human cancer.

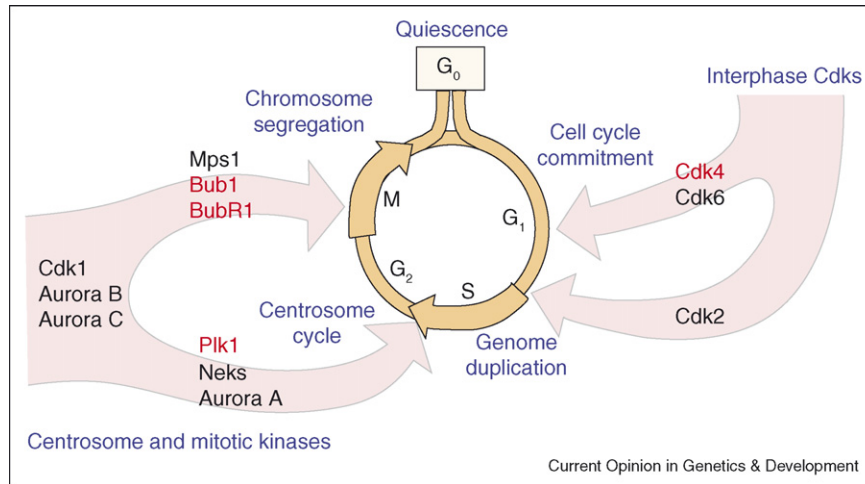
Cyclin-dependent kinases: controlling unscheduled proliferation of cancer cells

Cyclin-dependent kinases (Cdks) are heterodimeric protein kinases composed of a catalytic subunit known as Cdk and a regulatory subunit known as Cyclin. The mammalian genome has twelve loci encoding Cdks, although only five of them, *Cdk1*, *Cdk2*, *Cdk3*, *Cdk4* and *Cdk6* have been directly implicated in driving the cell cycle (Figure 1) [4,5]. Whereas Cdk1 is generally considered to be a mitotic kinase (see below), the other Cdks are believed to play a role in the early phases of cell division (interphase) [4]. To date, only *Cdk4* has been found mutated in human cancer, albeit only in a few cases of hereditary melanoma. In addition, *Cdk6* overexpression has also been documented in lymphomas, leukemias and melanomas as a consequence of chromosomal translocations [4]. However, a significant fraction of human cancers carry mutations that result in misregulation of Cdk activity. They include overexpression of their cognate Cyclins and inactivation of Cdk inhibitors, including members of the INK4 (Inhibitor of kinase 4) and Cip/Kip families. This information has been previously reviewed [2,4] and will not be further discussed here.

Cdks as targets for therapeutic intervention

The drugable nature of kinases in general, along with the frequent misregulation of Cdk activity in human cancer has led to intensive efforts to develop selective Cdk inhibitors. To date, none of them have successfully completed the early phases of clinical development, mainly due to toxic effects [3]. Yet recent genetic evidence suggests that at least some Cdks might be suitable targets for therapeutic intervention, at least in those tumors overexpressing D-type Cyclins. Ablation of Cyclin D1, one of the activating partners of Cdk4 and Cdk6, conferred resistance to mammary carcinogenesis induced by certain oncogenes such as Ras and ErbB2 [6]. Given that Cyclin D1 is essential for proper mammary gland development, the resistance of these mice to breast tumors could be due to a developmental defect rather than a lack of Cdk4 and Cdk6 activity. More recently, however, it has been shown that mice expressing a Cyclin

Figure 1



Main cell cycle kinases and their involvement in cell cycle progression. Kinases mutated in human cancer are shown in red.

D1 mutant that binds, but does not activate, Cdk4 or Cdk6 are resistant to breast cancer initiated by ErbB2, in spite of having normal mammary gland development (Table 1) [7^{**}]. Similarly, *Cdk4* null mice, which display minor defects in normal mammary gland development, are also resistant to ErbB2-driven breast tumors (Table 1) [8^{**},9^{**}]. These results strongly support the concept that Cdk4 and/or Cdk6 kinases might be relevant targets for therapeutic intervention, at least for breast cancers over-expressing *HER2*, the human homologue of *ErbB2* [10]. Another common defect observed in human tumors is loss or severe reduction in p27Kip1 protein levels, a defect linked to poor tumor prognosis [2]. p27Kip1 is a member of the Cip/Kip family of cell cycle inhibitors assumed to block cell division by directly interacting with Cdk2–CyclinE and Cdk2–CyclinA complexes, an interaction that results in inhibition of their kinase activity. Thus, it has been widely assumed that blocking Cdk2 activity with selective inhibitors should provide a therapeutic benefit. Unfortunately, ablation of Cdk2 in *p27Kip1* knockout mice has no effect on either tumor incidence or latency (Table 1) [11[•],12[•]], thus raising doubts about the efficacy of this potential therapeutic strategy.

Mitotic kinases: protecting cells from chromosome aberrations

Aneuploidy is a landmark of many human cancers [13]. Recent evidence indicates that proper chromosome segregation is tightly controlled by mitotic kinases such as Cdk1 (also known as Cell division cycle 2 [Cdc2]), Polo-like kinases (Plks), and Aurora and Nek kinases (Figure 1). These enzymes are involved in regulating the centrosome cycle and formation of the mitotic spindle. Once the spindle is formed, the proper bipolar attachment of sister chromatids is mediated by the spindle assembly checkpoint (SAC), a signaling pathway that ensures proper connections between kinetochores and spindle microtubules [13]. Alterations in this pathway can result in either mitotic catastrophe that triggers apoptosis or exit from mitosis with aberrant chromosomal distribution. The SAC is controlled by the Bub kinases, Bub1 and BubR1, Aurora B and the kinetochore kinase Mps1 (Monopolar spindle 1), a dual Serine/Threonine and Tyrosine kinase also known as Ttk. Recent biochemical and genetic data have shed light on the role of these protein kinases in cell cycle regulation as well as on their implication in human cancer (Table 2).

Table 1

Genetic approaches for preclinical evaluation of Cdks as therapeutic targets.

Kinase	Model	Phenotype	References
Cdk2	<i>Cdk2</i> ^{-/-} ; <i>p27Kip1</i> ^{-/-}	These mice develop tumors with incidence and latency similar to <i>p27Kip1</i> ^{-/-} mice, suggesting that tumor suppressor function of p27Kip1 is independent of Cdk2	[11 [•] ,12 [•]]
Cdk4	<i>Cdk4</i> ^{-/-} ; <i>MMTV-ErbB2</i>	Resistant to ErbB2-induced breast tumors	[8 ^{**} ,9 ^{**}]
Cdk4/6	<i>Cyclin D1</i> ^{K112E/K112E} ; <i>MMTV-ErbB2</i>	Resistant to ErbB2-induced breast tumors	[7 ^{**}]

Abbreviations: MMTV, mouse mammary tumour virus.

Table 2

Representative mouse tumor models of cell cycle kinases.

Kinase	Model	Phenotype	References
Cdk4	<i>Cdk4</i> ^{R24C/R24C}	Mice expressing an endogenous INK4-insensitive Cdk4 ^{R24C} mutant protein develop a variety of tumor types with complete penetrance after long latency (12–28 months).	[45]
Cdk4	<i>Cdk4</i> ^{R24C/R24C} +DMBA	Mice develop invasive melanoma with properties (S100 expression and progressive loss of melanin) similar to those observed in human patients.	[46]
Cdk4	<i>Cdk4</i> ^{R24C/R24C} ; <i>p27Kip1</i> ^{-/-}	Mice develop aggressive pituitary tumors with short latency (8–10 weeks).	[47]
Aurora A	Aurora A transgenics	Mice develop mammary gland hyperplasia with significant presence of binucleated cells.	[48]
Plk4	<i>Plk4</i> ^{+/-}	Mice develop lung and liver tumors. Wild type allele is retained in tumors.	[28**]
BubR1	<i>Bub1B</i> ^{+/-}	Mice display progeroid syndrome and infertility. They also show increased susceptibility to lung and intestinal neoplasias.	[36**,37**]
BubR1	<i>Bub1B</i> ^{+/-} ; <i>Apc</i> ^{Min/+}	Lower levels of BubR1 increases incidence and aggressiveness of tumors in <i>Apc</i> ^{Min/+} mutant mice.	[49]

Abbreviations: Apc, adenomatous polyposis coli.

Cdk1

Cdk1, when bound to Cyclin A or Cyclin B, promotes centrosome duplication, spindle assembly and chromosome condensation, among other functions [4]. Specific inhibition of Cdk1 before mitosis results in G₂ arrest, whereas inhibition during mitosis provokes a quick exit from mitosis without cytokinesis [14]. Although the role of this kinase during the cell cycle has been extensively analyzed, its implication in tumor development and, hence, as a target for cancer therapy has not been properly evaluated. Yet it is currently assumed that tampering with Cdk1 will result in intolerable toxic effects.

Aurora kinases

Aurora kinases, including Aurora A, B and C, are key regulators of mammalian cell division. Aurora A localizes to centrosomes and spindle poles during mitosis, and its inhibition results in centrosome separation defects [15]. Aurora B, by contrast, is a chromosomal passenger implicated in SAC. The localization of this kinase at the mitotic apparatus varies depending upon the stage of the cell cycle. Aurora C is structurally and functionally related to Aurora B, although its expression is restricted to certain cell lineages [15]. Aurora kinases are essential to ensure error-free cell division, and their overexpression appears to be intimately linked to centrosome amplification, malignant transformation and resistance to microtubule poisons [15,16]. Aurora A phosphorylates tumor suppressors such as p53, thereby modulating their activities [16]. More recently, Aurora A and B have also been shown to cooperate with Ras-mediated cell transformation [17–19]. Inhibition of Aurora A by RNA interference or by small molecule inhibitors results in a monopolar phenotype that prevents chromosome segregation [15,20*]. By contrast, inhibition of Aurora B provokes exit from mitosis without cytokinesis, and loss of viability, suggesting distinct therapeutic values for these two kinases [20*]. Recently, Aurora kinases have been implicated in a gene expression signature for chromosomal instability [21**]. Among the 70 genes represented in this signature, overexpression of TPX2 (Targeting protein for *Xenopus* kinesin-like protein

2), an activator of Aurora A, showed the highest correlation to chromosomal instability. Overexpression of Aurora A is also included in this signature along with other genes encoding mitotic kinases such as Aurora B, Cdk1, Nek2 and Mps1 (see below). Overexpression of these genes correlates with poor clinical outcome in tumors with chromosomal instability [21**]. These observations, taken together, have led to intense efforts to develop Aurora kinase inhibitors, some of which are currently under clinical evaluation [16].

Plk1 and other Polo-like kinases

The best characterized member of the mammalian Polo-like family is Plk1. Plk1 specifically localizes to centrosomes, the spindle midzone and the post-mitotic bridge, and it participates in both mitotic entry and mitotic progression [22,23]. Depletion of *Plk1* by RNA interference results in metaphase arrest and formation of abnormal chromatin structures. Knockdown of *Plk1* also reduces cell survival and elevates drug sensitivity of tumor, but not normal, cells [24,25]. *Plk1* is overexpressed in a broad spectrum of cancer types, and its expression often correlates with poor prognosis. Thus, inhibition of Plk1 kinase activity might represent a promising approach for the development of novel anticancer therapies [23].

The other members of the Plk family, Plk2, Plk3 and Plk4, have been less studied. Plk2 and Plk3 were identified in response to mitogenic stimulation. However, they are possibly involved in other functions such as DNA damage checkpoint response or apoptosis [22]. Indeed, *Plk2* is a target of p53 and participates in the G₂ checkpoint and in modulation of apoptosis. Recently, *Plk2* has been found to be silenced by hypermethylation in B-cell neoplasia, suggesting a tumor suppressor role in this disease [26]. Plk4, the most divergent Plk family member, is involved in centrosome separation and mitotic fidelity [27]. Surprisingly, this kinase appears to be a tumor suppressor, because *Plk4* heterozygous mice develop liver and lung tumors due to high frequency of mitotic errors (Table 2) [28**]. These tumors do not lose the normal

allele, indicating that *Plk4* is haploinsufficient for tumor suppression [28**]. These findings indicate that Plks might have opposite roles in controlling cell division. Thus, therapeutic strategies against Plk1 must be highly selective to avoid those side-effects likely to result from inhibiting other Plks.

NIMA-related kinases

The NIMA (Never-in-mitosis *Aspergillus*)-related kinases (Nek) consist of eleven proteins with limited homology to the NIMA kinase of *Aspergillus nidulans* [29]. Some family members, such as Nek2, Nek6, Nek7 and Nek9, are involved in mitotic progression. Nek1 and Nek8, by contrast, might play a role in cilium formation, because they are mutated in polycystic kidney disease. Finally, Nek1, Nek2 and Nek11 participate in the DNA damage response [29]. Nek2 exhibits the greatest sequence identity to NIMA and is the best known member of the family. Nek2 has been implicated in SAC and in centriole function in cooperation with Plk1 [30,31]. Nek2 protein levels peak during S and G₂ phases, but are degraded by the proteasome after recognition by the anaphase-promoting complex (APC). Interestingly, targeting of Nek2 is independent of the APC adaptor proteins Cdc20 and Frizzled-related 1 (Fzr1), suggesting that degradation of Nek2 is uncoupled to SAC [32*]. Nek2 is overexpressed in a variety of human tumors and might be responsible for the appearance of multiple centrosomes and aneuploidy. Depletion of Nek2 prevents centrosome separation, delays mitosis and results in increased apoptosis, possibly as a result of mitotic errors, suggesting possible therapeutic uses in cancer [30].

The SAC kinases Bub1, BubR1 and Mps1

Bub1 and BubR1 (encoded by the *Bub1B* gene) are involved in the regulation of the chromosome-spindle attachment by SAC [13,33]. They are mutated in several colorectal, lung, breast and hematopoietic malignancies [13]. Biallelic mutations of the *Bub1B* gene have also been found in mosaic variegated aneuploidy syndrome and premature chromatid separation syndrome [34**,35**]. These rare autosomal recessive disorders are characterized by growth retardation, microcephaly and childhood cancer. These mutations result in lost or reduced checkpoint function, suggesting a role for these kinases in protecting from genomic instability. Deletion of *Bub1B* in the mouse germline results in early embryonic lethality. Heterozygous animals display increased chromosome instability accompanied by early aging phenotypes and increased cancer susceptibility (Table 1) [36**,37**]. Knockdown of *BubR1* or inhibition of its kinase activity in human cancer cells results in strong genomic abnormalities, massive chromosome loss and apoptotic cell death in a few cell divisions, suggesting potential therapeutic uses [38].

Mps1 is the mammalian homologue of the yeast Mps1p, a kinase involved in the regulation of APC during SAC [39].

Mps1 is a target of APC that controls Mps1 protein levels during mitosis, suggesting the existence of an Mps1–APC feedback circuit to irreversibly inactivate the SAC during anaphase [40]. Recent results indicate that Mps1 phosphorylates the Bloom syndrome protein Blm, a helicase required for genome stability [41]. Blm phosphorylation by Mps1 primes it for interaction with Plk1, which modulates Blm function. Although no mutations in *MPS1* have been found in human cancer, a hypomorphic Mps1 in zebrafish causes meiotic errors, aneuploidy and developmental defects [42], suggesting a relationship between this kinase and genomic stability. Inhibition of the yeast Mps1p by cincreasein [43*], a novel small molecule inhibitor, causes lethal chromosome mis-segregation only in mutants that display chromosomal instability as a result of defective SAC. An unrelated Mps1 inhibitor, SP600125, previously known as a Jnk (Janus kinase) inhibitor, cooperates with spindle poisons in triggering apoptosis due to aberrant mitotic progression [44*]. These observations have raised the possibility that Mps1, and possibly Bub kinases, can be exploited as cancer targets by selectively killing cancer cells that display chromosomal instability.

Conclusions

Abnormal cell division is one of the hallmarks of cancer cells. Evidence accumulated during the 90s pointed at misregulation of the early phases of the cell cycle as one of the pathways most frequently mutated in human cancer [2]. Many of these mutations result in Cdk misregulation, thus making these targets likely candidates for the development of selective inhibitors. Unfortunately, most current Cdk inhibitors have not been successful in the clinic, mostly owing to undesired side effects. Genetic evidence in mice indicates that interphase Cdks are not essential for the basic cell cycle but for proper homeostasis of specific cell types [4]. These findings are making it possible to genetically interrogate the therapeutic potential of these kinases in animal tumor models. Emerging evidence indicates that, whereas Cdk4 and/or Cdk6 kinase activity might be essential for HER2-driven mammary tumorigenesis, Cdk2 is dispensable for pituitary tumors induced by loss of p27Kip1 [10]. This information should be useful to design more rational therapeutic strategies based on selective targeting of individual Cdks in specific tumor types (Table 1).

Although aneuploidy has for decades been known to be a landmark of cancer cells, it is only recently that mitotic kinases have been implicated in cancer development. Some of these kinases such as Aurora kinases and Plk1 could be direct targets for therapeutic intervention [16,23]. Others, such as Mps1 and Bub, might prove to be novel therapeutic strategies that take advantage of the genetic instability of cancer cells to trigger apoptosis under conditions in which normal cells should not be affected. As discussed above for the Cdks, the success of

these novel therapeutic approaches will require a more detailed interrogation of the role of the mitotic kinases in genetically defined preclinical tumor models.

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