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SUMMARY

The decision to enter mitosis is linked to the activation of cyclin B1-Cdk1. Without cyclin B1-Cdk1, cells are not able to complete the cell cycle by producing two daughter cells in mitosis, but instead continue cycling in the absence of mitosis. In this thesis, we investigated the roles and regulation of cyclin B1-Cdk1 and other factors that critically direct mitosis. We identified the human orthologue of Greatwall kinase, MASTL, as an effector of the positive-feedback loop that activates cyclin B1-Cdk1 in G2 phase (**Chapter 2**). The identification of this kinase provided insight into the regulation of the B55 subunit-associated form of PP2A (PP2A-B55), a *bona fide* Cdk1-opposing phosphatase. MASTL suppresses the antagonizing activity of PP2A through its substrates, Arpp19 and Ensa (**Chapter 2, addendum**) These two closely related proteins belong to the endosulfine family and act as direct inhibitors of PP2A-B55. The inhibition of PP2A-B55 allows for complete phosphorylation of mitotic substrates by cyclin B1-Cdk1. This is also required in a negative feedback loop at mitotic exit: MASTL-dependent PP2A repression supports the efficient degradation of cyclin B1, which is required for Cdk1 inactivation at metaphase (**Chapter 3**). Using a chemical-genetic screen, we further confirmed the necessity of PP2A inhibition for mitosis (**Chapter 4**). We identified potential effectors of Cdk1 that require tight regulation to allow orderly mitotic progression. Our results indicate that the rise in cyclin B1-Cdk1 activity during mitosis is crucial to the formation of identical daughter cells once cells exit mitosis again. Here, we discuss how the main governor of mitosis, Cdk1, coordinates key steps in both entry into as well as exit out of mitosis.

DISCUSSION

A Cell Cycle Without Mitosis: Lessons Learned From Knockout Studies

Unicellular organisms such as yeast have been very useful to study the roles of cell cycle regulators. In particular, they have proven their effectiveness in the analysis of gene deletions due to the ease of creating knockout collections for screening purposes. However, such model systems often do not resemble multicellular organisms due to the lack of complexity. For instance, the cell cycle of yeast is dependent on only a single Cdk that binds to different cyclins in order to direct different steps in the cell cycle (reviewed in Bloom and Cross, 2007). In contrast, mammalian cells use multiple Cdks (Cdk2, Cdk4, and Cdk6) to drive cells through interphase, as well as Cdk1 to proceed through G2 phase and mitosis. Despite their presence, the interphase Cdks are not strictly essential for the cell cycle or mitosis (Berthet et al., 2006; Malumbres et al., 2004; Santamaría et al., 2007). Apparently, in the absence of other Cdks, Cdk1 can bind to all the different mammalian cyclins, and execute, for instance, the phosphorylation of pRb, to modulate the expression of E2F target genes. In absence of the interphase Cdks, however, cell cycle duration is extended, indicating that Cdk1 may not regulate interphase processes with similar efficiencies as the other Cdks. In addition, mouse embryos lacking *CDK2* and *CDK4/6* do not develop to normally sized mice. So, while Cdk1 may compensate for most interphase Cdk functions, it is not able to sustain the complexity of a mature animal. Accordingly, interphase Cdks probably evolved to support the complexity of multicellular organisms.

Genetic studies demonstrated that cell division only occurs when Cdk1 is present (Diril et al., 2012; Itzhaki et al., 1997; Santamaría et al., 2007; Th'ng et al., 1990). In absence of Cdk1, however, all interphase events are still executed. Cells lacking *CDC2* undergo endoreduplication, a cell cycle consisting of the gap phases G1 and G2, separated by an intervening S phase (G1-S-G2) (Figure 1) (reviewed in Edgar and Orr-Weaver, 2001). So, these cells replicate their entire genome in the absence of mitosis, leading to elevation of the DNA content (also known as polyploidization). Endoreduplication can also occur naturally for instance in the salivary glands of flies (resulting in the formation of polytene chromosomes), but also in trophoblast stem cells or mammalian megakaryocytes, the progenitors of blood platelets (Hammond and Laird, 1985; Ullah et al., 2008; reviewed in Ravid et al., 2002).

In many of these cell types, modulation of Cdk activity by the CKIs is thought to contribute to the observed endoreduplication cycles. For instance, the differentiation process of trophoblast stem cells into trophoblast giant cells requires the temporal expression of p57(Kip2) in order to inhibit Cdk1 activity (Ullah et al., 2008). This CKI inhibits Cdk1 during the Gap phases, while its expression is lost upon S phase entry, allowing for Cdk2-directed DNA replication. Interestingly, endoreduplication may also contribute to regeneration of the liver after its partial surgical resection (Diril et al., 2012). Apparently, liver regeneration can be achieved by cell growth, rather than cell division, which is why it is one of the few tissues that can grow in the absence of Cdk1.

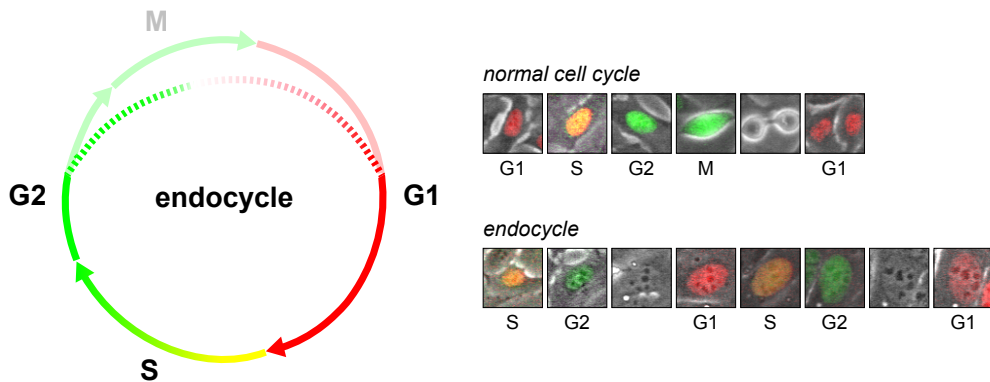


Figure 1 | The Cell Cycle in Absence of Cdk1 Activity

A schematic depiction of the cell cycle in cells lacking Cdk1 activity. Without Cdk1, cells are unable to progress from G2 phase to mitosis. Instead, mitosis is bypassed, leading to so-called endocycles consisting of G1-S-G2-G1 etc. As a result, uncontrolled DNA replication will facilitate cellular polyploidization. The filmstrip shows U2OS cells stably expressing the Fucci system to mark the different cell cycle phases. Control cells degrade the geminin fusion protein (in green) specifically in mitosis, whereas the Cdt1 fusion (in red) is degraded in S phase. Cdk1 inhibition induces DNA endoreduplication, demonstrated by the oscillating behaviour of both Cdt1 and geminin fusion proteins, in the absence of mitosis. See text for details.

An essential molecular component driving endoreduplication is the APC/C, together with its substrate binding co-factor Cdh1. In mitosis, Cdk1 phosphorylates Cdh1 to reduce its affinity for the APC/C (Visintin et al., 1998; Zachariae et al., 1998), and suppression of Cdk1, from the exit of mitosis until the end of G1 phase, promotes the formation of APC/C-Cdh1 complexes. Apart from Cdk1, the Emi1 protein is a very prominent inhibitor of the APC/C: *FBXO5* (the gene that encodes Emi1) depletion by RNAi leads to robust APC/C^{Cdh1} activation, which prevents the onset of mitosis by destroying cyclin A and B (Di Fiore and Pines, 2007; Grosskortenhaus and Sprenger, 2002; Ma et al., 2009; Machida and Dutta, 2007). Subsequent oscillations in APC/C^{Cdh1} activity, due to the E2F-dependent re-accumulation of Emi1 in G1 phase, and loss of Emi1 upon cyclin A and Plk1 activation at the end of G2 phase, explain why Emi1 supports completion of the cell cycle. Depletion of *FBXO5*, which leads to loss of the replication inhibitor geminin, or depletion of *GMNN* itself, causes repetitive S phase cycles, known as DNA re-replication (Machida and Dutta, 2007; Melixetian et al., 2004). DNA re-replication differs from endoreduplication in that cells no longer maintain the temporal separation of both licensing and firing of the origins of replication (reviewed in Porter, 2008). Thus, during re-replication, origins can fire more than once within a single S phase leading to a continuous increase in DNA content. A schematic overview of the molecular components driving the oscillations in APC/C activity, necessary for cell cycle progression is summarized in Figure 2.

Cell cycle-dependent oscillations in APC/C activity can be detected by studying the proteolysis of APC/C substrates, which is also part of the so-called Fucci system. This system uses the APC/C degradation motif of geminin and the SCF degradation motif of Cdt1, fused to a green (mAG) or red (mKO2) fluorescent protein, respectively (Sakaue-Sawano et al.,

2008). Geminin is an APC/C substrate that is effectively destroyed in mitosis (Clijsters et al., 2013). It is initially targeted for degradation by APC/C^{Cdc20}, but also APC/C^{Cdh1} may direct its proteolysis. The MKO2-Cdt1 is a substrate of the SCF^{Skp2}, that operates in S and G2 phases. The APC/C^{Cdh1} regulates the stability of the SCF co-factor Skp2, thereby ensuring the inactivation of SCF^{Skp2} in G1 phase (Wei et al., 2004). As a result, the activities of APC/C^{Cdh1} and SCF^{Skp2} oscillate reciprocally during the cell cycle (reviewed in Vodermaier, 2004) (Figure 1). During genome endoreduplication these oscillations occur without any intervening mitosis. Endoreduplication can be induced by the use of small-molecule Cdk1 inhibitors such as RO-3306 (Vassilev et al., 2006). The development of selective Cdk1 inhibitors has gained access to powerful tools in order to study the temporal regulation of cyclin B1-Cdk1-directed processes. Completely inhibiting Cdk1 prevents mitotic commitment, while its partial inhibition allows entry into mitosis (**Chapter 4**).

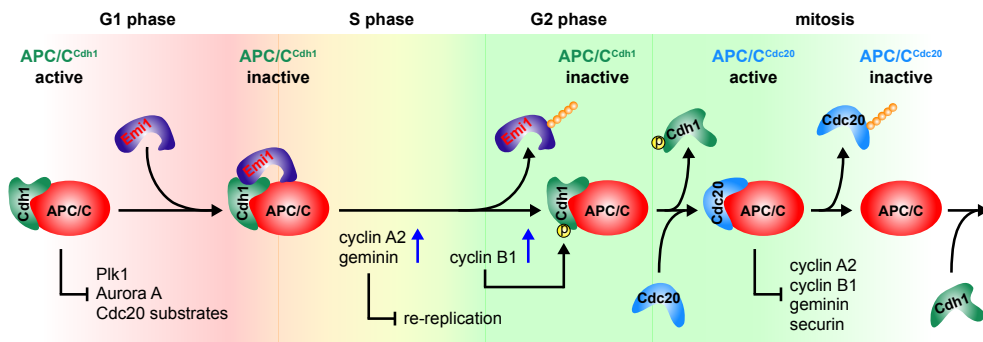


Figure 2 | Oscillations in APC/C Activity Direct Cell Cycle Progression

Schematic working model of how the APC/C controls normal cell cycle progression. In early G1 phase, APC/C^{Cdh1} prevents the accumulation of mitotic cyclins by targeting them for proteasomal destruction. The expression of Emi1 at the end of G1 phase ensures APC/C^{Cdh1} inhibition, which is required to establish Cdk2 activity and drive DNA replication. At this point, the APC/C substrates cyclin A and geminin re-accumulate to suppress re-initiation of S phase. Completion of DNA replication is followed by G2 phase, where cyclin B1 starts to be synthesized. Towards the end of G2 phase, Emi1 is destroyed and subsequent phosphorylation of Cdh1 by cyclin B1-Cdk1 safeguards against unscheduled APC/C activation. In mitosis, Cdc20 takes over from Cdh1, and APC/C^{Cdc20} targets a bunch of substrates including mitotic cyclins, securin, and geminin for degradation. The auto-ubiquitylation of Cdc20, together with the destruction of cyclin B1, allows the activation of APC/C^{Cdh1} complexes, thereby completing the cycle.

Checkpoints in Mitosis

The determinants of mitotic entry have been studied extensively. Especially the use of *in vitro* model systems, such as *Xenopus* egg extracts supported progress in the characterization of mitotic modulators. Cyclin B1, which starts to be expressed at the end of S phase, is a limiting factor for the decision to enter mitosis. Only when a certain threshold level is reached, will cyclin B1 starts to direct the activation of Cdk1 (Solomon et al., 1990). The subsequent activation of the double positive-feedback loop makes entry into mitosis an all-or-nothing response (Pomerening et al., 2003; Sha et al., 2003).

The initiation of mitosis is accompanied by the nuclear translocation of cyclin B1-Cdk1, which depends on the presence of active cyclin B1-Cdk1 (Gavet and Pines, 2010a).

One might assume that a sudden drop in cytoplasmic cyclin B1-Cdk1 could, in principle, cease the continuation of its own activation (Lindqvist et al., 2007). Instead, the activation progressively increases, which is now thought to depend on the inhibition cytoplasmic PP2A-B55 (Álvarez-Fernández et al., 2013; Wang et al., 2013).

Prophase, which basically represents the onset of mitosis, is believed to be reversible, dependent on cellular insults (e.g. microtubule poisons) that threaten the proper inheritance of chromosomes. A checkpoint active in early prophase, known as the antepause checkpoint, is able to pull cells back into G2 phase, resulting in a temporal cell cycle block (Matsusaka and Pines, 2004; Rieder and Cole, 1998; Rieder and Cole, 2000). This checkpoint requires the presence of an E3 ubiquitin ligase called checkpoint with FHA and RING finger domains (CHFR) and active p38 stress kinases (Matsusaka and Pines, 2004; Scolnick and Halazonetis, 2000). How exactly CHFR and p38 contribute to the reversal of mitotic commitment is poorly understood, but they are thought to inhibit the activities of several mitotic kinases including Aurora A, Plk1, and cyclin B1-Cdk1 (Matsusaka and Pines, 2004; Summers et al., 2005). The cytoplasmic sequestration of cyclin B1 is likely to be the key event that delays the onset of mitosis. The negative role of p38 kinases in unperturbed mitotic entry has been demonstrated previously (Cha et al., 2007). Live-cell imaging of synchronised cells allows us to study the effects of different variables in the mitotic entry network. For instance, we also find that inhibition of p38 kinases, using the small-molecule inhibitor SB 203580, speeds up entry into mitosis (Figure 3). As expected, inhibiting the Cdc25 phosphatases significantly impairs entry into mitosis. In line with this, the partial inhibition of Cdk1 using roscovitine noticeably delays the G2-to-M transition. Interestingly, the inhibition of Plk1 using BI 2536 (Lénárt et al., 2007; Steegmaier et al., 2007) also strongly prevents the onset of mitosis. This may be explained by the intimate regulation between Plk1 and Cdk1: Cdk1 promotes the activation of Plk1 (Chan et al., 2008), whereas Plk1 in turn is required for the activation of cyclin B1-Cdk1 (Qian et al., 2001; Toyoshima-Morimoto et al., 2001; Toyoshima-Morimoto et al., 2002). Fully activating cyclin B1-Cdk1 is necessary to promote timely entry into prometaphase.

Cells in prophase can still decide to go back to G2 phase, whereas mitotic progression becomes irreversible after the nuclear envelope breaks down and cells enter prometaphase. Apparently, this decision is dependent on the amount of Cdk1 substrates that is phosphorylated: when Cdk1 substrates approach their peak level of phosphorylation, cells become capable of proper M-to-G1 phase transition (Potapova et al., 2011). This so-called “forward M-to-G1 phase transition” requires active APC/C^{Cdc20} in order to process mitotic substrates and promote mitotic exit. Inhibiting Cdk1 kinase activity in prophase, using 10 μ M flavopiridol, blocks mitotic progression and even reverts cells into G2 phase (Kaur et al., 1992; Potapova et al., 2011). In **Chapter 4**, we describe that Cdk1 inhibition by 3 μ M RO-3306 allows cells to enter mitosis, but subsequently delays spindle checkpoint satisfaction and mitotic exit. The discrepancy between these studies is likely related to the doses of the Cdk inhibitors used. While we found that 3 μ M RO-3306 only partially inhibits Cdk1, a dose

of 10 μM flavopiridol is expected to result in near complete Cdk1 inhibition. Consequently, flavopiridol treatment prevents normal Cdk1 substrate phosphorylation needed to promote mitosis. Partial Cdk1 inhibition only allows limited Cdk1 substrate phosphorylation. Consequently, cells will maintain the mitotic state, but delay in the spindle checkpoint since maximal substrate phosphorylation is needed to promote mitotic progression (Lindqvist et al., 2007). We believe that gradually increasing Cdk1 activity in mitosis, like in meiosis, may function as a timer that supports the stabilization of kinetochore-microtubule interactions (Davydenko et al., 2013). Partially blocking Cdk1 activity will delay the timer and therefore postpone satisfaction of the spindle checkpoint.

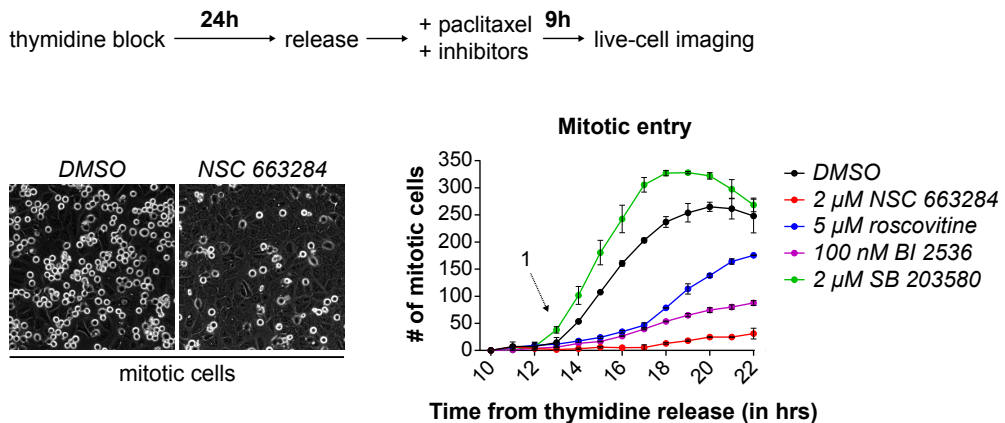


Figure 3 | Monitoring the Effects of Different Effectors on Mitotic Entry
 U2OS cells were synchronised in mitosis as indicated by the experimental setup. Cells were monitored by phase contrast using a wide-field microscope. Representative images demonstrate the presence of mitotic cells after 18 hours of paclitaxel treatment. The arrow (1) indicates the moment that cells start to enter mitosis due to activation of the positive-feedback loop. DMSO, control; NSC 663284, Cdc25A/B/C inhibitor; roscovitine, pan-Cdk inhibitor; BI 2536, Plk1 inhibitor; SB 203580, p38 α / β inhibitor.

The spindle checkpoint is the major checkpoint that halts mitotic progression until all chromosomes are bi-oriented and correctly attached to microtubules. This checkpoint, composed of the molecular components BubR1, Mad2, and Bub3, prevents premature sister chromatid separation and safeguards genomic stability by inhibiting APC/C^{Cdc20} activity (Sudakin et al., 2001; reviewed in Foley and Kapoor, 2013). The spindle checkpoint is gradually satisfied by the establishment of correct attachments (Collin et al., 2013), triggering the metaphase-anaphase transition and segregation of chromosomes to form two identical daughter cells. During anaphase, certain defects may impact the genomic integrity of the newly formed daughter cells. We have shown in **Chapter 4** that lagging chromosomes segregate erroneously and therefore are a cause of genomic instability. When sister chromatid pairs are not separated properly (e.g. due to the presence of catenated DNA persisting between sister chromatids) anaphase bridges may arise that block the process of abscission (**Chapter 2** and **3**). These chromosome bridges form a physical barrier that

maintains Aurora B activity in order to protect cells against tetraploidization (Steigemann et al., 2009). This Aurora B-dependent abscission checkpoint was initially discovered in budding yeast and named NoCut as it prevents chromosome breakage by the cytokinetic machinery (Norden et al., 2006). The NoCut pathway is thought to monitor the clearance of chromatin from the cell equator to ensure completion of cytokinesis only takes place after all chromosomes have migrated to the poles. Recent findings have, however, contradicted the existence of the NoCut pathway, since non-segregating chromosomes rarely inhibit cell division by cleavage furrow regression. Apparently, chromosome arm segregation requires the combined action of Aurora B and the Condensin I complex (Bembenek et al., 2013; Cuylen et al., 2013). Together, these players prevent chromosome breakage once DNA ends up in the cleavage furrow by coordinating the resolution of chromatin obstructions and delaying abscission. The abscission checkpoint is possibly unable to handle gross segregation errors, which may be a cause of DNA damage and structural chromosome aberrations (Janssen et al., 2011). An overview of the checkpoints that coordinate normal cell division are summarized in Figure 4.

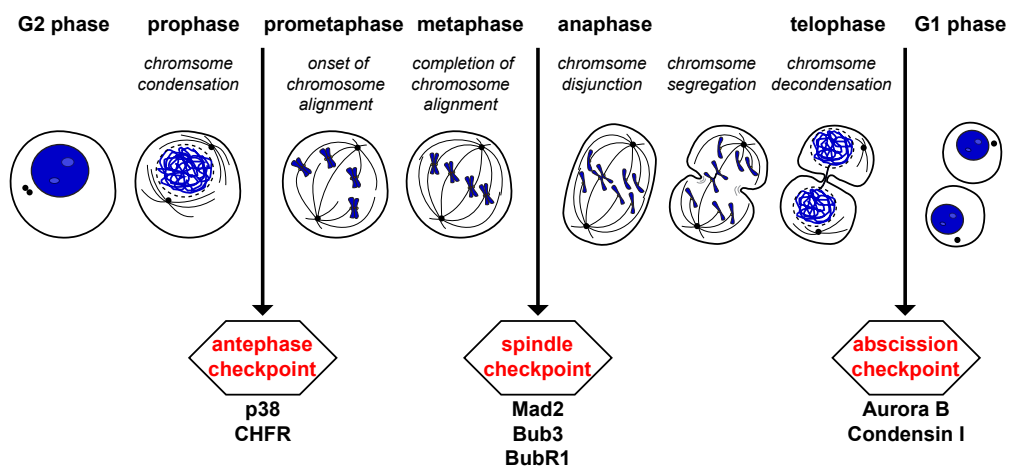


Figure 4 | The Checkpoints That Function in Mitosis

A schematic overview of the checkpoints that regulate transition through the different stages of mitosis. During prophase, the antepause checkpoint, dependent on p38 kinase and CHFR, may prevent mitotic progression as a result of certain exogenous stresses. Subsequently, the spindle checkpoint proteins Mad2, Bub3, and BubR1 ensure that anaphase follows metaphase by correctly attaching each sister chromatid to spindle microtubules. In this example, one sister chromatid pair is not completely separated, leading to the formation of an anaphase bridge. This DNA bridge is sensed by Aurora B, which, together with Condensin I, prevents abscission until the bridge is resolved. This checkpoint safeguards the cellular ploidy, resulting in the formation of two identical daughter cells.

Mitotic Exit: Reversal of Cdk1 Phosphorylation Events

As soon as cells enter mitosis, the activities of Cdk1-antagonizing phosphatases are repressed. In **Chapters 2 and 3** we discussed how MASTL supports cyclin B1-Cdk1 activity by inhibiting PP2A-B55. Also, the activity of PP1, another Cdk1-counteracting phosphatase is, at least in part, regulated by direct cyclin B1-Cdk1 phosphorylation (see **General Introduction**

for more details). How exactly the PP2A-B55 and -B56 phosphatases become active during mitosis is not well understood, but it is thought to involve the inactivation of Cdk1 by APC/C^{Cdc20}-mediated cyclin B1 proteolysis. PP1, which is activated by auto-dephosphorylation (Wu et al., 2009), is thought to stimulate PP2A-B55 activity. Once activated, PP2A-B55 starts dephosphorylating cyclin B1-Cdk1 substrates. MASTL is one of these substrates and is dephosphorylated at the essential Cdk1 site Thr¹⁹⁴ (Blake-Hodek et al., 2012; Hégarat et al., 2014). As a result, MASTL activity is blocked by PP2A-B55. Interestingly, another phosphatase called Fcp1 is responsible for dephosphorylation of Arpp19 and Ensa (Hégarat et al., 2014). Fcp1 activity is controlled in a proteasome-dependent manner, but the exact mode of regulation is still poorly understood. Fcp1 may become active before PP2A-B55 in order to dephosphorylate Arpp19 and Ensa. Subsequently, PP2A-B55 is relieved from its inhibitors and may mediate the dephosphorylation of MASTL and other crucial cyclin B1-Cdk1 substrates.

The activation state of PP2A-B56 is controlled by a small inhibitory protein, in a way similar to that of PP2A-B55 complexes. This inhibitory protein, termed Biorientation defective 1 (Bod1), directly binds B56 thereby suppressing the phosphatase activity of PP2A-B56 (Porter et al., 2007; Porter et al., 2013). The underlying mechanisms that mediate Bod1 control over PP2A-B56 are unknown, but it is believed that Bod1 is activated by cyclin B1-Cdk1. The crucial Thr⁹⁵ residue is probably a Cdk1 target, which, upon phosphorylation, converts Bod1 into a potent PP2A-B56 inhibitor (Porter et al., 2013). The declining cyclin B1 levels later in mitosis permit the PP1-mediated activation of PP2A-B55, which in turn promotes the dephosphorylation and activation of PP2A-B56 (Grallert et al., 2014). PP2A-B56 activity is thought to promote spindle checkpoint silencing (Espert et al., 2014). Direct substrates of PP2A-B56 are KNL1, a target of the checkpoint kinase Mps1, and probably also other kinetochore proteins. Altogether, the joint action of multiple phosphatases including at least Fcp1, PP1, PP2A-B55 and PP2A-B56, reverses most mitotic phosphorylations in order to promote exit from mitosis.

Cancer Mutations in the Cyclin-Cdk Pathway

Genetic alterations in crucial mitotic regulators may contribute to aneuploidy and facilitate tumorigenesis at a later stage. Stable aneuploidy can occur without chromosomal instability (CIN), the gain and loss of whole chromosomes during cell division, whereas the aneuploidy observed in cancer is often caused by CIN (Lengauer et al., 1997). Most alterations, associated with various cancer types, are found in genes involved in the spindle checkpoint, sister chromatid cohesion factors, and centrosome maturation (reviewed in Kops et al., 2005). None of the cancer-related mutations are found in essential genes, such as *CCNB1* or *CDC2*. However, these genes are appear overexpressed in various cancer types as shown by the CIN signature associated with cancer (Carter et al., 2006). This CIN signature consists of 70 genes and 29 of these are considered mitotic regulators according to their function. Interestingly, also the cytokinesis regulators *KIF4* and *PRC1* are included in the signature. Apart from the

CIN signature, negative cell cycle regulators, appear frequently downregulated, rather than overexpressed. For instance, the expression of CKI family members *CDKN2A* (p16), *CDKN2B* (p15), and *CDKN1B* (p27) often is completely lost by epigenetic inactivation (reviewed in Malumbres and Barbacid, 2001).

Many human tumours harbour defective p53 or pRb pathways. Mutations in the tumour suppressor gene *RB1* generally inactivate pRb and are associated with the development of retinoblastoma and other cancers (Lee et al., 1987; reviewed in Weinberg, 1995). The other tumour suppressor gene, *TP53*, is found mutated in more than 50% of human cancers and p53 loss is directly linked to tumorigenesis (Donehower et al., 1992; Hollstein et al., 1991).

Also mutations in genes other than *RB1* and *TP53* have been causally linked to tumour formation. For instance, the gene encoding for the PP2A scaffold (A) subunit, *PPP2R1A* (a gene we also describe in **Chapter 4**), is found mutated particularly in ovarian carcinoma but is also identified in other cancer subtypes (Calin et al., 2000; Jones et al., 2010). Many of the mutations identified are located in regions near the interface between the A subunit and the regulatory B subunit (Shih et al., 2011). These mutations may alter the binding affinity between PP2A A and B subunits and thereby the catalytic activity of the PP2A complex. It is interesting to note that the interaction between A and B subunits is abolished by the small-t (ST) antigen, a protein originating from a DNA tumour virus called simian virus 40 (SV40) (Ruediger et al., 1992; Ruediger et al., 2001; Yang et al., 1991). The ST antigen is a potent oncogene that inhibits PP2A phosphatase activity. Of all PP2A complexes, there are specific subtypes of the B56 family that may act as true tumour suppressors (Chen et al., 2004). Whether or not the oncogenic properties of PP2A inactivation are related to the activity state of cyclin B1-Cdk1 remains enigmatic. Future work may elucidate the key players involved in tumorigenesis and whether targeting mitosis, with particular attention to cyclin B1-Cdk1, may be a rationale for the treatment of PP2A-mutated cancers.

Concluding remarks

In this thesis, we studied the regulators that contribute to cyclin B1-Cdk1 activation in G2 phase and mitosis as well as the factors that are under direct control of Cdk1. We have uncovered the function of the previously uncharacterized kinase MASTL, and provide evidence that this kinase is the functional human orthologue of Greatwall kinase. The work presented sheds light onto the molecular control of mitosis with emphasis on the positive-feedback loop required to activate cyclin B1-Cdk1. In addition, we identified KIF4 and PRC1 as crucial effectors downstream of cyclin B1-Cdk1. Fine-tuning their activity in mitosis is vital for the formation of microtubule attachments to chromosomes, resulting in the division of equal sets of chromosomes over the newly formed daughter cells. It will be important to gain insight into the substrates whose phosphoregulation confers control of cyclin B1-Cdk1 over the spindle checkpoint and the stability of kinetochore-microtubule attachments. Future work should therefore be directed at identifying the key molecular events that drive spindle checkpoint satisfaction.

We believe our work highlights the importance of proper cyclin B1-Cdk1 activation in the execution of cell division. Any perturbation in this process could affect genome integrity, having disastrous consequences for successive cell cycle events. Our work may help to revisit the use Cdk1 inhibitors in the clinic, starting with the identification of biomarkers that sensitize cells to Cdk1 inhibition. The documentation of these biomarkers will be essential in order to predict tumor responsiveness to Cdk1 inhibitory strategies.

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