

G₁ control in mammalian cells

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SUMMARY

Cyclin-dependent kinases (Cdks) control the major cell cycle transitions in eukaryotic cells. On the basis of a variety of experiments where cyclin function either is impaired or enhanced, D-type cyclins as well as cyclins E and A have been linked to G₁ and G₁/S phase roles in mammalian cells. We therefore sought to determine if agents that block the G₁/S phase transition do so at the level of regulating the Cdk activities associated with these cyclins. A variety of conditions that lead to G₁ arrest were found to correlate with accumulation of G₁-specific Cdk inhibitors, including treatment of fibroblasts with ionizing

radiation, treatment of epithelial cells with TGF- β , treatment of HeLa cells with the drug lovastatin, and removal of essential growth factors from a variety of different cell types. Mechanistically, inhibition of Cdks was found to involve the stoichiometric binding of Cdk inhibitor proteins. p21^{Waf1/Cip1} was associated with DNA damage induced arrest while p27^{Kip1}/p28^{Ick1} accumulated under a variety of antiproliferative conditions.

Key words: cell cycle, G₁, cyclin, Cdk

INTRODUCTION

Understanding of the eukaryotic cell cycle has been revolutionized by the discovery that all of the major regulatory points are controlled by a class of protein kinases known as cyclin-dependent kinases, or Cdks (for reviews see Sherr, 1993; Reed, 1992; Pines and Hunter, 1991). The functional paradigm of these kinases is that they are composed of a catalytic subunit that has no intrinsic activity and a requisite positive regulatory subunit known as a cyclin. In simple eukaryotic organisms such as yeast, a single Cdk catalytic subunit interacts with numerous different classes of cyclin to mediate diverse cell cycle phase transitions. In mammalian cells, the regulatory environment is complicated by the presence of multiple Cdks (Meyerson et al., 1992) as well as cyclins (Xiong and Beach, 1991; Lew and Reed, 1992). It has been our goal to elucidate the roles of these kinases and cyclins in the regulation of the G₁ to S phase transition.

RESULTS AND DISCUSSION

G₁ cyclins

A number of lines of evidence implicate three types of cyclin in G₁ and S phase functions. Cyclins D1 and E were identified on the basis of their ability to rescue a deficiency of G₁ cyclin function in the simple eukaryote yeast (Lew et al., 1991; Xiong et al., 1991; Koff et al., 1991). At the same time, the cyclin D1 cDNA was isolated on the basis of the growth factor inducibility of the corresponding mRNA (Matsushime et al., 1991) and because of its location at a chromosomal breakpoint associated with malignancy (Motokura et al., 1991; Withers et al., 1991).

After the identification of cyclin D1, two other closely related cyclins, D2 and D3, were identified on the basis of their homology to cyclin D1 (Matsushime et al., 1991). Patterns of expression suggested that cyclins D and E were associated with G₁ and/or G₁/S phase functions (Dulic et al., 1992; Koff et al., 1992; Baldin et al., 1993; Won et al., 1992). Finally, cyclin A, shown to accumulate beginning at the G₁/S phase boundary, was suggested to have a potential role during S phase (Pines and Hunter, 1990).

Several lines of evidence confirm G₁ or G₁/S phase roles for these three classes of cyclin. Antibody microinjection experiments using IgGs specific for cyclins A and D1 have demonstrated that these cyclins are required for initiation or progression through S phase (Girard et al., 1991; Pagano et al., 1992; Zindy et al., 1992; Baldin et al., 1993; Quelle et al., 1993). Similar experiments using cyclin E-specific antibodies have been unsuccessful, possibly for technical reasons (G. Mondesert and S. Reed, unpublished). However, cyclin E has been shown to be essential for entry into S phase in *Drosophila* (Knoblich et al., 1994), suggesting an essential S phase initiation function in mammalian cells as well. Conversely, constitutive expression of these three cyclins can lead to premature entry into S phase, suggesting that they control functions that are rate-limiting for passage through G₁ into S phase (Ohtsubo and Roberts, 1993; Quelle et al., 1993; Resnitzky et al., 1994; D. Resnitzky and S. Reed, unpublished; Table 1). However, expression of no cyclin alone appears to be able to advance the G₁/S phase to the degree that G₁ can be eliminated. This suggests either that several individual rate-limiting transitions within G₁ are controlled by different cyclins or that compartments exist within the G₁ interval that cannot be influenced by the action of cyclin-dependent kinases.

Table 1. Effect of cyclin E and cyclin D1 on asynchronous cells versus cells emerging from quiescence

Clone	% G ₁ in asynchronous populations		Length of G ₁ in asynchronous populations (h)		Decrease in length of G ₁ in asynchronous populations (h)	Decrease in length of G ₀ /G ₁ after serum starvation/stimulation (h)
	+tet	-tet	+tet	-tet		
D5	48.4	41.8	6.78	5.85	0.93±0.17	4.7±0.7
D3	44.1	39.9	6.17	5.58	0.53±0.11	3.1±1.1
E2	52.2	39.9	7.31	5.59	1.72±0.04	2.5±0.9
E19	49.2	36.9	6.89	5.17	1.72±0.18	1.7±0.7

The percentage of G₁ cells in asynchronous populations was determined by flow cytometric analysis and was used with the population doubling time to determine the length of the G₁ phase. The relative lengths of G₀/G₁ in populations emerging from quiescence was determined by direct measurement using flow cytometric analysis to monitor entry into S phase. In all experiments, comparisons were based on cultures growing in the presence of tetracycline (cyclins repressed) versus in the absence of tetracycline (cyclins repressed) (Resnitzky et al., 1994). Clones D5 and D3 are Rat1 fibroblasts expressing human cyclin D1 and clones E2 and E19 express human cyclin E.

It is of interest to note that whereas constitutive expression of cyclins D1 and E have a more profound effect on advance of S phase in cells emerging from quiescence as compared to cycling cells, expression of cyclin E confers an equivalent S phase advance in either circumstance, suggesting participation in distinct pathways (Resnitzky et al., 1994; Table 1).

Finally, with the demonstration that mammalian cells contain a number of different Cdk catalytic subunits, it was important to establish which combinations of G₁ cyclins and catalytic subunits contribute to the activities described above. Although a large number of combinatorial possibilities have been detected, the biologically critical complexes for G₁/S-phase functions appear to be cyclins A and E combined with catalytic subunit Cdk2 (Pines and Hunter, 1990; Dulic et al., 1992; Koff et al., 1992) and D type cyclins combined with Cdk4 (Matsushime et al., 1992; see Fig. 1).

Targets of cyclin-dependent kinase action

Of all the potential targets for the G₁ cyclin-dependent kinases, the retinoblastoma susceptibility gene product, pRb is the one most often invoked to explain regulation of the G₁/S phase transition. It is known that pRb inhibits cell cycle progression when in a hypophosphorylated form and that phosphorylation reverses these inhibitory functions (Buchkovich et al., 1989; Chen et al., 1989; DeCaprio et al., 1992; Ludlow et al., 1993; Mihara et al., 1989). A mounting body of evidence suggests that the inhibitory function of pRb is based on the ability of hypophosphorylated pRb to sequester some members of a family of essential transcription factors known together as E2F (Helin et al., 1992; Kaelin et al., 1992; Nevins, 1992). Phosphorylation of pRb is thought to lead to the release of transcription-competent E2F. Furthermore, the *in vivo* phosphorylation sites on pRb correspond to Cdk consensus phosphorylation sites and a variety of Cdk's have been shown to be capable of phosphorylating pRb *in vitro* (Lees et al., 1991; Lin et al., 1991; Kato et al., 1993). The most compelling evidence for an *in vivo* role for Cdk's in pRb phosphorylation comes from experiments in SAOS-2 osteosarcoma cells where ectopic expression of pRb caused G₁ arrest but co-expression of pRb with either cyclin D, E or A did not (Hinds et al., 1992; Ewen et al., 1993). It could be shown that, concomitant with the release from G₁ arrest, pRb became hyperphosphorylated. These data suggest that all of the proposed G₁ and G₁/S phase Cdk activities have the capacity to phosphorylate pRb directly

or to stimulate its phosphorylation by other protein kinases *in vivo*. These experiments have the caveat, however, that both pRb and cyclins are highly overexpressed, perhaps imbuing them with abnormal properties. Therefore the issue of which Cdk's (cyclins and catalytic subunits) actually contribute to pRb phosphorylation under normal cellular growth circumstances remains to be resolved. It is noteworthy that D-type cyclins contain motifs that allow them to bind directly to pRb, presumably facilitating the direction of kinase activity toward this potential substrate (Ewen et al., 1993; Dowdy et al., 1993).

Several other proteins with Rb-like physical properties have been identified. p107 and p130 have structural homology with pRb, can bind viral oncoproteins, as can pRb, and can bind E2F as well (Ewen et al., 1991; Hannon et al., 1993). However the relationship of these proteins to cell cycle control is less well understood than that of pRb. High levels of expression of p107 in some cell types confer G₁ arrest, suggesting an inhibitory role similar to that of pRb (Zhu et al., 1993). The relationship of cell cycle control to sequestration of E2F is less clear. Although p107 and p130 bind E2F, it appears that different isoforms are involved relative to pRb (Lees et al., 1993). The roles of these isoforms have not yet been elucidated nor has the relationship between phosphorylation of p107 and p130 and release of E2F. However, it has been shown that cyclin

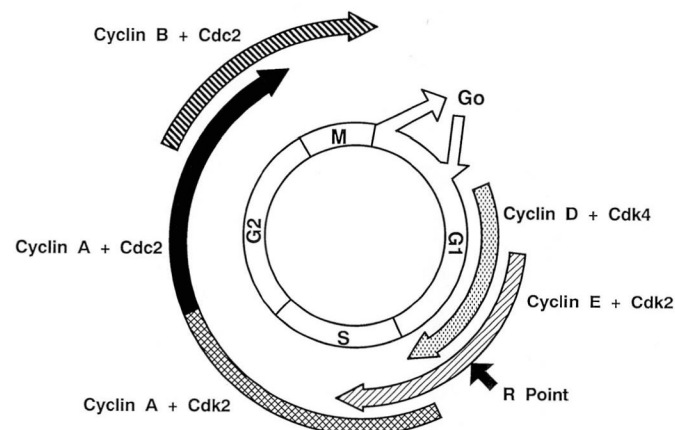


Fig. 1. The roles and temporal participation of various cyclins and cyclin-dependent kinases in the mammalian cell cycle.

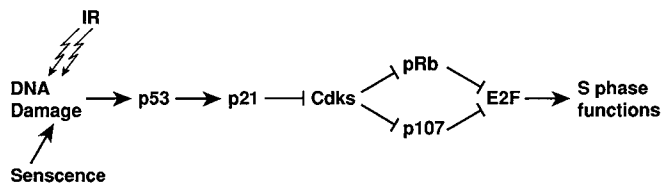


Fig. 2. The functions of p53 and p21 in mediating cell cycle control in response to DNA damage. DNA damage incurred from external sources such as ionizing radiation (IR) or internal sources, such as the transition to senescence, leads to elevation of p53 levels. p53 promotes elevated expression of p21, which in turn inhibits G₁ Cdk. This ultimately has the effect of inhibiting functions essential for S phase, notably the release of E2F isoforms from antagonists such as pRb and p107.

E/Cdk2 is included in p107/E2F complexes in late G₁ and early S phase whereas cyclin A/Cdk2 is in similar complexes during S phase and G₂ (Lees et al., 1992). This suggests a regulatory role for cyclin E and cyclin A in regulation of p107 functions. If p107 functions analogously to pRb, then cyclin E/Cdk2 may control release of E2F isoforms associated with p107 by direct phosphorylation of p107. Other potential targets of G₁ Cdk are proteins directly involved in initiation of DNA replication, such as origin binding proteins. However, these remain to be identified before this idea can be explored.

The Role(s) of Cdk inhibitors

In budding yeast, developmental control of the cell cycle occurs at G₁ and is implemented at the level of controlling G₁-specific Cdk (Reed, 1992). Therefore, investigation of G₁ control in mammalian cells has focused on G₁ Cdk, as well (Sherr, 1993). Several model systems have been explored including the effects of DNA damage (Dulic et al., 1994), negative growth factors (Koff et al., 1993; Polyak et al., 1994; Slingerland et al., 1994), antiproliferative drugs (Hengst et al., 1994) and growth factor deprivation (Dulic et al., 1994; Hengst et al., 1994; Polyak et al., 1994; Slingerland et al., 1994). A common theme has emerged, namely that G₁ control in response to a variety of signals is mediated at the level of proteins that inhibit the kinase activities of Cdk via stoichiometric binding (Dulic et al., 1994; Hengst et al., 1994; Polyak et al., 1994; Slingerland et al., 1994).

When human diploid fibroblasts are synchronized by growth to confluence followed by replating, they can be prevented from entering S phase by high doses of ionizing radiation such as γ -rays (Little and Nagasawa, 1985). Unirradiated cells enter S phase at approximately 18 hours after release from contact inhibition. Cells blocked in G₁ were found to accumulate normal levels of cyclin E and D1 and to form normal levels of cyclin E/Cdk2 and cyclin D1/Cdk4 complexes. However, these complexes were found not to be active (Dulic et al., 1994). It was shown that cyclin/Cdk complexes under these conditions contained a heat stable Cdk inhibitory protein whose presence was dependent on the wild-type status of the tumor suppressor p53. Further investigation indicated that this inhibitor corresponded to p21^{Waf1/Cip1} (El-Deiry et al., 1993; Harper et al., 1993; Xiong et al., 1993; Gu et al., 1993), shown to be a p53-inducible Cdk inhibitor (Dulic et al., 1994). These data establish a p53-dependent signal transduction pathway linking DNA damage to cell cycle control (Fig. 2). The loss of genome

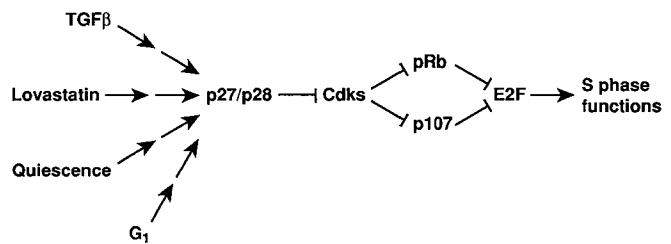


Fig. 3. Mediation of cell cycle control by p27/p28. A variety of conditions, including response to TGF β (epithelial cells), treatment with lovastatin, starvation for serum or contact inhibition, and passage through the G₁ phase of the cell cycle, lead to accumulation of the Cdk inhibitor p27^{Kip1}/p28^{Ick1}. As with p21, this is likely to prevent the release of the essential S phase transcription factor E2F.

stability in response to negation of p53 function is likely to arise from the uncoupling of cell cycle control from DNA damage responses. This is likely to be an important modality in the transition to malignancy. Similar data have been obtained for senescent fibroblasts (Dulic et al., 1993) where DNA damage signals have been invoked to explain the block to proliferation.

The response of epithelial cells to epithelial antiproliferative agent, TGF- β , is phenomenologically similar to the response to DNA damage. In human breast epithelial cells presynchronized by growth factor depletion and refeeding, and then treated with TGF- β , cyclin E accumulates on schedule, associates with Cdk2, but cyclin/Cdk complexes are inactive (Slingerland et al., 1994). Similarly, in the situation with ionizing radiation, a heat stable Cdk inhibitor could be detected in lysates from TGF- β treated cells (Slingerland et al., 1994; E. Bailly and S. Reed, unpublished). However it is unlikely that this inhibitor is p21^{Waf1/Cip1}. Similar studies on mink lung epithelial cells suggest that the inhibitor induced by treatment with TGF- β is a 27/28 kDa protein that is distinct from p21 (Polyak et al., 1994). This protein has been alternately designated p27^{Kip1} and p28^{Ick1}.

p27/p28 accumulates under a number of conditions associated with G₁ arrest of the cell cycle (Fig. 3). HeLa cells treated with the drug lovastatin, which confers G₁ arrest, accumulate p27/p28 in inactive cyclin/Cdk complexes (Hengst et al., 1994). Since p27/p28 is heat stable, it can be released from these complexes by boiling. p27/p28 also accumulates in fibroblasts and epithelial cells deprived of essential growth factors (Hengst et al., 1994). It has also been shown to fluctuate through the cell cycle in proliferating cells, with maximal levels in mid-G₁ (Hengst et al., 1994). Finally, like p21, it has been shown to have the ability to bind and inhibit a broad spectrum of Cdk (Hengst et al., 1994). These data suggest that a variety of conditions that confer G₁ arrest in mammalian cells lead to the production or maintenance of a Cdk inhibitor, p27/p28 that has the capacity to arrest the cell cycle in G₁. In addition, this inhibitor fluctuates through the cell cycle, presumably to prevent premature activation of Cdk during the G₁ interval. Finally, p27/p28 and p21 appear to play complementary roles in cell cycle control mediating the antiproliferative responses associated with distinct signals. In particular, p21 seems to be associated with responses to DNA damage, whereas p27/p28 appears to mediate a more general antiproliferative response.

In summary, the primary motif of cell cycle regulation in G₁ appears to be through the action of cell cycle inhibitory proteins that bind to and inhibit Cdks by a stoichiometric mechanism. This is distinct from control of the G₂/M phase transition, which is mediated primarily at the level of negative phosphorylation of the Cdk1 catalytic subunit (Gould and Nurse, 1989). One possible reason for the prevalence of broad spectrum Cdk inhibitors in G₁ control is that it would allow coordinate control of several distinct Cdks thought to collaborate in progression through G₁ to S phase. It is not yet clear whether p21 and p27/p28 define all of the Cdk inhibitors involved in cell cycle control or whether they are only the first members of a larger family to be identified.

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