Chemical genetic analyses of quantitative changes in Cdk1 activity during the human cell cycle

Polly Gravells, Kazunori Tomita†, Alexander Booth‡, Joshua Poznansky and Andrew C.G. Porter∗

Gene Targeting Group, Centre for Haematology, Imperial College Faculty of Medicine, Hammersmith Hospital Campus, Du Cane Road, London W12 0NN, UK

Received February 13, 2013; Revised and Accepted March 19, 2013

Cyclin-dependent kinase 1 (Cdk1) controls cell proliferation and is inhibited by promising anticancer agents, but its mode of action and the consequences of its inhibition are incompletely understood. Cdk1 promotes S- and M-phases during the cell-cycle but also suppresses endoreduplication, which is associated with poly-ploidy and genome instability. The complexity of Cdk1 regulation has made it difficult to determine whether these different roles require different thresholds of kinase activity and whether the surge of activity as inhibitory phosphates are removed at mitotic onset is essential for cell proliferation. Here, we have used chemical genetics in a human cell line to address these issues. We rescued cells lethally depleted of endogenous Cdk1 with an exogenous Cdk1 conferring sensitivity to one ATP analogue inhibitor (1NMPP1) and resistance to another (RO3306). At no 1NMPP1 concentration was mitosis in rescued clones prevented without also inducing endoreduplication, suggesting that these two key roles for Cdk1 are not simply controlled by different Cdk1 activity thresholds. We also rescued RO3306-resistant clones using exogenous Cdk1 without inhibitory phosphorylation sites, indicating that the mitotic surge of Cdk1 activity is dispensable for cell proliferation. These results suggest that the basic mammalian cycle requires at least some qualitative changes in Cdk1 activity and that quantitative increases in activity need not be rapid. Furthermore, the viability of cells that are unable to undergo rapid Cdk1 activation, and the strong association between endoreduplication and impaired proliferation, may place restrictions on the therapeutic use of a Cdk1 inhibitors.

INTRODUCTION

Cyclin-dependent kinase 1 (Cdk1) is a key cell-cycle regulator that is required for cell proliferation. Small molecules that inhibit Cdk1 are potential anticancer agents (1–5), but their modes of action are unclear, partly because they lack complete specificity but, more importantly, because of our incomplete understanding of the way in which Cdk1 activity controls cell-cycle progression.

Cdk1 has three key roles in the cell cycle: promotion of S- and M-phases, and the suppression of replication origin licensing during G2. Failure of the latter role leads to endoreduplication (consecutive S-phases without an intervening M-phase). To achieve such different roles, Cdk1 must phosphorylate different sets of substrates at different phases of the cell cycle (6,7). In principle, these different sets may respond either to different Cdk1 specificities, achieved by the association of Cdk1 with different cyclins, or to different threshold levels of a single Cdk1 specificity as it rises and falls with each cycle (8). Support for the latter (quantitative) model was recently provided by work in fission yeast showing that a single Cdk1-cyclin combination can fully support cell proliferation (9). Furthermore, using chemical genetics (10), Cdk1 was rendered analogue sensitive (AS; specifically sensitive to the ATP analogue 1NMPP1) by introducing an F80G mutation into its ATP-binding site (9). In this way, varying the concentration of inhibitor experimentally separated the different roles for Cdk1. The extent to which threshold values of Cdk1 activity similarly control the cell cycle in higher eukaryotes remains unclear.

†Present address: Chromosome Maintenance Group, University College London Cancer Institute, Paul O’Gorman Building, 72 Huntley Street, London, WC1E 6DD, UK.
‡Present address: MRC-Laboratory of Molecular Biology, Cambridge CB2 0QH, UK.
∗To whom correspondence should be addressed. Tel: +44 20 83838276; Fax: +44 20 87409679; Email: andy.porter@imperial.ac.uk

© The Author 2013. Published by Oxford University Press. All rights reserved.
For Permissions, please email: journals.permissions@oup.com
In higher eukaryotes, there are multiple Cdk paralogues but, apart from Cdk7, which activates Cdk1 (11,12), Cdk1 is the only Cdk required for viability of cells, or indeed animals (13–15). These results reflect essential roles for Cdk1 in mitosis and suppressing endoreduplication that, in the absence of Cdk1, are not adopted by Cdk2 or any other Cdk parologue. Depletion or inactivation of Cdk1, therefore, prevents mitosis and, in many though not all cell types, promotes endoreduplication (16–18), leading to polyploidy and genome instability (19,20). The role for Cdk1 in promoting S-phase (40). HT2-19 cells, therefore, depend on the inducer IPTG for only Cdk required for viability of cells, or indeed animals becomes essential when Cdk2 is absent. Thus, DT40 chicken has also been conserved, but is shared with Cdk2 and only endoreduplication (16–18), leading to polyploidy and genome vents mitosis and, in many though not all cell types, promotes paralogue. Depletion or inactivation of Cdk1, therefore, pre-absence of Cdk1, are not adopted by Cdk2 or any other Cdk mitosis and suppressing endoreduplication that, in the quantitative model of Cdk1. Cdk1 inactivation in DT40 cells does not cause endoreduplication, however, making DT40 cells unsuitable for assessing how endoreduplication responds to quantitative changes in Cdk1 activity. Inhibition of Cdk1 in other cell types can be achieved by the use of ATP analogues such as RO3306 that preferentially inhibit DT40 cells unsuitable for assessing how endoreduplication results in Cdk1 activity, including the G2/M surge, affect the viability and undergo endoreduplication and apoptosis in its absence (40). To generate 1NMPP1-sensitive cell lines, HT2-19 cells were transfected with plasmids encoding PAC (puromycin N-acetyltransferase) and either wild-type or F80G-mutated *Xenopus laevis* Cdk1 (xCdk1-WT or xCdk1-AS), as previously used in chicken B cells (21). xCdk1-AS, but not xCdk1-WT, rescued HT2-19 cells from IPTG dependence and puromycin sensitivity in a manner that was completely sensitive to 1NMPP1 (Table 1). Several puromycin resistant, IPTG-independent clones were isolated and screened for sensitivity to 10 μM 1NMPP1 in the presence or absence of IPTG. 10 μM 1NMPP1 (Table 2). Because the xCdk1 expression plasmids linked xCdk1-coding DNA to a GFP reporter gene, clones were also screened for GFP as an initial measure of xCdk1 expression. None of the xCdk1-WT-rescued clones (WT1 to WT7) showed sensitivity to 1NMPP1, regardless of GFP expression levels, whereas all xCdk1-AS-rescued clones (AS1 to AS13) were AS in the absence of IPTG. Interestingly, all clones except AS5 expressed detectable levels of GFP and were sensitive to 1NMPP1 even in the presence of IPTG, suggesting that robust expression of xCdk1-AS confers dominant 1NMPP1 sensitivity.

### RESULTS

**Xenopus Cdk1-AS rescues HT2-19 cells and confers 1NMPP1 sensitivity**

In the parental HT2-19 cells used for these studies, one *CDK1* allele is disrupted and the other is repressed by the *lac* repressor (40). HT2-19 cells, therefore, depend on the inducer IPTG for viability and undergo endoreduplication and apoptosis in its absence (40). To generate 1NMPP1-sensitive cell lines, HT2-19 cells were transfected with plasmids encoding PAC (puromycin N-acetyltransferase) and either wild-type or F80G-mutated *Xenopus laevis* Cdk1 (xCdk1-WT or xCdk1-AS), as previously used in chicken B cells (21). xCdk1-AS, but not xCdk1-WT, rescued HT2-19 cells from IPTG dependence and puromycin sensitivity in a manner that was completely sensitive to 1NMPP1 (Table 1). Several puromycin resistant, IPTG-independent clones were isolated and screened for sensitivity to 10 μM 1NMPP1 in the presence or absence of IPTG. Because the xCdk1 expression plasmids linked xCdk1-coding DNA to a GFP reporter gene, clones were also screened for GFP as an initial measure of xCdk1 expression. None of the xCdk1-WT-rescued clones (WT1 to WT7) showed sensitivity to 1NMPP1, regardless of GFP expression levels, whereas all xCdk1-AS-rescued clones (AS1 to AS13) were AS in the absence of IPTG. Interestingly, all clones except AS5 expressed detectable levels of GFP and were sensitive to 1NMPP1 even in the presence of IPTG, suggesting that robust expression of xCdk1-AS confers dominant 1NMPP1 sensitivity.

### Table 1. Complementation of HT2-19 by xCdk1-AS

<table>
<thead>
<tr>
<th>No. of Cells</th>
<th>Selection reagent</th>
<th>Colonies&lt;sup&gt;b&lt;/sup&gt;</th>
<th>Colonies&lt;sup&gt;b&lt;/sup&gt;</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Puromycin</td>
<td>IPTG</td>
<td>1NMPP1</td>
</tr>
<tr>
<td>10&lt;sup&gt;6&lt;/sup&gt;</td>
<td>-</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>10&lt;sup&gt;6&lt;/sup&gt;</td>
<td>+</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>10&lt;sup&gt;6&lt;/sup&gt;</td>
<td>+</td>
<td>+</td>
<td>+</td>
</tr>
</tbody>
</table>

<sup>a</sup>Number of HT2-19 cells electroporated.

<sup>b</sup>Colony numbers (frequencies, normalised with row 1 set at 100%) resulting from transfection with expression plasmids for xCdk1-WT (WT) or xCdk1-AS (AS).

### Table 2. Preliminary analysis of HT2-19 clones rescued by xCdk1-WT or xCdk1-AS

<table>
<thead>
<tr>
<th>Clone&lt;sup&gt;b&lt;/sup&gt;</th>
<th>1NMPP1 sensitivity&lt;sup&gt;a&lt;/sup&gt;</th>
<th>GFP&lt;sup&gt;c&lt;/sup&gt;</th>
<th>Clone&lt;sup&gt;b&lt;/sup&gt;</th>
<th>1NMPP1 sensitivity&lt;sup&gt;a&lt;/sup&gt;</th>
<th>GFP&lt;sup&gt;c&lt;/sup&gt;</th>
</tr>
</thead>
<tbody>
<tr>
<td>WT1</td>
<td>-</td>
<td>++</td>
<td>AS1</td>
<td>+</td>
<td>++</td>
</tr>
<tr>
<td>WT2</td>
<td>-</td>
<td>++</td>
<td>AS2</td>
<td>+</td>
<td>++</td>
</tr>
<tr>
<td>WT3</td>
<td>-</td>
<td>+</td>
<td>AS3</td>
<td>+</td>
<td>NT</td>
</tr>
<tr>
<td>WT4</td>
<td>-</td>
<td>+</td>
<td>AS4</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>WT5</td>
<td>-</td>
<td>+</td>
<td>AS5</td>
<td>+</td>
<td>-</td>
</tr>
<tr>
<td>WT6</td>
<td>-</td>
<td>+</td>
<td>AS6</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>WT7</td>
<td>-</td>
<td>+</td>
<td>AS7</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>AS8</td>
<td>+</td>
<td>+</td>
<td>AS9</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>AS10</td>
<td>+</td>
<td>+</td>
<td>AS10</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>AS11</td>
<td>+</td>
<td>+</td>
<td>AS12</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>AS12</td>
<td>+</td>
<td>+</td>
<td>AS13</td>
<td>+</td>
<td>+</td>
</tr>
</tbody>
</table>

<sup>a</sup>Proliferation judged by phase-contrast microscopy was unaffected (+) or impaired (−) by the addition of 10 μM 1NMPP1 in the presence or absence of IPTG.

<sup>b</sup>WT and AS colonies selected in puromycin but no IPTG after transfection with xCdk1-WT or xCdk1-AS expression constructs, respectively, were analysed.

<sup>c</sup>GFP expression judged by fluorescence microscopy was strong (+ +), detectable (+) or undetectable (−).

NT, not tested.
More detailed analyses of clones AS1, AS4 and AS5 confirmed that all ceased to proliferate and died in response to 1NMPP1 (Fig. 1A), undergoing endoreduplication (Fig. 1B), so phenocopying parental HT2-19 cells deprived of IPTG (40). As expected, an xCdk1-WT-rescued clone (WT1) showed no such response. The dominant effect of xCdk1-AS in clones AS1 and AS4 was also confirmed, IPTG failing to rescue them from 1NMPP1 sensitivity as it did in AS5. Immunoblots with an antibody recognizing both hCdk1 and xCdk1, or an antibody to the myc-tag on xCdk1, confirmed that xCdk1 was less abundant in AS5 than in AS1, AS4 and WT1, but still more abundant than endogenous IPTG-induced hCdk1 (Fig. 2A and B). Flow cytometry and immunoblots with anti-GFP antibody confirmed that relative levels of GFP expression approximated those for xCdk1 expression, although xCdk1 was clearly detectable in AS5 while GFP was not (Fig. 2B and C). Together, these results show that xCdk1-AS can substitute for hCdk1 and confer 1NMPP1 sensitivity, and that such sensitivity is dominant over 1NMPP1-insensitive hCdk1 unless xCdk1-AS is expressed at physiological levels.

Experiments similar to those described in Table 1 and Figure 1 were also carried out using expression vectors for human Cdk1 carrying mutations F80G or F80A (Supplementary Material, Tables S1 and S2), but these yielded clones with only modest sensitivities to ATP analogues (e.g. Supplementary Material, Fig. S1) that were not analysed further.

Cells expressing xCdk1 are resistant to the Cdk1 inhibitor RO3306

As expected from studies in other cell types (17,22), the Cdk1 inhibitor RO3306 induced endoreduplication in parental HT2-19 cells (Fig. 3A). Unexpectedly, however, we found that RO3306 did not induce endoreduplication in AS5 cells (Fig. 3A). Similarly, growth curves showed that AS5 cells, though fully sensitive to 1NMPP1, were resistant to RO3306 (Fig. 3B). Furthermore, WT1 cells were also resistant to RO3306 (Fig. 3B). These results suggest that cellular xCdk1, unlike hCdk1, is resistant to RO3306, at least under the conditions used here. Importantly, they also show that residual hCdk1 in IPTG-independent HT2-19 derivatives, such as AS5, is unnecessary for the rescue of Cdk1-depleted cells by xCdk1.

Titrating 1NMPP1 does not induce stable G2 arrest in AS clones

If the amount of Cdk1 activity required to promote mitosis is greater than the amount required to prevent endoreduplication, it should be possible to find an intermediate concentration of 1NMPP1 that prevents Cdk1 from promoting mitosis while still allowing it to suppress endoreduplication. Under such conditions cells are expected to accumulate in G2 with a 4N DNA content and with no accompanying accumulation of higher ploidies. To test this, we treated xCdk1-AS-rescued clones with a range of 1NMPP1 concentrations and measured the effect on DNA content. Arrest in G2 without endoreduplication will increase the 4N/2N ratio without increasing the 8N/2N ratio. Primary data (Supplementary Material, Fig. S2) were, therefore, analysed to determine the 4N/2N and 8N/2N DNA content ratios (Fig. 4A). In all clones, except the WT1 control, the 4N/2N ratio was increased by treatment with the higher concentrations of 1NMPP1, but this was always accompanied by parallel increases in the 8N/2N ratio, indicating that
no stable G2 arrest occurred. All three AS clones, despite their different doubling times and kinetics of endoreduplication, appeared to have a threshold of \( \approx 100 \text{ nM} 1\text{NMPP1} \), above which endoreduplication was induced. This threshold was not sharp: above it the extent of endoreduplication increased gradually with increasing 1NMPP1 concentrations, while below it low levels of endoreduplication could still be detected at the latest time points. Similarly, increasing 1NMPP1 concentrations between 0 and 310 nM resulted in increasingly delayed impairments to cell proliferation (Fig. 4B). Thus, although a main threshold at \( \approx 100 \text{ nM} 1\text{NMPP1} \) is detectable, reducing the amount of Cdk1 activity appears to reduce the probability of entering mitosis while increasing the probability of undergoing endoreduplication over a wide range of Cdk1 activities.

Rescue of HT2-19 by xCdk1-AS with T14A/Y15F mutations

To test whether inhibitory phosphorylation sites are essential for complementation by xCdk1-AS, T14A and Y15F mutations (AF) were introduced into the xCdk1-AS expression plasmid. When transfected into HT2-19, this construct did not generate IPTG-independent HT2-19 clones (Supplementary Material, Table S2). We reasoned that this might reflect Cdk1AF expression that was too robust, as this is known to promote premature and lethal entry into mitosis (30,33,35). We, therefore, replaced the powerful CMV promoter driving xCdk1 with the human CDK1 promoter region. When HT2-19 cells were transfected with this modified construct, IPTG-independent, puromycin-resistant colonies were obtained in a 1NMPP1-sensitive manner (Table 3). To confirm that their survival was dependent on xCdk1-AS/AF, three of these clones (AS/AF4, 6 and 7) were expanded and treated with 1NMPP1 (Fig. 5). In two clones (AS/AF6 and 7), proliferation was impaired and polyploid cells accumulated. The third clone (AS/AF4) was incompletely sensitive to 1NMPP1, however, suggestive of clonal impurity, possibly due to up-regulation of residual hCdk1 activity in a minority of cells (40). The low frequency of complementation by xCdk1-AS/AF (Table 3) relative to xCdk1-AS (Table 1) suggests that, even when driving xCdk1-AS/AF expression with the CDK1 promoter, only those clones expressing the smallest amounts of xCdk1-AS/AF are viable. Consistent with this, immunoblots showed that xCdk1 was less abundant in xCdk1-AS/AF-rescued clones than in AS5 (Fig. 5C).

In previous work, HT2-19 cells rescued by exogenous hCdk1AF appeared to depend on residual endogenous hCdk1 for viability (39). We were, therefore, interested to know whether the same was true in cells rescued by xCdk1-AS/AF. To test this, we treated AS/AF7 cells with RO3306, in order to inhibit residual endogenous hCdk1 activity, and found that proliferation was unaffected, even though the cells remained sensitive to 1NMPP1 (Fig. 6A). Moreover, when a late passage of clone AS/AF4, which had become largely insensitive to 1NMPP1, was challenged with RO3306, proliferation slowed temporarily and the emerging population showed renewed sensitivity to 1NMPP1 (Fig. 6B). Thus, RO3306 can be used to enrich for xCdk1-rescued cells at the expense of any xCdk1-independent cells. These results suggest that proliferation of mammalian cells does not depend on the ability of Cdk1 to undergo inhibitory phosphorylation of T14 and Y15.
DISCUSSION

Cell-cycle control by Cdk1 is fundamental to eukaryotic biology, and an attractive target for the control of malignant disease (1–5), but it remains incompletely understood. In this study, we have established a chemical genetic system for specifically inhibiting Cdk1 activity in mammalian cells, and have used it to study the effects of quantitative variations in Cdk1 activity and the importance of inhibitory Cdk1 phosphorylation for cell proliferation.

Our system was based on human HT2–19 cells that undergo endoreduplication and apoptosis when endogenous Cdk1 is depleted. These cells displayed a similar phenotype when rescued with a Xenopus-derived, AS Cdk1 (xCdk1-AS) and treated with the ATP analogue 1NMPP1. Thus, while enzyme inhibition and depletion can have different biochemical and phenotypic effects (41,42), this does not appear to be the case for Cdk1. Even when xCdk1-AS was greatly overexpressed (e.g. in clones AS1 and AS4), the same 1NMPP1-induced phenotype was observed, and was dominant over endogenous hCdk1. The same clones grew normally in the absence of 1NMPP1, albeit somewhat slower than parental cells. These results suggest that excess xCdk1 out-competes endogenous Cdk1 for binding to its normal cyclin partners, and has minimal non-physiological interactions with other host proteins.

On the basis of the quantitative model of Cdk1 action, we expected that partial inhibition of Cdk1 might prevent its ability to promote mitosis but not to suppress endoreduplication. Over a range of 1NMPP1 concentrations, however, none was found to prevent mitosis without also inducing endoreduplication. In principle this could be explained if HT2-19 cells endoreduplicate only after entering but failing to complete mitosis, as appears to happen in some cells, including chicken B cells with inhibited Cdk1 (21), and spontaneously endoreduplicating...
Table 3. Complementation of HT2-19 by xCdk1-AS/AF

| No. of cells ×10⁶ | Selection reagent | Colonies b | | | |
|------------------|------------------|------------|---|---|
| Puromycin | IPTG | 1NMPP1 | AS | AS/AF |
| 10⁶ | + | - | 140 (100) | 123 (100) |
| 3 × 10⁶ | + | - | 239 (57) | 12 (3) |
| 3 × 10⁶ | + | - | 0 (0) | 0 (0) |

aNumber of HT2-19 cells electroporated.
bColony numbers (frequencies, normalised with row 1 set at 100%) resulting from transfection with expression plasmids for xCdk1-AS (AS) or xCdk1-AS/AF (AS/AF).

An attractive model to explain the observed link between inhibiting mitosis and inducing endoreduplication can be found by considering the subcellular localization of the only essential Cyclin partners for Cdk1, CyclinA2 and CyclinB1 (13). CyclinA2 is the most likely Cdk1 partner involved in preventing endoreduplication because its nuclear location during G2 (46) allows access to the replication origin licensing factors implicated in mediating the suppression of endoreduplication by Cdk1 (47). In contrast, Cyclin B1 is cytoplasmic during G2 (46), and so prevented, until nuclear membrane breakdown, from acting on the nuclear Cdk1 targets implicated in promoting mitosis. Our results may, therefore, be explained by the co-inhibition of CyclinA2/Cdk1 and CyclinB1/Cdk1 by 1NMPP1, making it impossible to prevent mitosis without also permitting endoreduplication. This model could be qualitative or quantitative in that CyclinA2/Cdk1 and CyclinB1/Cdk1 may have different substrate specificities or similar specificities but different levels of activity. Another possibility is that there are indeed two distinct thresholds, as predicted in the quantitative model, but that cells maintain Cdk1 activity at a level between these thresholds only briefly before a mechanism is activated allowing cyclin degradation without the normal requirement for reaching anaphase. Further chemical genetic studies involving Cdk1-Cyclin fusion proteins and more detailed analyses of cell-cycle kinetics are required to explore these possibilities.

The chemical genetic approach used in this study relied on the unexpected observation that the F80G mutation confers 1NMPP1 sensitivity more effectively in xCdk1 than in hCdk1. We also discovered a further unexpected benefit in using xCdk1, namely that rescued cells are resistant to 0.5 μM RO3306. This may facilitate chemical genetic analyses of Cdk1 in other RO3306-sensitive host cells by avoiding the need to modify host cell CDK1 alleles. The basis of RO3306 resistance in xCdk1-rescued cells requires further investigation, however, given that xCdk1 immunoprecipitated from Xenopus egg extracts is inhibited by 0.5 μM RO3306 (48). This apparent discrepancy could be explained if xCdk1 is more RO3306-resistant when bound to human cyclins than Xenopus cyclins, although a structural basis for this is hard to envisage. Alternatively, differences (e.g. in ATP concentrations) between in vitro assay conditions and the cellular environment may be responsible.

Here, we exploited the RO3306 resistance of xCdk1-rescued cells to clarify the role of inhibitory phosphorylation of Cdk1. Although theoretical models predict that inhibitory phosphorylation of Cdk1 need not be essential for establishing sustained cell-cycle oscillations (49–51), most experimental
evidence has been to the contrary (29–37). Our previous observation that Cdk1-depleted HT2-19 cells could be rescued by a hCdk1AF provided the first experimental evidence in support of a non-essential role for inhibitory phosphorylation (38). Further analysis, nevertheless, suggested that rescue by hCdk1AF was impaired when the small amount of residual endogenous Cdk1 was depleted by RNA interference (39). In the present study, however, rescue of Cdk1-depleted HT2-19 cells by xCdk1-AS/AF was not only sensitive to 1NMPP1 but also resistant to RO3306, indicating that xCdk1-AS/AF is able to support cell proliferation without the assistance of any endogenous Cdk1. The apparent difference in the abilities of hCdk1AF and xCdk1-AS/AF to complement Cdk1-depleted cells may be genuine. Thus, full complementation may only be possible within a narrow window of Cdk1AF expression, and this may be more difficult to achieve with hCdk1AF than with xCdk1-AS/AF. Alternatively, although the siRNA used to deplete residual Cdk1 did not affect hCdk1AF expression (39), it may have impaired proliferation via other off-target effects.

Our results suggest that the basic cell cycle, in mammalian cells as in fission yeast, can support cell proliferation without the need for inhibitory phosphorylation of Cdk1. This conclusion contrasts with previous reports showing that the transient expression of Cdk1AF causes aberrant mitoses (33,37), suggesting that inhibitory phosphorylation is indispensable. Transient expression, however, allows little control over the level of Cdk1AF, which is clearly a key variable in its influence on the cell cycle. Furthermore, transient expression only allows the effects of gene expression to be observed for a limited number of cycles. In contrast, our analysis depends on the stable expression of Cdk1AF at levels that are not only compatible with, but also necessary for, cell viability. The fact that inhibitory phosphorylation is so well conserved presumably reflects its importance in both mediating G2-arrest as a response to DNA damage (52,53) and refining the efficiency of the fundamental Cdk-based cell-cycle oscillator (36). These roles are almost certainly required to ensure genome stability during extensive cell proliferation, and it will be interesting to assess genome stability in clones such as AS/AF7. Given that the first Cdk-based cell cycles to evolve presumably lacked the ability to undergo inhibitory phosphorylation, it is less surprising that such simplified cycles can be effective than that they can still be effective in human cells. The ability of cell proliferation to persist after ablating the mechanism responsible for the late G2 surge in Cdk1 activity suggests again that the potential of therapies based on inhibiting only Cdk1 may be limited.

MATERIALS AND METHODS

Construction of Cdk1 expression plasmids

The key plasmids used in this study are summarized in Table 4.

Human Cdk1 (hCdk1) expression plasmids were as follows. To express hCdk1 and hCdk1-AS a derivative of pBSgptCDK1-WT-HA (39) lacking the haemagglutinin tag was made (pBSgpt/CDC) and oligonucleotide-mediated mutagenesis (QuikChange, Agilent) was used to introduce the F80G (TTT>GGT) mutation, generating pBSgpt/CDC2as. The 6.3 kb BamH1 fragments from pBSgpt/CDC and pBSgpt/CDCas were then cloned into the BamH1 site of pBL-Puro (54) to generate pPuroCDC and pPuroCDCas, respectively. To express hCdk1 with an F80A mutation (hCdk1-AS’), a PCR mutagenesis protocol was used to introduce the F80A
mutation (TTT→GCT) into pPuroCDC, generating pPuroCD-C2as'.

Xenopus laevis Cdk1 (xCdk1) expression plasmids were as follows. The previously described (21) constructs for expressing xCdk1-WT and xCdk1-AS were used initially. These (here named pXICdkWT-mycEGFP and pXICdkAS-mycEGFP) contained Xenopus laevis Cdk1myc cloned into pIRES2-EGFP (Clontech) with or without the F80G mutation (TTT→GCT). To express xCdk1-AS/AF, QuikChange mutagenesis was used to introduce the AF mutation (T14A, ACATAT→CACTTTT) into pXICdkAS-mycEGFP, generating pXICdkASAS/AF-mycEGFP. To allow co-selection for puromycin resistance, these three plasmids were cotransfected with pBL-Puro (54). Alternatively they were modified to carry a puromycin resistance cassette by linearizing at their unique AflII site, end-filling and ligating to a 1.4 kb phosphoarginine transferase; Puro, puromycin N-acetyl-transferase; Neo, aminoglycoside 3'-phosphotransferase) conferring resistance to mycophenolic acid, puromycin and neomycin, respectively.

Table 4. Summary of plasmids

<table>
<thead>
<tr>
<th>Plasmid name</th>
<th>Cdk1 encoded</th>
<th>Pro&lt;sup&gt;a&lt;/sup&gt;</th>
<th>Mark&lt;sup&gt;b&lt;/sup&gt;</th>
<th>Ref</th>
</tr>
</thead>
<tbody>
<tr>
<td>pBL-Puro</td>
<td>–</td>
<td>–</td>
<td>Puro</td>
<td>(54)</td>
</tr>
<tr>
<td>pBSgptCDK1-WT-HA</td>
<td>xCdk1-WT</td>
<td>xCdk1</td>
<td>Gpt</td>
<td>(39)</td>
</tr>
<tr>
<td>pBSgptCDC</td>
<td>xCdk1-WT</td>
<td>xCdk1</td>
<td>Gpt</td>
<td></td>
</tr>
<tr>
<td>pBSgptCDCas</td>
<td>xCdk1-AS</td>
<td>xCdk1</td>
<td>Gpt</td>
<td></td>
</tr>
<tr>
<td>pPuroCDC</td>
<td>xCdk1-WT</td>
<td>xCdk1</td>
<td>Puro</td>
<td></td>
</tr>
<tr>
<td>pPuroCDCas</td>
<td>xCdk1-AS</td>
<td>xCdk1</td>
<td>Puro</td>
<td></td>
</tr>
<tr>
<td>pXICdkWT-mycEGFP</td>
<td>xCdk1-WT</td>
<td>CMV</td>
<td>Neo</td>
<td>(21)</td>
</tr>
<tr>
<td>pXICdkAS-mycEGFP</td>
<td>xCdk1-AS</td>
<td>CMV</td>
<td>Neo</td>
<td></td>
</tr>
<tr>
<td>pXICdkAS/AF-mycEGFP</td>
<td>xCdk1-AS/AF</td>
<td>CMV</td>
<td>Neo</td>
<td></td>
</tr>
<tr>
<td>pXICdkWT-mycEGFP-puro</td>
<td>xCdk1-WT</td>
<td>CMV</td>
<td>Neo, Puro</td>
<td></td>
</tr>
<tr>
<td>pXICdkAS-mycEGFP-puro</td>
<td>xCdk1-AS</td>
<td>CMV</td>
<td>Neo, Puro</td>
<td></td>
</tr>
<tr>
<td>pXICdkAS/AFmycEGFP-puro</td>
<td>xCdk1-AS/AF</td>
<td>CMV</td>
<td>Neo, Puro</td>
<td></td>
</tr>
<tr>
<td>pXICdkAS/AFmycEGFP-puro-HP</td>
<td>xCdk1-AS/AF</td>
<td>hCdk1</td>
<td>Neo</td>
<td></td>
</tr>
</tbody>
</table>

<sup>a</sup>Promoters driving Cdk1 expression: CMV, cytomegalovirus immediate early promoter; hCdk1, promoter region from human CDK1 gene. 
<sup>b</sup>Markers encoding proteins (Gpt, guanosine-hypoxanthine phosphoribosyltransferase; Puro, puromycin N-acetyl-transferase; Neo, aminoglycoside 3'-phosphotransferase) conferring resistance to mycophenolic acid, puromycin and neomycin, respectively.

Stock solutions of 1NMPP1 (Toronto Research Chemicals) and RO3306 (Calbiochem) were dissolved in dimethyl sulphoxide before diluting in medium to the indicated final concentrations.

**Generation of 1NMPP1-sensitive clones**

HT2-19 cells were transfected with 10 μg (unless stated otherwise) of the following plasmids. pXICdkWT-mycEGFP-puro or pXICdkAS-mycIRESeGFP-puro (both linearized with FspI) (Table 1). pXICdkWT-mycEGFP or pXICdkAS-mycIRESeGFP (each cut with PvuII and cotransfected with 1 μg pBL-Puro) (Table 2). Spel-linearized pXICdkAS-mycIRESeGFP-puro or BstB1-cut pXICdkAS/AFmycIRESeGFP-puro-HP (Table 3). SpeI-linearized pPuroCDC or pPuroCDCas (Supplementary Material, Table S1). SpeI-linearized (5 μg) pPuroCD-C1 or pPuroCDCas' (Supplementary Material, Table S2).

**Flow cytometry**

Known numbers of cells, e.g. 25 000, 12 500 and 5000, cells were plated into three wells (2.5 cm diameter) of a 12-well plate, harvested 2, 4 or 7 days later, respectively, and counted in a haemocytometer to determine the number of doublings. Error bars show the average and standard deviations for at least three-independent experiments.

**Western blotting**

Cells were lysed in RIPA buffer (0.75 M NaCl, 5%v/v NP40, 2.5% v/v DOC, 0.5% w/v SDS and 0.25 M Tris, pH8) containing protease inhibitors (Complete; Roche). Samples (40 μg total protein each) were separated on SDS–polyacrylamide gels and transferred to Hybond ECL membranes (Amersham). Membranes were probed overnight with the following antibodies conjugated secondary antibody and further washes, proteins were visualized using ECL reagents (Thermo Scientific) following manufacturers’ instructions.

**SUPPLEMENTARY MATERIAL**

Supplementary Material is available at HMG online.
ACKNOWLEDGEMENTS

We are grateful to Helfrid Hochegger for supplying xCdk1 expression plasmids, and to Simak Ali, William Brown, Helfrid Hochegger and Tim Humphrey for their comments on the manuscript.

Conflict of Interest statement. None declared.

FUNDING

This work was funded by the Biotechnology and Biological Research Council (grant number BB/H003371/1).

REFERENCES