Cyclin E Deregulation Impairs Mitotic Progression through Premature Activation of Cdc25C

Rozita Bagheri-Yarmand, Angela Nanos-Webb, Anna Biernacka, Tuyen Bui, and Khandan Keyomarsi

Abstract

The cyclin E–cyclin-dependent kinase 2 (CDK2) complex accelerates entry into the S phase of the cell cycle and promotes polyploidy, which may contribute to genomic instability in cancer cells. The effect of low molecular weight isoforms of cyclin E (LMW-E) overexpression on mitotic progression and its link to genomic instability were the focus of this study. Here, we show that full-length cyclin E (EL) and LMW-E overexpression impairs the G2-M transition differently by targeting dual-specificity phosphatase Cdc25C activity. We identify Cdc25C as an interaction partner and substrate for cyclin E/CDK2 kinase. Specifically, the cyclin E/CDK2 complex phosphorylates Cdc25C on Ser214, leading to its premature activation, which coincides with higher cyclin B/CDK1 and Polo-like kinase 1 (PLK1) activities in an S-phase–enriched population that result in faster mitotic entry. Whereas EL overexpression leads to hyperactivation of Cdc25C, cyclin B/CDK1, and PLK1 in a G2-M–enriched population, LMW-E overexpression causes premature inactivation of Cdc25C and PLK1, leading to faster mitotic exit. In addition, LMW-E–overexpressing cells showed a reduction in the mitotic index in the presence of a spindle poison and faster degradation of cyclin B, suggesting an increased rate of mitotic slippage and adaptation to the spindle checkpoint. Lastly, downregulation of Cdc25C inhibits LMW-E–mediated chromosome missegregation, anaphase bridges, and centrosome amplification. These results suggest that the high levels of LMW-E isoforms found in breast cancer may contribute to cellular transformation and genomic instability by impairing mitotic progression involving Cdc25C. Cancer Res; 70(12); 5085–95. ©2010 AACR.

Introduction

Cyclin E, a regulatory subunit of cyclin-dependent kinase 2 (CDK2; ref. 1), is critical for entry into the S phase in mammalian cells (2–4). Cyclin E induces histone biosynthesis at the G1-S transition and DNA replication and centrosomal duplication during S phase. However, cyclin E deregulation also has a direct effect on mitosis that leads to genomic instability. When full-length cyclin E is overexpressed through inhibition of proteasome-mediated degradation, high levels of cyclin E–associated kinase activity are found in the G2-M phases (5). Additionally, overexpression of full-length cyclin E in U2OS cells resulted in the accumulation of cells with impaired chromosomal alignment and delayed mitotic progression in prometaphase (6). Full-length cyclin E/CDK2 can phosphorylate and inactivate the mitotic ubiquitin ligase APC/C<sup>Cdh1</sup>, thereby increasing cyclin B accumulation in prometaphase and metaphase (6). The regulation of cyclin B expression and its role in activating CDK1 are crucial for controlling the timing of both entry into and exit from mitosis (7). Before mitosis, cyclin B–CDK1 complexes are kept in an inactive state by phosphorylation of CDK1 at Thr<sup>14</sup> and Tyr<sup>15</sup>, which is catalyzed by the protein kinases Wee1 and Myt1 (reviewed in ref. 8). This complex is dephosphorylated by the dual-specificity protein phosphatase Cdc25C. CDK1 activation, on entry into mitosis, results from simultaneous inhibition of Wee1 and Myt1 and activation of the phosphatase Cdc25C. The phosphorylation of Cdc25C by Polo-like kinase 1 (PLK1) or cyclin B–CDK1 complex is required for its activation, suggesting the presence of a positive feedback loop. Exit from mitosis requires inactivation of cyclin B–CDK1 by APC/C<sup>Cdk20</sup>–targeted proteasomal degradation of cyclin B, which occurs during metaphase–anaphase transition. Any modulation of this finely orchestrated process of activation and inactivation of cyclin B/CDK1 can result in mitotic defects, resulting in altered chromosome segregation and formation of aneuploid cells (9).

In the most aggressive cancers, which metastasize, full-length cyclin E is proteolytically cleaved to its low molecular weight (LMW-E) isoforms from the NH<sub>2</sub>-terminal elastase cleavage of the 50-kDa full-length cyclin E1 (termed EL; refs. 10, 11). The LMW-E isoforms are tumor specific, are predominantly cytoplasmic (12), and have enhanced biochemical...
and biological properties that differ from those of EL. The LMW-E isoforms are resistant to inhibition by the CDK inhibitors p21 and p27 (13, 14). Because both EL and LMW-Es are overexpressed in tumors from breast cancer patients (10), we questioned which phenotype, EL or LMW-E, predominates. We have recently addressed this question (15) by overexpressing both EL and LMW-E in cells and asking which one can take over the phenotype when length of mitosis is the readout. The result revealed that when EL and LMW-E are co-overexpressed, the LMW-E takes over as shown by the genomic instability and shortening of the period between nuclear envelope breakdown and anaphase A compared with EL expression. In this article, we hypothesized that overexpression of either the EL or LMW-E isoforms alters the timing of the M-phase progression (entry and exit) by targeting specific phosphorylation events and upregulating mitotic kinases, leading to polyploidy and genomic instability.

Materials and Methods

Plasmids

Human pEX2T Cdc25C, GST-25(200–256), and GST-25 (200–256) S216A were kindly provided by Yolanda Sanchez (Dartmouth Medical School, Hanover, NH; refs. 15, 16), and human Cdc25C/p-CDK-Myc was kindly provided by Jian Kuang (University of Texas M.D. Anderson Cancer Center, Houston, TX). The QuikChange Site-Directed Mutagenesis kit (Stratagene) was used according to the manufacturer’s instructions with the following oligonucleotides to substitute human Cdc25C Ser216 to Ala: 5′-cctatatcgcgccccgtc-gatcgcagagaac-3′ and 5′-gttctctggcatcgacggggcgcgatatagg-3′.

Cell cultures and transfections

The generation of the EL-inducible and LMW-E-inducible MCF-7 cell lines is described in the accompanying article (15). MRC50 human primary fibroblasts (American Type Culture Collection) derived from normal lung tissue of a 14-week-old male fetus is a normal diploid human cell line with 46,XY karyotype with only a 3.6% rate of polyploidy (12). The antibodies used were as follows: anti-cyclin A, –β-tubulin, and monoclonal anti-Flag (all from Sigma); and polyclonal anti-γ-tubulin (1:1,000; Sigma-Aldrich), rabbit anti-pericentrin (1:500; Abcam); and polyclonal anti-Flag (1:200; BD Pharmingen), and rabbit anti-Cdc25C (1:100; Santa Cruz Biotechnology).

Synchronization, cell cycle analysis, and measurement of mitotic index

To generate synchronized populations, MCF-7 stable pTRE-EL/LMW-E cells were arrested at the G1-S boundary by aphidicolin block (5 μg/mL) for 24 hours. After release, cells were collected, fixed in ice-cold 70% ethanol, and stained with propidium iodide for flow cytometry analysis. These experiments were repeated seven times with each cell line, and results are provided as Western blot analysis (with representative experiments) and flow cytometric and kinase analyses (where the values of all experiments were combined and averaged and statistical analysis on time points showing the significant differences is provided as bar graphs). MRC50 human primary fibroblasts were treated with nocodazole (100 ng/mL), fixed, and stained with propidium iodide for flow cytometry analysis. To measure the mitotic index in live cells, we used HeLa H2B green fluorescent protein (GFP) stable cells (18), which were infected with adenovirus EL or LMW-E for 24 hours and then treated with nocodazole (100 ng/mL) for 16 hours, and mitotic cells were counted microscopically.

RNA interference

Cdc25C protein was depleted using four different small interfering RNA (siRNA) duplex oligonucleotides (Dharmacon Research). siRNA transfections were performed using the X-tremeGENE siRNA transfection reagent (Roche). ON-TARGETplus SMARTpool siRNA Cdc25C oligonucleotides (Dharmacon Research) were made with the following sequences: GAAACUUUGUGGACAGUGA, AGGAAGGCUUAUGUUA, GAGAGAGACACUUCCUUUA, and GGGCAAAUUUCUGUGUGAU. Experiments using siRNAs were harvested at 72 hours after transfection unless otherwise specified.

Immunofluorescence staining

pTRE-EL and pTRE-LMW cells were grown in six-well plates with cover slides, induced or uninduced with doxycycline, and then treated with control siRNA or with Cdc25C siRNA. Immunofluorescence staining was performed as described in the accompanying article (15). Primary antibodies included mouse anti-β-tubulin (1:1,000; Sigma-Aldrich), rabbit anti-γ-tubulin (1:1,000; Sigma-Aldrich), rabbit anti-pericentrin (1:500; Abcam), mouse anti-PLK1 (1:200; BD Pharmingen), and rabbit anti-Cdc25C (1:100; Santa Cruz Biotechnology).

SDS-PAGE electrophoresis, Western blotting, immunoprecipitation, and kinase assay

SDS-PAGE, Western blotting, immunoprecipitation, and kinase assay were performed as previously published (12). The antibodies used were as follows: anti-cyclin A, anti-cyclin E (HE-12), anti-c-Myc, polyclonal anti-cyclin B1, and anti-Cdc25C (all from Santa Cruz Biotechnology); monoclonal anti-β-tubulin, polyclonal and monoclonal anti-γ-tubulin, and monoclonal anti-Flag (all from Sigma); polyclonal anti-pericentrin (Abcam); and polyclonal anti-PLK1 and vinculin (Sigma).

Substrates used for kinase assays were 5 μg of histone H1 (Roche Diagnostics) and α-casein or 10 to 20 μg of glutathione S-transferase (GST)–Cdc25C. Where roscovitine was used, beads were incubated at final step of the kinase assay in reaction buffer plus 80 μmol/L roscovitine at 37°C for 30 minutes.

GST pull-down assay

In vitro transcription and translation of cyclin E constructs (EL and LMW-E) and Cdc25C proteins were performed using the TNT T7 Quick Coupled Transcription/Translation system (Promega) as previously described (19).
Phosphatase activity assay

Cdc25C activity was measured using 3-0-methylfluorescein phosphate (3-OMFP) as described previously (20). Values were corrected for background activity by measuring the activity of GST-Cdc25C lacking its catalytic domain or of lysates immunoprecipitated with IgG antibody. The activity of GST-Cdc25C was used as a positive control.

Statistical analysis

Statistical analyses were performed using GraphPad Prism software with two-way ANOVA or StatsDirect software. All statistical tests were two-sided and were considered to be significant at \( P < 0.05 \).

Results

LMW-E overexpression induces premature activation of Cdc25C and cyclin B/CDK1

To examine the effect of EL and LMW-E overexpression on the progression of cells through mitosis, we measured the expression of key cell cycle proteins and the activity of key mitotic enzymes, including CDK1 and PLK1, in synchronized populations of cells. MCF-7 cells inducibly expressing Flag-tagged EL or LMW-E were synchronized at the G1-S boundary with aphidicolin, induced for 24 hours, and harvested at different time points following release from aphidicolin arrest. Flow cytometric analysis revealed that 10 hours after release from aphidicolin arrest, 20% more EL-overexpressing cells than uninduced cells had accumulated in the G2-M phase of the cell cycle (\( n = 3, P < 0.001 \); Fig. 1A). In contrast, the G2-M population of LMW-E-overexpressing cells was 20% to 30% less than that of uninduced cells 10 to 12 hours after aphidicolin release (Fig. 1B). This occurred concomitantly with an increase in the G1-G2-phase and S-phase populations (Fig. 1B). The EL-overexpressing cells showed no significant change in cyclin B1 expression 10 to 12 hours after aphidicolin release (Fig. 1C), whereas the LMW-E-overexpressing cells showed a 45% to 70% reduction in cyclin B1 levels (Fig. 1D).

Next, we examined whether the activity of cyclin B1/CDK1 is differentially altered by EL versus LMW-E induction using histone H1 as a substrate. The results revealed the premature activation of CDK1 on induction of both EL (30–40% increase) and LMW-E (40–58% increase) 6 to 8 hours after aphidicolin release compared with uninduced cells (Fig. 2A and B). CDK1 activity is regulated by phosphorylation of residues Thr\(^{14}\) and Tyr\(^{15}\) by the Wee1/Myt kinases and by dephosphorylation of these residues by Cdc25C phosphatases (21–23). Thus, we next examined whether the EL-mediated and LMW-E-mediated premature activation of cyclin B/CDK1 was caused by regulation of Cdc25C phosphatase activity. We measured the activity of Cdc25C in aphidicolin-synchronized populations of EL-induced and LMW-E-induced cells using 3-OMFP as a substrate (Fig. 2C). These analyses showed that on induction of EL and LMW-E, the initial burst of Cdc25C activation in the early S phase was larger than that in the uninduced control cells (Fig. 2C). These results coincide with the higher activity of cyclin B/CDK1 in these cells on induction of EL and LMW-E. Specifically, at 10 hours

![Figure 1. Overexpression of EL and LMW-E impairs G2-M transition differently. pTRE-EL (A) and pTRE-LMW-E (B) MCF-7 cells were synchronized at the G1-S transition by aphidicolin block, induced for cyclin E expression with doxycycline (Dox; 1 μg/mL) for 24 h, released for the indicated times, and analyzed by flow cytometry. The graphs show the percentages of cells in the G1, G2-M, and S phases. Columns, percentage of cells in G2-M relative to control cells obtained from seven independent experiments; bars, SD. C and D, representative Western blot analysis of cell lysates described in A and B using specific antibodies against cyclins E, A, and B and vinculin. Changes in cyclin B expression as percentage of control after densitometry of uninduced and induced cells. *, \( P < 0.05 \).](https://cancerres.aacrjournals.org/)
after aphidicolin release in the LMW-E–expressing cells, the Cdc25C activity dropped by 27%, whereas it remained high in the EL-expressing cells. This LMW-E–mediated decrease in Cdc25C activity is consistent with a drop in cyclin B1/CDK1 activity in these cells (Fig. 2B).

Cdc25C is a binding partner and substrate of the cyclin E/CDK2 complex

To understand the mechanism by which EL and LMW-E deregulate Cdc25C activity, we first sought to determine whether there is a functional interaction between Cdc25C and cyclin E. GST pull-down assays revealed that both EL (Fig. 3A, left) and LMW-E (Fig. 3A, right) bind to full-length Cdc25C. We also observed an interaction between both EL and LMW-E and Cdc25A (Fig. 3A), as previously described (24). To confirm these in vitro interactions in an ex vivo setting, we transiently transfected human embryonic kidney 293T cells with Flag-tagged EL or LMW-E and c-Myc-tagged Cdc25C expression constructs and examined complex formation in cell lysates (Fig. 3B). Both EL and LMW-E formed immune complexes with Cdc25C, but the EL/Cdc25C complexes were more abundant than LMW-E/Cdc25C complexes (Fig. 3B, right). In addition, Western blot analysis showed that Cdc25C from LMW-E–overexpressing cells migrated more slowly 4 hours after aphidicolin release, suggesting a posttranslational event (Fig. 3C). Specifically, on induction of LMW-E, there was a 3-fold increase in the slower migrating Cdc25C band compared with uninduced LMW-E or induced EL cells (Fig. 3C, bar graph). Next, we asked whether the migration shift is caused by...
Cdc25C phosphorylation, leading to its activation and subsequent cyclin B/CDK1 activation. Using a specific phospho-CDK1 antibody, we observed a lower level of CDK1/pY15 in LMW-E–overexpressing cells, suggesting an increase in CDK1 activity (Fig. 3C). Next, we measured the ability of the EL/CDK2 versus LMW-E/CDK2 complexes to phosphorylate full-length GST-Cdc25C. HeLa cells were used as they (a) do not have the machinery to process full-length cyclin E, (b) have similar population doubling times to MCF-7 (HeLa, 24 h; MCF-7, 29 h), and (c) both have similar cell cycle profiles following release from aphidicolin arrest (25). EL or LMW-E was overexpressed in HeLa cells by adenoviral infection (Fig. 3D, left) and assayed for cyclin E–associated kinase activity using full-length Cdc25A and Cdc25C (Fig. 3D, middle) as substrates. Although both EL-overexpressing and LMW-E–overexpressing HeLa cells could phosphorylate full-length GST-Cdc25A and GST-Cdc25C, the amount of phosphorylated GST-Cdc25C was 3-fold higher in EL-overexpressing than in LMW-E–overexpressing cells (Fig. 3D, middle). This difference was specific to GST-Cdc25C, as the EL and LMW-E complexes phosphorylated GST-Cdc25A to the same extent. In addition, the GST-Cdc25C phosphorylation was specific, as the CDK2 inhibitor roscovitine attenuated the phosphorylation by ∼80% in both EL-overexpressing and LMW-E–overexpressing cells (Fig. 3D, middle). Lastly, we examined the site(s) on Cdc25C, which cyclin E/CDK2 can phosphorylate (Fig. 3D, right). During interphase, Cdc25C is inhibited by Ser216 phosphorylation, but during mitosis, Cdc25C is phosphorylated on Ser214, which in turn prevents phosphorylation of S216 (26). HeLa cells were infected with LMW-E adenovirus, synchronized in G1-S with aphidicolin, and subjected to a cyclin E–associated kinase activity assay using S214A or S216A GST-Cdc25C(200–256) as substrates. We

Figure 3. EL and LMW-E interact with and phosphorylate Cdc25C. A, GST pull-down assay showing the interaction of 35S-labeled EL (left) and LMW-E (right) with GST-tagged fusion proteins. Ponceau-stained gel is shown below. B, 293T cells were cotransfected with Flag-tagged EL or LMW-E and c-Myc–Cdc25C for 24 h. Left, total lysates were analyzed by Western blot analysis to show expression of transfected proteins. Vinculin used as loading control. Right, immunoprecipitation was performed with monoclonal anti-Flag or a polyclonal anti-c-Myc followed by Western blotting with the indicated antibodies. C, pTRE-LMW-E MCF-7 cells were synchronized with aphidicolin for 24 h, induced for 24 h, released for 4 h, and analyzed by Western blotting for cyclin E, Cdc25C, and CDK1. Bottom, densitometric values of the Cdc25C slower-migrating band. D, left, Western blot analysis showing cyclin E expression in HeLa cells infected with control (LacZ), EL-expressing, or LMW-E–expressing adenovirus for 24 h. Middle, HeLa cells overexpressing cyclin E were immunoprecipitated with a cyclin E antibody and kinase activity was measured using full-length GST-Cdc25C or GST-Cdc25A as substrates. The CDK2 inhibitor roscovitine (80 μmol/L) was added to the kinase reaction as indicated. Right, HeLa cells were synchronized with aphidicolin for 24 h and infected with EL or LMW-E adenovirus. Cell lysates were prepared from cells released for 6 h and subjected to a kinase assay using GST-Cdc25C(200–256) S214A or S216A GST-Cdc25C(200–256) as substrates.
observed that only GST-Cdc25C(200–256) containing S216A, and not the construct containing S214A, was phosphorylated by both the EL/CDK2 and LMW-E/CDK2 complexes (Fig. 3D, right). Collectively, these experiments suggest that EL and LMW-E directly interact with and phosphorylate Cdc25C on Ser214, leading to its premature activation during the S phase, followed by dephosphorylation of CDK1 on T14 and Y15 and activation of cyclin B/CDK1, which promotes premature mitotic entry. The difference between the EL and LMW-E complexes is the extent of Cdc25C phosphorylation. Specifically, it is the transient activity of LMW-E/CDK2 in G2-M transition that leads to a transient activation of cyclin B/CDK1 via phosphorylation of Cdc25C, which results in the faster mitotic exit in LMW-E-overexpressing cells.

**LMW-E overexpression abrogates the mitotic arrest caused by nocodazole.**

We next assessed whether the LMW-E-mediated alteration of mitotic exit could render these cells resistant to mitotic arrest using a spindle poison. HeLa H2B-GFP cells were infected with adenovirus to EL and LMW-E and treated with nocodazole, followed by counting of the mitotic cells (Fig. 4A and B). More than 50% of cells infected with LacZ- or EL-expressing adenovirus were arrested in mitosis compared with only 30% of the LMW-E–expressing cells (Fig. 4B), suggesting that LMW-E, but not EL, abrogates the nocodazole-mediated mitotic arrest in HeLa cells. To examine these results in a different system, we overexpressed EL or LMW-E for 24 hours in MRC50 normal human fibroblasts, treated the cells with nocodazole for 3 to 18 hours, and then analyzed the cells by flow cytometry. LMW-E–expressing cells accumulated in prometaphase less efficiently than the control or EL-expressing cells, suggesting that overexpression of LMW-E results in a faster exit from mitosis after nocodazole treatment (Fig. 4C). Cyclin B1 protein levels accumulated in both the control and EL-expressing cells after 13 or 18 hours of nocodazole treatment, whereas the level of cyclin B1 in LMW-E–overexpressed cells was not increased (Fig. 4D). In fact, the level of cyclin B1 is increased by ~2-fold after 18 hours of incubation with nocodazole, whereas cyclin B1 remained at its lowest levels in the LMW-E–overexpressed cells. Collectively, these data suggest that LMW-E–expressing cells have an increased rate of mitotic slippage and adaptation to the...
spindle checkpoint, resulting in a faster mitotic exit, compared with EL-overexpressing cells.

**Downregulation of Cdc25C inhibits LMW-E–mediated chromosome missegregation and centrosome amplification**

Our results thus far suggest that Cdc25C may mediate the effects of LMW-E on deregulation of the G2-M transition, spindle defects, chromosome segregation, centrosome amplification, and polyploidy. To directly address this hypothesis, we transfected pTRE-EL (Supplementary Fig. S1) or pTRE-LMW-E MCF-7 cells with siRNA targeting Cdc25C (Fig. 5A), which was capable of downregulating Cdc25C protein >80% as depicted in Western blot analysis and immunostaining (Fig. 5A; Supplementary Fig. S1A). Next, cells were stained for β-tubulin and γ-tubulin to analyze mitotic defects (Fig. 5B and D; Supplementary Fig. S1C and D) or for pericentrin and γ-tubulin to detect centrosomes (Fig. 5C and D). We noted that LMW-E–overexpressing cells displayed increases in supernumerary centrosomes (12%), micronuclei (15%), and chromosome missegregation in mitosis (50% of mitotic cells). Depletion of Cdc25C completely inhibited centrosome amplification (Fig. 5C and D), micronuclei formation (Fig. 5D, right), or chromosome missegregation (Fig. 5D, right) in these cells and brought the level of abnormalities comparable with that of uninduced LMW-E or EL–induced cells.

![Figure 5](image-url)

**Figure 5.** Depletion of Cdc25C protein prevents LMW-E–mediated centrosome amplification and chromosome missegregation. A, left, pTRE-LMW-E MCF-7 cells were transfected with control siRNA or Cdc25C-specific siRNA for 72 h, and Cdc25C and cyclin E expression was analyzed by Western blotting. Cyclin E immunofluorescence (right) was also used to examine cyclin LMW-E levels in the presence or absence of pTRE-LMW-E induction. Cdc25C immunofluorescence was used to examine Cdc25C levels in the siRNA control or siCdc25C pTRE-LMW-E–induced cells. B, pTRE-LMW-E cells were treated with control or Cdc25C-specific siRNA for 72 h, treated with or without LMW-E induction, and stained for β-tubulin (green), γ-tubulin (red), and DAPI (blue) to analyze the mitotic defects. C, cells treated as in B were costained with pericentrin (green), γ-tubulin (red), or DAPI (blue) to analyze the number of centrosomes. D, left, centrosomes were counted in cells (n = 500) stained with γ-tubulin and pericentrin for each condition in three independent experiments. *, P < 0.01. Right, mitotic cells (n = 100) were analyzed for abnormalities such as micronuclei and chromosome missegregation for each condition in three independent experiments. *, P < 0.01.
Overexpression of EL did not show a significant increase of centrosome amplification, micronuclei, or chromosome missegregation during mitosis (Supplementary Fig. S1). Depletion of Cdc25C in EL-overexpressing cells did not further alter chromosome missegregation during mitosis of these cells (Supplementary Fig. S1). These findings suggest that Cdc25C is a critical target of LMW-E for induction of chromosomal instability in cancer cells.

EL and LMW-E overexpression differentially modulates PLK1 activity

We next assessed the downstream consequences of EL-mediated versus LMW-E-mediated altered Cdc25C activation. One of the proteins that is involved in a feedback loop with Cdc25C and Myt1 is PLK1, which also functions as a key regulator of CDK1 activity. Hence, we asked whether induction of either EL or LMW-E could alter the activation of PLK1 as they did Cdc25C by measuring PLK1 kinase activity. We used the MCF-7 EL-inducible or LMW-E-inducible cells, induced with doxycycline and synchronized in the G1-S boundary by aphidicolin. At different time intervals following release, cells were harvested and PLK1 kinase activity was measured using α-casein as a substrate (Fig. 6A and B). The left panels depict the autoradiogram of the α-casein kinase gels at each time interval in either EL-induced (Fig. 6A) or LMW-E-induced (Fig. 6B) cells. The right panels depict the densitometric measurement of each band. These analyses revealed that induction of EL or LMW-E results in the

Figure 6. Overexpression of EL and LMW-E differentially deregulates PLK1 and leads to its mislocalization. pTRE-EL (A) and pTRE-LMW-E (B) cells were synchronized at the G1-S transition by aphidicolin block, induced with doxycycline for 24 h, released for the indicated times, and subjected to immunoprecipitation with anti-PLK1 antibody. Kinase activity was measured using α-casein as a substrate. Coomassie-stained gel of IgG was used as a loading control. Right, PLK1 kinase activity in A and B was measured by densitometry and normalized to the activity in the uninduced condition ± SD obtained from at least three independent experiments. C, pTRE-LMW-E cells were treated with doxycycline for 24 h, including a 16-h nocodazole treatment, and analyzed by Western blotting for cyclin E, PLK1, and vinculin. Kinase activity was measured as in A and the bands corresponding to α-casein were quantitated and depicted as bar graphs. D, pTRE-LMW-E cells were induced to express LMW-E by treatment with doxycycline for 24 h or depleted of Cdc25C by treating with a Cdc25C-specific siRNA for 72 h. Cells were costained for cyclin E (red), PLK1 (green), and DNA (blue; top) and for PLK1 (green) or Cdc25C (red; bottom).
premature activation of PLK1 activity 4 to 8 hours after aphidicolin release by about 68% to 70% or 37% to 68%, respectively (Fig. 6A and B). However, the PLK1 activity remained high 12 hours after release in the EL-overexpressing cells, whereas it dropped 3.5-fold 10 hours after release in the LMW-E-overexpressing cells when the G2-M population was the largest (Fig. 6A and B). The results from these synchronisation experiments show that the changes in Cdc25C activity coincided with the time intervals where there were also changes in cyclin B/CDK1 and PLK1 activities in both EL-expressing and LMW-E-expressing cells (Fig. 2C). Together, these experiments suggest that cyclin B/CDK1 and PLK1 activity are modulated by EL and LMW-E expression differently and through a mechanism involving direct activation of Cdc25C.

Normal exit from mitosis requires the inactivation of PLK1, which can occur by its either degradation or dephosphorylation (27). Because we observed a significant reduction in the PLK1 activity in LMW-E-overexpressing cells enriched in the G2-M phase, we asked whether LMW-E induction affects PLK1 activity in cells treated with nocodazole. MCF-7 LMW-E cells were induced by doxycycline in the presence and absence of nocodazole and examined for cyclin E and PLK1 expression and PLK1 kinase activity (Fig. 6C). Treatment with nocodazole resulted in a 2-fold reduction in PLK1 activity in LMW-E-expressing cells compared with uninduced cells (Fig. 6C, bar graphs). These results are consistent with the aphidicolin time course study, suggesting that the decrease in PLK1 activity in LMW-E-expressing cells during mitosis may force cells to exit mitosis and bypass the spindle assembly checkpoint, and potentially resulting in the mislocalization of PLK1.

Under normal conditions, PLK1 associates with centrosomes from G2 to metaphase, translocates to the kinetochores at metaphase, and localizes to the midbody during anaphase and telophase. It has been shown that the activation state of CDK1 controls the translocation of PLK1 from the centrosomes and kinetochores during metaphase to the central spindles during anaphase (28). We hypothesized that overexpression of LMW-E deregulates the localization of PLK1. We tested this hypothesis in our inducible system and found that on induction of LMW-E, PLK1 is no longer associated with the central spindles during anaphase and telophase and is now dispersed nonspecifically throughout the cellular structure (Fig. 6D, top). We also examined PLK1 localization in LMW-E-overexpressing cells in which Cdc25C was depleted by siRNA. We observed that in uninduced cells following Cdc25C siRNA depletion, PLK1 does not localize to the midbody but to the centrosome (Fig. 6D, bottom). Cdc25C is not detectable in control cells at the telophase stage, but it is when LMW-E is induced. Additionally, in LMW-E–induced cells depleted of Cdc25C, PLK1 was mislocalized in the same manner as in the Cdc25C-depleted uninduced cells (Fig. 6D, bottom). These results suggest that both overexpression of LMW-E and depletion of Cdc25C lead to mislocalization of PLK1. Because inhibition of PLK1 activity abolishes the correct localization of PLK1 (29), these results suggest that inhibition of PLK1 activity caused by induction of LMW-E may also lead to its mislocalization and may cause cytokinesis failure by affecting important targets of PLK1.

Discussion

In this report, we describe a novel regulatory pathway involving activation of Cdc25C protein phosphatase, which is differentially phosphorylated by EL and LMW-E to regulate mitotic entry and exit. We also show that deregulation of mitotic progression and chromosomal instability is mediated by the interaction between cyclin E and Cdc25C. EL and LMW-E directly interact with and phosphorylate Cdc25C on residue Ser214, leading to its premature activation during S phase. Ser214 is the major phosphorylation site on Cdc25C during mitosis and prevents phosphorylation of Ser216 (26). This premature activation of Cdc25C causes dephosphorylation of CDK1 on Thr14 and Tyr15, which forms the core of feedback loops that control the activation of cyclin B/CDK1 and PLK1 and promote mitotic entry. A fraction of Cdc25C localizes to the centrosome during the S phase and throughout G2 and mitosis, and cyclin E localizes to the centrosomes (30). Thus, it is likely that cyclin E interacts with Cdc25C at the centrosomes and activates Cdc25C by phosphorylating Ser214, leading to activation of CDK1–cyclin B1, which in turn activates PLK1 and Cdc25C. However, we cannot exclude the possibility that the cyclin E/CDK complex phosphorylates and directly activates PLK1.

The EL-expressing and LMW-E–expressing cells displayed different mitotic exit phenotypes. LMW-E–expressing cells exited mitosis faster than the control cells and exhibited an accelerated mitotic transition, whereas EL-overexpressing cells were arrested in mitosis (15). Inactivation of Cdc25C is a key upstream event in M-phase–promoting factor inactivation during mitotic exit (30). We propose that the weak binding of LMW-E to Cdc25C during mitosis may result in a rapid exit from mitosis through the premature inactivation of Cdc25C and further inactivation of CDK1 and PLK1. In contrast, in EL-overexpressing cells, high levels of S214 phosphorylation and hyperactivation of both CDK1 and PLK1 arrest cells in mitosis and delay mitotic exit. These results with EL are consistent with a previous study showing that EL overexpression causes mitotic arrest by inhibiting APC/C^{cdh1} (6). Normal exit from mitosis has been shown to require the inactivation of PLK1 by either degradation or dephosphorylation (27). Thus, the drop in PLK1 activity observed during mitosis may be the cause of the premature mitotic exit in LMW-E–expressing cells, whereas the high PLK1 activity observed in EL-expressing cells arrests them in mitosis, resulting in delayed mitotic exit.

We also observed mislocalization of PLK1 in LMW-E–expressing cells in metaphase and anaphase, suggesting that such mislocalization may deregulate the activity of the target genes of PLK that are necessary for proper cytokinesis (32, 33). These results may explain the failure of cytokinesis in the LMW-E–expressing cells. We found that expression of LMW-E induced genomic instability by causing the cells to progress faster through mitosis before the
chromosomes were properly segregated, leading to an increase in the number of multipolar anaphase spindles, a failure of cytokinesis, and the generation of multinucleated cells with supernumerary centrosomes (15). Failure to execute a crucial step in the cell division process, such as late anaphase and cytokinesis, leads to the formation of cells with two nuclei; these 4N cells can then undergo either bipolar or multipolar mitosis with amplified centrosomes (34). Furthermore, we showed that depletion of Cdc25C in LMW-E-overexpressing cells inhibited centrosome amplification, decreased the number of abnormal mitotic spindles, and reduced chromosome missegregation. Our findings suggest that the LMW-E-mediated polyplody and centrosome amplification require a premature transition through mitosis.

Another key finding from our study is that LMW-E-overexpressing cells showed a reduction in the mitotic index in the presence of nocodazole, suggesting an increased rate of mitotic slippage and adaptation to the spindle checkpoint, a feature that is commonly seen when checkpoint-defective cells are accelerated out of mitosis. In contrast, EL-overexpressing cells accumulated in G2-M and had an increased mitotic index when treated with nocodazole, suggesting delayed entry into and exit from mitosis. These results suggest the spindle assembly checkpoint is defective in LMW-E-overexpressing cells but not in EL-overexpressing cells. The mechanism by which LMW-E overexpression bypasses the spindle assembly checkpoint needs further investigation. Collectively, these results suggest that the generation of LMW-E isoforms only in tumor cells primes these cells to accrue chromosomal instability by affecting the transition of cells through mitosis, leading to the generation of supernumerary centrosomes and contributing to transformation in cancer cells.

Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

Acknowledgments

We thank Said Akli and Yan Liu for generation of the cyclin E-expressing adenovirus; Wendy D. Schober and Nalini Patel for assistance with the flow cytometry analysis; and Helen Piwnica-Worms, Stephen J. Elledge, Yolanda Sanchez, and Jian Kuang for providing the Cdc25C constructs.

Grant Support

NIH grants CA87458 and P50CA116199 and Clayton Foundation (K. Keyomarsi) and Susan G. Komen grant PDF0707621 (A. Biermacka and K. Keyomarsi). The costs of publication of this article were defrayed in part by the payment of page charges. This article must therefore be hereby marked advertisement in accordance with 18 U.S.C. Section 1734 solely to indicate this fact.

Received 11/06/2009; revised 03/29/2010; accepted 04/22/2010; published OnlineFirst 06/08/2010.

References

23. Hoffmann I, Dretta G, Karsenti E. Activation of the phosphatase


Cancer Research


Cyclin E Deregulation Impairs Mitotic Progression through Premature Activation of Cdc25C

Access the most recent version of this article at:
doi:10.1158/0008-5472.CAN-09-4095

Access the most recent supplemental material at:
http://cancerres.aacrjournals.org/content/suppl/2010/06/07/0008-5472.CAN-09-4095.DC1

E-mail alerts
Sign up to receive free email-alerts related to this article or journal.

Reprints and Subscriptions
To order reprints of this article or to subscribe to the journal, contact the AACR Publications Department at pubs@aacr.org.

Permissions
To request permission to re-use all or part of this article, contact the AACR Publications Department at permissions@aacr.org.