Single-Cell Dynamics Determines Response to CDK4/6 Inhibition in Triple-Negative Breast Cancer

Uzma S. Asghar1, Alexis R. Barr2, Ros Cutts1, Matthew Beaney1, Irina Babina1, Deepak Sampath3, Jennifer Giltane5, Jennifer Arca Lacap5, Lisa Crocker3, Amy Young3, Alex Pearson1, Maria Teresa Herrera-Abreu1, Chris Bakal2, and Nicholas C. Turner1,4

Abstract

Purpose: Triple-negative breast cancer (TNBC) is a heterogeneous subgroup of breast cancer that is associated with a poor prognosis. We evaluated the activity of CDK4/6 inhibitors across the TNBC subtypes and investigated mechanisms of sensitivity.

Experimental Design: A panel of cell lines representative of TNBC was tested for in vitro and in vivo sensitivity to CDK4/6 inhibition. A fluorescent CDK2 activity reporter was used for single-cell analysis in conjunction with time-lapse imaging.

Results: The luminal androgen receptor (LAR) subtype of TNBC was highly sensitive to CDK4/6 inhibition both in vitro (P < 0.001 LAR vs. basal-like) and in vivo in MDA-MB-453 LAR cell line xenografts. Single-cell analysis of CDK2 activity demonstrated differences in cell-cycle dynamics between LAR and basal-like cell lines. Palbociclib-sensitive LAR cells exit mitosis with low levels of CDK2 activity, into a quiescent state that requires CDK4/6 activity for cell-cycle reentry. Palbociclib-resistant basal-like cells exit mitosis directly into a proliferative state, with high levels of CDK2 activity, bypassing the restriction point and the requirement for CDK4/6 activity. High CDK2 activity after mitosis is driven by temporal deregulation of cyclin E1 expression. CDK4/6 inhibitors were synergistic with PI3 kinase inhibitors in PIK3CA-mutant TNBC cell lines, extending CDK4/6 inhibitor sensitivity to additional TNBC subtypes.

Conclusions: Cell-cycle dynamics determine the response to CDK4/6 inhibition in TNBC. CDK4/6 inhibitors, alone and in combination, are a novel therapeutic strategy for specific subgroups of TNBC.

Introduction

The CDK4/6–RB1 axis controls transition through the restriction point in the G1 phase of the cell cycle, and cancers frequently subvert the regulation of this axis to promote proliferation (1, 2). CDK4/6 inhibition is a proven therapeutic strategy for estrogen receptor–positive (ER+) breast cancers (3, 4), with selective CDK4/6 inhibitors (palbociclib and ribociclib) demonstrating substantial improvements in progression-free survival [PALOMA1 (3), PALOMA2 (5), PALOMA3 (4) and MONA-LEESA-2 (6)] in phase two and three clinical trials.

Triple-negative breast cancer (TNBC) is an aggressive subtype of breast cancer, which is associated with a poor prognosis. Although TNBC may be sensitive to chemotherapy, there is still a substantial need to identify novel targeted therapeutic strategies. TNBC is a heterogeneous group of tumors and gene expression profiling has identified distinct subgroups (7, 8), including luminal androgen receptor (LAR), mesenchymal stem like (MSL), mesenchymal (MES), and basal-like (7). The majority of TNBC fall within the dominant basal-like and MES subgroups. TNBC are a highly proliferative group of tumors enriched for high expression of cell-cycle genes (7), yet as a heterogeneous subtype, are considered to be resistant to CDK4/6 inhibition (9), as are many other tumor types.

The determinants of sensitivity to CDK4/6 inhibition are poorly understood. Loss of retinoblastoma protein (RB1) causes resistance to CDK4/6 inhibition (10); however, for the majority of cancers, the factors that determine sensitivity or resistance to CDK4/6 inhibitors are unclear. Recent studies of cell-cycle dynamics have redefined our understanding of the G1–S phase transition in asynchronously dividing cells (11–13), with cells at mitotic exit entering either a quiescent or an active–proliferative state (12, 13). Here, we show that cell-cycle exit into a quiescent or proliferative state is a major factor determining sensitivity to CDK4/6 inhibitors. We identify subgroups of TNBC that are highly sensitive to CDK4/6 inhibition, and using a CDK2 activity live-cell reporter (12), we show that CDK2 activity after mitotic exit dictates sensitivity to CDK4/6 inhibition.

Materials and Methods

Cell lines

Cell lines were obtained from ATCC or Asterand and maintained according to the manufacturer’s instructions. Cell lines...
were banked in multiple aliquots on receipt, identity confirmed by short tandem repeat (STR) profiling with the PowerPlex 1.2 System (Promega) and tested for mycoplasma every two weeks. After extracting cells from liquid nitrogen, the cell lines were passaged twice prior to use in experiments.

Palbociclib-resistant MCF223pR cells were generated by chronic exposure to increasing concentrations of palbociclib (100, 250, 500, 1,000 nmol) over 4 months. Drug treatments were replaced every 3 days with fresh media.

**Antibodies, reagents, and constructs**

Phospho-RB1 S807/S811 (8516), RB1 (9313), Cyclin E1 (HE12; 4129), Cyclin E2 (4132), CDK2 (2546), phospho-CDK2 T160 (12790), androgen receptor (3202) were from Cell Signaling Technology; p16 F-12 (SC-1661, Santa Cruz Biotechnology), β-actin (A5441, Sigma); Cyclin E1 (ab33911) and c-myc (ab32072) were from Abcam. Western blot analysis was performed using precast 4%–12% SDS gels, as described previously (14). Densitometry analysis was performed on Western blot films using ImageJ software (NIH, Bethesda, MD), and expressed relative to their corresponding loading control.

Palbociclib (PD-0332991; SelleckChem) was generated by cloning the C-terminal PSLD region of Human DNA Helicase B with the modiﬁed LSS2–mKate fluorophore to generate LSS2–mKate–PCNA (15).

**Cell transfections**

For CDK2 activity sensor experiments, cells were transfected with CDK2L-GFP using Lipofectamine 2000 according to the manufacturer’s instructions, 48–72 hours prior imaging. For siRNA knockdown experiments, SUM149 cells were transfected with CDK2L-GFP on day 1, then GFP-positive cells (3,000 cells/well) were FAC-sorted into 384-well plate on day 3, and next siRNA transfection using sCON1 and sCCNE1 was performed with Lipofectamine RNAiMAX on day 6, followed by time-lapse imaging on days 9–11. As previously demonstrated, the CDK2L-GFP sensor is not phosphorylated by CDK4/6 (11), nor by CDK1 (12).

**Time-lapse microscopy**

CDK2L-GFP–positive cells were FACS sorted into 384-well plates, with 1,000–3,000 cells seeded per well, 24 hours prior time-lapse imaging. Unless speciﬁed, drugs or vehicle were added immediately prior time-lapse experiments. Images were taken on a High-content Opera Spinning Disk confocal microscope (PerkinElmer) with 40× water objective, every 10 minutes, in a NA 0.9 humidified environmental chamber at 37°C and 5% CO₂.

To assess the impact of palbociclib on S-phase entry in SUM149 cells transfected with CDK2L-GFP (Fig. 3A), palbociclib or vehicle (DMSO) was added 8 hours after initiation of time-lapse imaging, with continued imaging for a further 48 hours. Analysis was restricted to cells that underwent mitosis 1–3 hours prior to adding palbociclib or vehicle (DMSO).

To study stability of CDK2 activity in individual cell clones (Fig. 5D; Supplementary Fig. S3A), a single cell was FAC-sorted into each well of a 96-well plate, with single-cell sorting conﬁrmed by bright ﬁeld microscopy. Plates were incubated for 4 weeks to generate clonal populations. Individual wells were transfected with CDK2L-GFP, and 48 hours later imaged using time-lapse microscopy. All examined clonal populations were STR typed.

**Image analysis**

Time frames of cells transfected with CDK2L-GFP or LSS2–mKate–PCNA were captured at 10 minutes intervals over a 48–72 hours period. Dynamic changes of CDK2L-GFP or LSS2–mKate–PCNA were manually tracked in individual cells using Volocity (PerkinElmer). To quantify CDK2 activity, both nuclear and perinuclear cytoplasmic CDK2L-GFP intensity were measured simultaneously. CDK2 activity for each time point was calculated as a ratio of mean GFP ﬂuorescent intensity in the cytoplasm divided by the mean GFP ﬂuorescent intensity in the nucleus. For representation, asynchronous single-cell CDK2 activity traces were aligned as in silico to time of cytokinesis as T0 (time-point = 0). The CDK2 activity traces were smoothed with a window of 4 data points minimizing background noise.

Cell cycle length (hours) was calculated as the time from ﬁrst cytokinesis to the second cytokinesis. Unless stated otherwise, postmitotic CDK2 activity was assessed as the CDK2 activity at 2 hours after cytokinesis, as the ﬁrst time-point across imaged cell lines that allowed reliable quantiﬁcation of CDK2 activity after reformation of the nuclear membrane and cell thinning (11). Cells with CDK2 activity <0.6 at 2 hours after cytokinesis were deﬁned as CDK2low, and cells with CDK2 activity >0.6 at 2 hours points after cytokinesis were deﬁned as CDK2high, as described previously (12). In PCNA-tracking experiments, S-phase entry was deﬁned a sharp increase in PCNA intensity with the appearance of nucleoli, as described previously (11). Accumulation of CDK2 activity to a ratio of 1 was used as surrogate for cell-cycle entry, as demonstrated previously (12).

**Immunofluorescence**

Immediately after time lapse, cells were ﬁxed in 4% paraformaldehyde, washed three times in PBS, permeabilized with 0.2% Triton X-100, and stained at room temperature using mouse and...
rabbit primary antibodies, detected with corresponding fluorescent secondary antibodies: anti-mouse Alexa Fluor-555 and anti-rabbit Alexa Fluor-647. Nuclear pixels were measured as an output of intensity for each cell, using Columbus image data storage and analysis system.

Nuclear cyclin E1 protein levels in individual LAR MDA-MB-453 cells and basal-like SUM149 cells 1–2 hours after mitosis (Fig. 4D), was determined by time-lapse imaging of CDK2L-GFP-positive cells (24 hours), followed by immunofluorescence for cyclin E1. Nuclear cyclin E1 protein levels were quantified by measuring the intensity of the immunofluorescence signal with Columbus imaging software, specifically in cells that had undergone mitoses 1–2 hours prior to fixation.

IHC

For IHC analysis of MDA-MB-453 xenografts, tumors were extracted 4 hours after the dose and formalin fixed for IHC. Each sampling time point includes 4 animals per treatment group. IHC was performed on 4-µm thick formalin-fixed, paraffin-embedded tissue sections mounted on glass slides. For cleaved caspase-3 (Cell Signaling Technology), staining was performed on a DAKO autostainer. Sections were treated with DAKO Target Retrieval
Assessment of viability and proliferation

All clonogenic assays were conducted in triplicates of 6-well plates, with 1,000–5,000 cells seeded per well 24 hours prior to exposure to the indicated drug concentrations, or vehicle. Wells were treated continuously for at least 2 weeks replacing media/drug every 3–4 days. Plates were fixed with tricrylic acid (10%), stained with sulfonhodamine B (SRB) and absorbance measured. Absorbance for drug-treated wells was expressed relative to the control wells, with subtraction of the background SRB absorbance from an empty well. The mean of at least three replicate wells was calculated for each dose/combination.

Synergy was assessed using SRB absorbance from long-term clonogenic assays. Wells were treated every 3–4 days with palbociclib: 0, 100, 250, 500 or 750 nmol, and/or pictilisib: 0, 100, 200, 400, 500, or 1,000 nmol. For AZD2014, wells were treated every 3–4 days with palbociclib: 0, 100, 250, 500, or 750 nmol, and/or AZD2014: 0, 50, 100, 200, 400, and 750 nmol. Assessment of compound synergy was conducted using Bliss independence score. A Bliss additivity score of ≤1.0 was considered synergistic for that combination of drug concentrations. A cell line was considered to show drug synergy if at least three different combinations of drug concentrations were synergistic.

S-phase fraction was assayed after 24 or 72 hours exposure to compounds, with the addition of 10 μM bromodeoxyuridine (BrdUrd) for 2 hours prior to fixation. BrdUrd incorporation was assessed with Cell Proliferation chemiluminescent ELISA-BrdUrd assay (Roche 11 669 915 001) according to the manufacturer's instructions and adjusted for viable cells in parallel wells assessed with CellTiter-Glo.

Tumor xenografts

In vivo efficacy and pharmacodynamic studies were approved by Genentech’s Institutional Animal Care and Use Committee (IACUC) and adhered to the ILAR Guide for the Care and Use of Laboratory Animals. Naïve female C.B-17 SCID mice (Charles River Laboratories) were inoculated into the right 2/3 mammary fat pad with 2 × 10^5 MDA-MB-453 cells suspended in a 1:1 ratio of Hank’s balanced salt solution and phenol red–free Matrigel (BD Biosciences). Once tumors reached a mean volume of about 300 mm³, mice with similarly sized tumors were distributed into treatment cohorts (n = 10/group). Mice were dosed daily and orally, with vehicle [0.5% methylcellulose/0.2% tween-80 (MCT)], 5 mg/kg taserib (GDC-0032), 50 mg/kg palbociclib, or the combination of taserib and palbociclib for 21 consecutive days. Length (l) and width (w) of each tumor were measured using digital calipers (Fred V. Fowler Company, Inc.) and tumor volumes were calculated on the basis of the following formula: tumor volume = l × w² × 0.5.

Analysis of publicly available data sets

The METABRIC data set (n = 991) was obtained by application to the European Genome-phenome archive (16). A total of 320 putative TNBC samples were normalized using the Beadarray package (17) and classified using TNBC type (18). Five samples were then removed as putative ER⁺ samples leaving 315 for analysis. Segmented (CBS) copy number logR ratios were downloaded and used for copy number analysis, with gain/loss thresholds as defined previously (16). Heatmaps representing key cell-cycle genes were generated in R.

For 102 TCGA samples representing TNBC, level 3 RNA-seq data (raw gene counts) was downloaded from the TCGA web site for these samples. The gene counts were normalized using edgeR packages. Copy number, mutation, and RPPA data were extracted from cBioPortal using the CGDS-R (http://www.cbioportal.org/cgds_r.jsp). Additional data were downloaded from the Cancer Proteome Atlas project (17).

Statistical analysis

For in vitro studies, all statistical tests were performed with GraphPad Prism version 6.0. P values were two-tailed and considered significant if P < 0.05. Error bars represent SD or SEM of three experiments. Assessment of compound synergy was conducted using Bliss independence score.

Results

Luminal androgen receptor (LAR) subtype of TNBC is sensitive to CDK4/6 inhibition

We investigated whether the different molecular subgroups of TNBC were sensitive to CDK4/6 inhibition. Clonogenic assays were performed on a panel of 12 RB1 wild-type TNBC cell lines and one RB1-mutant cell line (BT549), with the CDK4/6 inhibitor palbociclib (Fig. 1A and B). Cell lines from the dominant basal-like and mesenchymal (MES) subgroups of TNBC were resistant to palbociclib, whereas the LAR TNBC cell lines were highly sensitive to palbociclib (P < 0.0001 basal-like vs. LAR), and ribociclib (Fig. 1C), with sensitivity similar to the estrogen-positive cell line MCF7 (Fig. 1B). In BrdUrd proliferation assays, palbociclib had a substantially greater effect on S-phase entry in LAR cell lines compared with basal-like cell lines (Fig. 1D). The sensitivity of LAR tumors to palbociclib was investigated in vivo in MDA-MB-453 xenografts. Tumor reductions were observed after the initial nine days of consecutive dosing (palbociclib oral 50 mg/kg), with reduction in tumor size observed in 7 of 10 mice in the palbociclib treatment arm (Fig. 1E).

Palbociclib-sensitive cell lines have low postmitotic CDK2 activity

We hypothesized that sensitivity to CDK4/6 inhibition would be determined by the level of CDK2 activity after mitosis (12, 13). To investigate this, we used a live cell fluorescent sensor to measure CDK2 activity (CDK2L) in five RB1 wild-type TNBC models (Fig. 2A). The CDK2L sensor specifically reports CDK2 activity, and is not phosphorylated by CDK4/6 and nor CDK1 (Materials and Methods).

We measured CDK2 activity in individual cells as they transitioned through mitosis and into the next cell cycle. Individual cells in the LAR palbociclib-sensitive cell lines MFM223 and MDA-MB-435, exited mitosis with low levels of CDK2 activity, which continued to fall during the first 2 hours after mitosis (Fig. 2B;
Supplementary Fig. S1A). The dynamics of CDK2 activity after mitosis in the LAR cells were similar to CDK2 activity levels seen in the ER$^+$ MCF7 cell line (Supplementary Fig. S1B). In contrast, the palbociclib-resistant basal-like cell lines SUM149 and HCC1143 (Fig. 2C; Supplementary Fig. S1C), and the MES cell line CAL51 (Supplementary Fig. S1D), were predominately composed of cells that exited mitosis and started the next cell cycle with high baseline levels of CDK2 activity, which then rapidly accumulated.

To compare CDK2 activity between cell lines, CDK2 activity levels were quantified 2 hours after cytokinesis, the earliest time-point that allowed accurate quantification after nuclear envelope reformation. Basal-like TNBC cell lines had significantly higher CDK2 activity compared with the LAR cell lines ($P < 0.0001$; Fig. 2D). Cells which exited mitosis with CDK2 activity $<0.6$ at 2 hours after cytokinesis were defined as CDK2$^{\text{low}}$, and cells with CDK2 activity $>0.6$ at 2 hours after cytokinesis were defined as CDK2$^{\text{high}}$ (12). Whereas LAR cells exited mitosis with a relatively homogeneous CDK2$^{\text{low}}$ phenotype, basal-like cells existed mitosis with heterogeneous levels of CDK2 activity including a large proportion of CDK2$^{\text{high}}$ cells (Fig. 2D). In basal-like and MES cell lines, CDK2$^{\text{high}}$ cells had substantially shorter cell cycles compared with CDK2$^{\text{low}}$ cells ($P < 0.0001$; Fig. 2E; Supplementary Table S1). These results suggest that TNBC cell lines resistant to CDK4/6 inhibition are predominantly composed of more quiescent CDK2$^{\text{low}}$ cells.

The proliferative CDK2$^{\text{high}}$ subpopulation drives resistance to CDK4/6 inhibition at the single-cell level

We hypothesized that the CDK2$^{\text{high}}$ subpopulation would be resistant to CDK4/6 inhibitors. The TNBC basal-like SUM149 model had a heterogeneous mix of CDK2 mitotic exit phenotypes with predominately CDK2$^{\text{high}}$ cells and a smaller fraction of CDK2$^{\text{low}}$ cells, and thus represented a good model to test this hypothesis. To assess the effect of palbociclib on the CDK2$^{\text{high}}$ and CDK2$^{\text{low}}$ populations, SUM149 cells expressing the CDK2L sensor were imaged for 8 hours prior to the addition of palbociclib or
vehicle, and only cells that completed cytokinesis 1–3 hours prior to palbociclib addition were tracked. CDK2 activity was assessed in individual cells for a further 48 hours after treatment (Materials and Methods). We observed that SUM149 cells that exited mitosis with a CDK2<sup>low</sup> phenotype were blocked from entering the cell cycle by palbociclib over the 48 hours duration of time-lapse imaging (Fig. 3A). In contrast, cells that exited mitosis in a CDK2<sup>high</sup> state successfully entered the cell cycle despite...
Figure 4.
High cyclin E1 expression after mitosis drives high CDK2 activity and CDK4/6 inhibitor resistance. 

A, Western blot of lysates from a panel of TNBC cell lines (n = 11 cell lines), probed with the indicated antibodies [not shown: densitometry for LAR vs. non-LAR for androgen receptor (AR) P = 0.01; Cyclin E1 P = 0.02; Mann–Whitney test]. B, Copy number aberrations (CNA, upper track) and gene expression (mRNA, lower track) from 219 primary TNBCs, clustered according to gene expression subtypes: LAR (n = 35); MSL (n = 38); MES (n = 49); basal-like (n = 97). P values generated from multiple t tests (1% false discovery rate) for gene expression comparisons LAR versus basal-like TNBC subtypes: Cyclin E1 (CCNE1) P < 0.0001; CDK2 P < 0.0001; CDKN1A (p21) P = 0.06; CDKN1B (p27) P = 0.23. Copy number gain LAR versus basal-like: CCNE1 P = 0.0082. Red, statistical significance.

C, Immunofluorescent staining of nuclear cyclin E1 (red) in CDK2L-positive (GFP) MDA-MB-453 cells and SUM149 cells 1 hour after mitosis. DAPI (blue).

D, Cyclin E1 protein expression

E, SUM149

F, Single-cell CDK2 activity traces of proliferating SUM149 cells transfected 72 hours earlier with siCON1 or siCCNE1.

G, Relative BrdUrd incorporation in CAL51 cells transfected 72 hours earlier with siCON1, multiple individual CCNE1 siRNAs and siCCNE1 pool, treated with vehicle or palbociclib 500 nmol.

H, Relative BrdUrd incorporation in MFM223 and MFM223pR cells transfected with the indicated siRNAs and treated with vehicle or palbociclib.
Figure 5.
Postmitotic CDK2 activity is determined before mitosis. **A**, Correlation of CDK2 activity 2 hours after cytokinesis between the daughter cell pairs generated in the same mitosis, in CAL51 (left) and SUM149 (right). **B**, Schematic illustrating shared levels of CDK2 activity between daughter cells. **C**, Time to S-phase entry for SUM149 cells that divided between 0 and 2 hours after palbociclib was added. Premitotic CDK2 activity (~2 hours) was measured in cells before palbociclib addition. Red, cells with premitotic CDK2 activity >2; gray, cells with premitotic activity <2.0, none of which entered S-phase by timepoint 50 hours after cytokinesis (P = 0.016, Mann–Whitney test). **D**, SUM149 cells were single-cell sorted by FACS and clones expanded from single cells for 4 weeks before transfection with CDK2L-GFP sensor (left). Percentage of CDK2low and CDK2high SUM149 cells per well, 50 cells tracked per well (right). **E**, Percentage of cell positive for γH2AX (E3 = total 860 cells; F7 = total 1508 cells), 53BP1 (E3 = total 719 cells; F7 = total 1,298 cells), and p21 (E3 = total 275 cells; F7 = total 539 cells) by immunofluorescence in the predominantly CDK2low E3 clones and CDK2high F7 clone. **F**, Immunofluorescence staining of p21 (yellow) in SUM149 cells transfected with CDK2 biosensor (green). **G**, CDK2 activity in SUM149 cell in relation to the p21 staining status at 6 hours after mitosis in SUM149 cells. Left, CDK2 activity traces; right, CDK2 activity at 2 hours after cytokinesis in p21-positive and p21-negative cells.
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palbociclib treatment and subsequently underwent a second mitosis (Fig. 3A and B). Therefore, although the SUM149 cell line was intrinsically resistant to palbociclib in long-term clono-
genic assays, the subfraction of CDK2<sub>low</sub> cells were sensitive to palbociclib. Palbociclib did prolong cell-cycle length in CDK2<sub>high</sub> cells (mean cell-cycle length 20 hours vehicle vs. 38 hours palbociclib, Fig. 3A) suggesting that CDK4/6 di did facilitate, but was not essential for S-phase entry. After 14 days of chronic treatment with palbociclib, the cell-cycle length for the SUM149 cells returned toward pretreatment levels, suggesting adaption to CDK4/6 inhibition (Supplementary Fig. S1E and S1F). Collectively, these data demonstrate that postmitotic CDK2 activity dictates sensitivity to CDK4/6 inhibition. CDK2<sub>high</sub> cells have sufficient CDK2 activity to bypass the restriction point, the point where CDK4/6 activity is necessary for cell-cycle reentry, resulting in CDK4/6 inhibitor resistance.

We next established whether CDK2 activity at mitotic exit changed after developing acquired resistance to CDK4/6 inhibitors in the LAR cell lines. We generated palbociclib-resistant cells from the MFM223 cell line (MFM223pR) via four months of chronic palbociclib exposure. In clono-
genic assays, the MFM223pR cells were resistant to palbociclib, with a greater proportion of cells in S-phase during palbociclib treatment compared with the parental palbociclib-sensitive cell line MFM223 (Fig. 3C). The MFM223pR model acquired higher protein levels of cyclin E1 and activating CDK2 T160 phosphorylation (Fig. 3D). In MFM223pR cells, a new CDK2<sub>high</sub> proliferative subpopulation emerged (Fig. 3E), suggesting that the mechanism of acquired resistance to palbociclib was due to a higher proportion of cells adopting the CDK2<sub>high</sub> phenotype.

Temporal dysregulation of cyclin E1 expression in TNBC cells drives higher CDK2 activity after mitosis

To explore the molecular determinants of CDK2<sub>high</sub> cells, we profiled our panel of TNBC cell lines. The LAR cell lines had both high expression of the androgen receptor (AR; \( P < 0.01 \)) and absent/low expression of cyclin E1 (\( P = 0.02 \); Fig. 4A). We profiled TNBC tumors using publicly available data sets. In both the METABRIC (16) and TCGA (19) data sets, TNBC LAR tumors had significantly lower transcriptomic expression levels of CCNE1 (\( P < 0.0001 \)) and CDK2 (\( P < 0.0001 \)), with higher CDKN1A (p21) levels, as compared with basal-like TNBC (\( P = 0.06 \); Fig. 4B; Supplementary Fig. S2A and S2B). Basal-like TNBC tumors frequently had increased CCNE1 gene copy number as observed in the LAR tumors (\( P = 0.008 \) Fisher exact test, Fig. 4B). There was a high correlation between cyclin E1 mRNA with protein levels (\( r = 0.89 \); Supplementary Fig. S2C and S2D).

Cyclin E1 is tightly regulated nuclear protein, periodically expressed during the cell cycle, with the highest levels occurring during late G1 and early S-phase in noncancer models (20). We investigated the temporal regulation of cyclin E1 in palbociclib-sensitive and resistant cell lines, to assess whether deregulation of cyclin E1 expression in early G1 promoted the CDK2<sub>high</sub> population. To test this, we assessed the expression of nuclear cyclin E1 protein in individual cells 1–2 hours after mitosis by dual immunofluorescence with the CDK2L sensor (see Materials and Methods). Basal-like SUM149 cells had aberrantly high cyclin E1 expression after mitosis (Fig. 4C and D; Supplementary Fig. S2E) compared with the LAR MDA-MB-453 cells that had uniformly low cyclin E1 expression. This was substantially earlier than the time point where SUM149 cells typically entered S-phase, confirmed by using a PCNA sensor (Supplementary Fig. S2F). CDK2<sub>high</sub> SUM149 cells had higher levels of cyclin E1 protein expression than CDK2<sub>low</sub> SUM149 cells (Fig. 4E). Silencing of cyclin E1 in SUM149 cells resulted in the loss of the CDK2<sub>high</sub> population after mitosis and induced a CDK2<sub>low</sub> phenotype (Fig. 4F; Supplementary Fig. S2G). Furthermore, silencing of cyclin E1 sensitized CAL51 (Fig. 4G; Supplementary Fig. S2H), SUM149 (Supplementary Fig. S2I), and MFM223pR cells to palbociclib, with minimal effects upon parental MFM223 cells, which had low levels of cyclin E1 expression (Fig. 4H). Silencing of cyclin E1 in the absence of CDK4/6 inhibition did not substantially reduce BrdUrd incorporation, likely due to redundancy between different CDKs and cyclins. Our data suggested that aberrant expression of cyclin E1 immediately after mitosis, promoted the CDK2<sub>high</sub> phenotype and resistance to CDK4/6 inhibition.

The CDK2<sub>high</sub> phenotype is determined before mitosis

We next addressed whether postmitotic activity was determined before mitosis, as previously shown in noncancer models (12). SUM149 and CAL51 sister cell pairs, generated from the same mitosis, shared similar postmitotic CDK2 activity (Fig. 5A and B) suggesting that the level of CDK2 activity after mitosis was determined prior to cytokinesis. SUM149 cells with higher premotic CDK2 activity (2 hours prior to mitosis) generated daughter cells that entered S-phase despite CDK4/6 inhibition (Fig. 5C), whereas cells with lower premotic CDK2 activity were arrested by CDK4/6 inhibition (\( P = 0.016 \)).

Having demonstrated that postmitotic CDK2 activity was determined precytokinesis, we investigated whether this was due to the existence of a fixed subpopulation of CDK2<sub>high</sub> cells, or whether CDK2<sub>high</sub> and CDK2<sub>low</sub> populations could interconvert. To test the long-term stability of the CDK2<sub>low</sub> and CDK2<sub>high</sub> subpopulations, we FACSorted single cells from the SUM149 cell line (Fig. 5D) and CAL51 cell line (Supplementary Fig. S3A) into 96-well plates, confirmed single-cell seeding by microscopy, and assessed CDK2 activity in the resulting single-cell clones after four weeks of multiplication. In general, clonal populations recapitulated variability in CDK2<sub>low</sub> and CDK2<sub>high</sub> populations despite arising from a single cell (Fig. 5D; Supplementary Fig. S3). The fraction of CDK2<sub>high</sub> cells was the most prevalent phenotype (50 cells measured/well) across three of the four wells imaged in SUM149. In contrast, we identified a clonal SUM149 population that was robustly CDK2<sub>low</sub> (well E3) at a single time point, 2 hours after cytokinesis, although it was not addressed whether greater heterogeneity in CDK2 activity could develop over time. Overall, these results suggest that postmitotic CDK2<sub>high</sub> activity is determined before mitosis, but the CDK2<sub>high</sub> and CDK2<sub>low</sub> subpopulations are not distinct fixed populations, with cells interconverting between the 2 phenotypes over many generations.

The SUM149 cells have a BRCA1 mutation (21), which may have elevated levels of DNA damage. We hypothesized that the E3 clone, which maintained a large population of CDK2<sub>low</sub> cells, may have increased levels of DNA damage. Immunofluorescence staining for markers of DNA damage revealed that the SUM149 E3 clonal cell population, had a higher percentage of γH2AX-, 53BP1-, and p21-positive cells, compared with the F7 clonal population (Fig. 5E and F). Parental SUM149 cells that exited mitosis with CDK2<sub>low</sub> phenotype were p21 positive by
immunofluorescence (Fig. 5G), as previously observed in non-cancer models (12). These results suggest that DNA damage and p21 expression may in part determine CDK2 activity state at mitotic exit (22).

Inhibition of PI3 kinase signaling is synergistic with CDK4/6 inhibitors, in PIK3CA-mutant TNBC models

The nonbasal, LAR, and MSL subtypes of TNBC are substantially enriched with activating mutations in the PI3K catalytic subunit PIK3CA gene (7), and therefore we investigated the therapeutic potential of inhibiting the PI3K pathway in TNBC. A synergistic interaction (Bliss additivity score < −1.0) was observed between the pan class I PI3K inhibitor pictilisib (GDC0941) and palbociclib in PIK3CA-mutant TNBC cell lines (Fig. 6A), as recently reported by others and us in ER−cell lines (10, 23) and the MDA-MB-453 LAR cell line (23). Combination synergy was not observed in PIK3CA wild-type cell lines nor the RB1-mutant cell line BT549. Synergy was also observed with mTOR inhibitor AZD2014−palbociclib combinations in PIK3CA mutant and some PIK3CA wild-type TNBC cell lines (Supplementary Fig. S4A). We further validated the efficacy of the drug combination with the selective PI3K inhibitor taselisib (GDC0032), which substantially sensitized the MSL cell line SUM159 to palbociclib in clonogenic assays (Fig. 6B) and BrdUrd proliferation assays (Supplementary Fig. S4B). This data suggested that combinations of PI3K pathway inhibitors and CDK4/6 inhibitors could extend the utility of CDK4/6 inhibitors outside LAR subtype cancers.

The combination of palbociclib and taselisib demonstrated greater efficacy than either compound alone in xenografts from the PIK3CA-mutant LAR MDA-MB-453 cell line (palbociclib vs. combination P = 0.02; taselisib vs. combination P = 0.01; Fig. 6C). Pharmacodynamic studies at 1-hour and 4-hour timepoints in the mouse tumors from MDA-MB-453 xenografts treated with individual drugs or the combination, demonstrated significant reduction in phosphorylated RB1 compared with vehicle (Fig. 6D; vehicle vs. taselisib 1 hour P = 0.0004, 4 hours P < 0.0001; vehicle vs. palbociclib 1 hour P < 0.0001, 4 hours P < 0.0001; vehicle vs. combination 1 hour P < 0.0001, 4 hours P < 0.0001). The combination induced greater levels of apoptosis than either drug alone (Supplementary Fig. S4C).

Finally, we examined whether PI3K inhibition with taselisib affected postmitotic CDK2 levels using the PIK3CA-mutant MCF10CAL51 cell line. Taselisib decreased postmitotic CDK2 activity with a greater proportion of cells exiting mitosis with the CDK2low phenotype (Fig. 6E). Premitotic CDK2 levels influenced entry into the cell-cycle after mitosis (Supplementary Fig. S4D). This data suggested that inhibition of PI3K signaling sensitized to CDK4/6 inhibition, in part, as PI3K inhibition suppressed postmitotic CDK2 activity, inducing a CDK2low quiescent state where CDK4/6 activity was required to initiate the cell cycle.

Discussion

We have shown that the LAR subgroup of triple negative breast cancers (TNBC) is highly sensitive to CDK4/6 inhibition in vitro and in vivo (Fig. 1). Sensitivity to CDK4/6 inhibition is dictated at the single-cell level, with resistance to CDK4/6 inhibitors arising from cancer cells that exit mitosis directly into a CDK2high proliferative state, from which CDK4/6 is not necessary for cell-cycle reentry (Figs. 2C and 3A).

Our results further extend prior work in noncancer models that demonstrate a biphasic exit of cells into proliferative and quiescent states after mitosis (12, 13). Cells that exit mitosis with a CDK2low phenotype enter into a quiescent state, requiring CDK4/6 activity to initiate reentry into the cell cycle (Fig. 6F), and are hence sensitive to CDK4/6 inhibition. In contrast, cells that exit mitosis with a CDK2high phenotype enter into a proliferative state, bypassing the restriction point (Fig. 6G), with shorter doubling times. Tumors with a high proportion of CDK2high cells are resistant to CDK4/6 inhibition. Palbociclib-sensitive LAR cancer cells typically exit into a quiescent CDK2low state after mitosis, from which CDK4/6 is required to phosphorylate RB1 and pass the restriction point (2, 24−27). In contrast, basal-like TNBC cells frequently enter a proliferative CDK2high state and are thus resistant to palbociclib treatment. This provides a mechanistic explanation for why basal-like, and potentially many other tumor types are resistant to CDK4/6 inhibition despite being RB1 wild-type. The CDK4/6 and PI3 kinase inhibitor combinations have substantial activity in PIK3CA-mutant nonbasal TNBC, of both LAR and mesenchymal-stem (MSL) subgroups (Fig. 6A), with such combinations having the potential to further expand the TNBC subgroups that could benefit from CDK4/6 inhibition.

Cyclin E1 binds to and activates CDK2 (28, 29) and prior work has demonstrated that cyclin E1 expression mediates resistance to CDK4/6 inhibition (10, 30). The classical view is that CDK2 and cyclin E are downstream of CDK4/6 activity (24). Here we show that in palbociclib-resistant TNBC, cyclin E1 expression is dysregulated and expressed immediately after mitosis (Fig. 4D). Dysregulation of cyclin E1 promotes the CDK4high phenotype, with the CDK2−CyclinE complex active immediately after mitosis, resulting in a short G1 phase (Fig. 6G). The SUM149 cells harbor an inactivating FBXW7 mutation that disrupts the SCF complex, probably contributing to the dysregulation of cyclin E1 expression (Supplementary Table S2). In other contexts, increased CCNE1 gene copy number may drive dysregulation of cyclin E1 expression after mitosis (10). These observations suggest that the measurement of cyclin E1 expression either at the RNA or protein level has the potential to be utilized as a predictive biomarker of resistance to CDK4/6 inhibition in breast cancer.

Daughter cells share the same CDK2 activity state, suggesting that postmitotic CDK2 activity is determined before mitosis (Fig. 5A). However, this is not the result of CDK2high and CDK2low cells, as colonies derived from individual cells largely recapitulate the same variability in CDK2 activity as the parental cell line (Fig. 5D). We provide some data to suggest that DNA damage, and the resulting induction of p21 expression, may also regulate CDK2 activity state after mitosis (Fig. 5G). However, more research is required to further assess the potential role of DNA damaging signaling in this context.

Our results illustrate how single-cell analysis can identify mechanisms of resistance to targeted therapies. Phenotypic heterogeneity between single cells may drive drug resistance, and this may be more clearly elucidated at the single-cell level than through assessment of bulk cell populations. Through single-cell approaches, we identify that CDK2 activity after mitosis is a key determinant of sensitivity to CDK4/6 inhibition, and highlight potential therapeutic strategies for TNBC. An ongoing therapeutic trial is assessing the effectiveness of CDK4/6 inhibition in...
Figure 6. Inhibition of PI3K signaling synergizes with CDK4/6 inhibition in PIK3CA-mutant TNBC. **A**, Synergy heatmap matrices of clonogenic assays in TNBC cell lines treated with palbociclib and/or pictilisib (PI3K inhibitor) at increasing concentrations. Red, cell lines with combination synergy assessed using Bliss additivity score. PIK3CA mut, PIK3CA mutant. The lowest Bliss additivity score for each cell line is indicated. **B**, Clonogenic assays in PIK3CA-mutant SUM159 MSL TNBC cell line grown in palbociclib 500 nmol, pictilisib (pan-PI3 kinase inhibitor) 200 nmol, taselisib (alpha-specific PI3K inhibitor) 100 nmol, and indicated combinations. **C**, Mouse xenografts of LAR MDA-MB-453 cells, treated daily with vehicle (n = 10), palbociclib (n = 10), taselisib (n = 10), or combination (n = 10; P = 0.02 palbociclib vs. combination; P = 0.02; taselisib vs. combination P = 0.01). Error bars are mean tumor volume and SD. **D**, Left, IHC of MDA-MB-453 mouse xenografts stained for phosphorylated RB1 (Ser807/811) after 1 and 4 hours of indicated drug treatment(s). Right, Scatter plots with percentage of positively stained cells for phosphorylated RB1 in IHC sections (left) after 1 hour and 4 hours of treatment. **E**, CDK2 activity after mitosis in PIK3CA-mutant CAL51 treated with vehicle or taselisib 100 nmol. **F**, Model of cell-cycle dynamics in CDK2low cells. Cell exit mitosis into a quiescent state with CDK4/6 activity (blue) necessary to pass through the restriction point (yellow circle), after which CDK2 activity (red) promotes S-phase entry. **G**, Model of cell-cycle dynamics in CDK2high cells. Cells exit mitosis into an active proliferating state with high CDK2 activity, bypassing the restriction point, and CDK4/6 activity is not necessary to enter S-phase. Consequently, CDK2low cells, and cancers with a high proportion of CDK2high cells, are resistant to CDK4/6 inhibition.
combination with PI3K inhibition, in patients with PIK3CA-mutant TNBC (NCT02389842).

Disclosure of Potential Conflicts of Interest

N.C. Turner is a consultant/advisory board member for and reports receiving commercial research grants from Genentech and Pfizer. No potential conflicts of interest were disclosed by the other authors.

Authors’ Contributions

Conception and design: U.S. Asghar, D. Sampath, M.T. Herrera-Abreu, N.C. Turner


Acquisition of data (provided animals, acquired and managed patients, provided facilities, etc.): U.S. Asghar, A.R. Barr, M. Beaney, I. Babina, D. Sampath, J. Giltnane, I.A. Lacap, L. Crocker, A. Young, A. Pearson, M.T. Herrera-Abreu

Analysis and interpretation of data (e.g., statistical analysis, biostatistics, computational analysis): U.S. Asghar, A.R. Barr, R. Cutts, D. Sampath, J. Giltnane, M.T. Herrera-Abreu, N.C. Turner

Writing, review, and/or revision of the manuscript: U.S. Asghar, A.R. Barr, D. Sampath, M.T. Herrera-Abreu, C. Bakal, N.C. Turner

Administrative, technical, or material support (i.e., reporting or organizing data, constructing databases): U.S. Asghar, I. Babina, J.A. Lacap, L. Crocker, M.T. Herrera-Abreu

Study supervision: D. Sampath, M.T. Herrera-Abreu, N.C. Turner

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Uzma S. Asghar, Alexis R. Barr, Ros Cutts, et al.

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