Cell cycle progression is an essential regulatory component of phospholipid metabolism and membrane homeostasis

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We show that phospholipid anabolism does not occur uniformly during the metazoan cell cycle. Transition to S-phase is required for optimal mobilization of lipid precursors, synthesis of specific phospholipid species and endoplasmic reticulum (ER) homeostasis. Average changes observed in whole-cell phospholipid composition, and total ER lipid content, upon stimulation of cell growth can be explained by the cell cycle distribution of the population. TORC1 promotes phospholipid anabolism by slowing S/G2 progression. The cell cycle stage-specific nature of lipid biogenesis is dependent on p53. We propose that coupling lipid metabolism to cell cycle progression is a means by which cells have evolved to coordinate proliferation with cell and organelle growth.

1. Introduction

Cell growth and proliferation requires the de novo synthesis of plasma membrane and organelle endomembranes. The composition of the specific lipid species which make up cell and organelle membranes in both growing cells, and in daughter cells, is also of the utmost importance for cell homeostasis. For example, the relative amounts of key components such as phosphatidylethanolamine (PE) and phosphatidylcholine (PC) species are essential for the optimal function of the endoplasmic reticulum (ER) [1–4]. In addition, the levels of lipid subspecies with specific acyl chain variants profoundly affect biological phenomena as diverse as macrophage differentiation, early embryo development and fertility [5–9].

In all eukaryotes the Protein Kinase B-Target of Rapamycin (PKB/AKT–TOR) pathway promotes phospholipid anabolism by activating sterol response element binding proteins (SREBPs), which are key transcriptional controllers of lipid and phospholipid metabolism. The AKT–TOR pathway also promotes phospholipid anabolism by regulating lipolysis and autophagy [10–16]. We have recently demonstrated that TOR–SREBP regulation of lipid metabolism is required for ER homeostasis [17]. Thus, in response to growth factors such as insulin, AKT–TOR coordinately upregulates protein translation and lipid anabolism [11,16,17]. But it still remains largely unclear as to how activation of AKT–TOR–SREBP signalling is coordinated with cell cycle progression in order to promote membrane homeostasis during growth and division.

While clearly lipid anabolism must be integrated with increased translation and DNA synthesis during growth and cell cycle progression in order to ensure daughter cells have similar lipid content to mother cells, the act of cell division itself also involves profound changes in the architecture of cell membranes [18–21]. For example, cytokinesis is driven by changes in the levels of several
lipid species, which have specific roles in the stepwise assembly and dynamics of regulatory complexes and cytoskeletal structures [22,23]. Consistent with a role of specific lipid species during cell proliferation, a number of early studies have suggested that the metabolism of specific lipids and phospholipids may be regulated in cell cycle specific fashions [20,21,24–26], and even demonstrated direct roles for cell cycle regulators such as the checkpoint factor Cdk1/Cdc28 in the control of lipid metabolism and trafficking in yeast [27]. But how lipid metabolism is regulated during periods of increased growth, such as during the G1 phase of the cell cycle, versus during other cell cycle phases, is very poorly understood.

Here, we show that lipid metabolism is tightly coordinated with cell cycle progression in metazoan cells. The production of key phospholipids that are essential for cell/organellar growth and homeostasis occurs during distinct phases of the cell cycle. Specifically, the G1/S transition is essential to sustain the balance of specific PC and PE species. Cells unable to progress through the G1/S transition are able to generate biomass de novo, but are unable to regulate PC and PE levels, which leads to ER stress. Such ER stress can be rescued through the exogenous supplementation of the relatively short, unsaturated fatty acid oleate (C18 : 1). We show that TOR-SREBP signalling is necessary, but not sufficient, for the regulation of lipid metabolism during growth and proliferation, as SREBP targets are fully activated only in cells that can progress through the G1/S transition. Furthermore, TOR promotes lipid anabolism not only by direct activation of SREBP, but also by regulating cell cycle progression itself. The compartmentalization of lipid metabolism across the cell cycle stages is dependent on p53 activity, because depletion of this regulator allows G1/S-stalled cells to synthesize the required phospholipid species and relieves ER stress derived from G1/S arrest. Moreover, analysis of isolated G1 versus S/G2 populations is compatible with a model by which lipid composition changes observed in insulin-treated cells are explained by changes in cell cycle distribution of the population. Kinetic control of cell cycle progression is thus an additional regulatory layer of lipid metabolism that is integrated with membrane homeostasis programmes.

2. Results

2.1. G1/S blockade during growth stimulation leads to defective lipidostasis and endoplasmic reticulum stress

We recently performed genome-scale RNA interference (RNAi) screens in *Drosophila* cells for genes whose depletion increases, or decreases, activation of the Inositol Requiring Enzyme 1-X-box Binding Protein 1 (IRE1-XBP1) pathway, which is triggered upon induction of ER stress. We found that depletion of genes that promote G1/S transition upregulate the Unfolded Protein Response (UPR), depletion of genes that promote G2/M transition downregulate the UPR (figure 1a; also see [17]). We validated these observations by real-time polymerase chain reaction (RT-PCR) analysis of endogenous XBP1 splicing, key regulators of cell cycle progression. Depletion of G1/S-positive regulators, such as Cyclin D (CycD), Dp, E2f transcription factor or the cyclin-dependent kinase 4 (CDK4) all resulted in increased levels of IRE1-dependent splicing of XBP1 (figure 1b). Conversely, depletion of different proteins required for G2 progression and mitotic entry such as the IplI-aurora-like kinase/aurora kinase B (ial) and polo kinase were associated with lower levels of IRE1 activity as compared with mock-transfected cells (figure 1c). Secondary screens further suggested that cell cycle control integrates with lipid metabolism through the action of SREBP, to ensure ER homeostasis [17]. These observations supported a key role of cell cycle regulatory networks in the control of lipid metabolism and ER homeostasis.

We hypothesized that cell cycle regulators are unlikely to play a role by directly modulating IRE1-XBP1 signalling, but rather that defects in cell cycle progression lead to imbalances in lipid composition that render cells unable to meet the requirements for sustained cell growth and proliferation. Consistent with this notion we found that insulin stimulation, which promotes cell and ER growth, leads to ER stress in *Drosophila* cells unable to progress through G1/S, but has little effect on ER stress in
nocodazole cells arrested at G2/M (figure 2a,1; electronic supplementary material, figure S1b). Insulin-mediated ER stress in thymidine-arrested cells is due to a deficiency in lipid metabolism because exogenous supplementation of relatively short unsaturated fatty acid species (sodium oleate, C18:1) can decrease ER stress in these cells (figure 2b) [3,17,28]. Insulin stimulation also further exacerbates the ER stress that occurs following RNAi-mediated depletion of the G1/S progression regulator Dp (electronic supplementary material, figure S1c,1). Thus, we reasoned that insulin stimulation increases the demand for lipid precursors needed for cell/ER growth, and G1/S progression is required to satisfy this increase.

We previously showed that insulin stimulation results in significant peripheral expansion and remodelling of the ER, and that insulin-driven changes in ER architecture are dependent on TOR and SREBP activity [17] (figure 2c,1). Therefore, we aimed to determine whether similar defects in ER structure occurred in cells sustaining ER stress during G1/S blockade by quantitative image analysis of the ER in single cells [17]. Thymidine exposure alone did not provoke significant alterations in ER morphology (figure 2c,1). Importantly,
insulin-dependent changes in ER architecture—namely, an increased peripheral occupation of ER and diminished texture features—were disrupted by blocking the progression of cells through the G1/S boundary with thymidine (figure 2c,d) [17]. These observations further support the idea that progression through G1/S is required for ER homeostasis and ER expansion/remodelling in proliferating cells, presumably through controlling the supply of lipid species to sustain membrane synthesis.

SREBP acts downstream of insulin-AKT–TOR signalling to regulate lipid metabolism, so that the availability of lipid building blocks such as specific fatty acid species, matches the demand for cell growth and concomitant ER expansion [11,16,17]. Thus, the fact that insulin stimulation increases ER stress in G1/S arrested cells, which can be prevented by addition of exogenous fatty acids, could be explained by dysfunctional SREBP activity during the G1/S blockade. To investigate SREBP activation and cell growth signalling during G1/S arrest, we compared, by western blot analysis, the pattern of relative activation of SREBP between normal and G1/S-blocked cells following insulin stimulation. Despite a moderate reduction (approx. 20%) as compared with unsynchronized cells, insulin stimulation still robustly activates AKT in G1/S-arrested cells, and results in cleavage of ER-localized SREBP to its nuclear localized form to levels equivalent to those of cells allowed to progress to G2/M (figure 3a). Paradoxically, qRT-PCR analysis revealed a dramatic decrease in mRNA levels of specific SREBP transcriptional targets, such as the sphingosine kinase 1 (Sk1) and the fatty acid synthase homologue (Fasn), in G1/S arrested cells, both in the absence or the presence of insulin stimulation (figure 3b). Microarray-based transcriptome profiling (figure 3c; electronic supplementary material, table S1) further revealed that, despite the cleavage and nuclear accumulation of SREBP in G1/S-arrested cells, targets of SREBP transcription were downregulated in cells unable to progress through G1/S (figure 3d). Thus, G1/S arrest does not directly affect insulin signalling or SREBP processing, but diminishes SREBP-dependent transcriptional output.

Figure 3. G1/S blockade neither provokes insulin resistance, nor attenuates SREBP processing, but diminishes SREBP-dependent transcriptional output. (a) Whole-cell lysates were obtained from cells grown under the indicated conditions, and analysed by western blotting for the indicated proteins. *: unspecific, low molecular weight band detected. (b) Total RNA was isolated from cells grown under the indicated conditions, and analysed by qRT-PCR for the expression levels of the indicated genes. 1: control S2R+ cells; 2: insulin (500 nM), 18 h; 3: thymidine (2 mM), 18 h; 4: insulin (500 nM)/thymidine (2 mM), 18 h. (c) Enrichment analysis of genes whose levels of mRNA are reduced (by at least 30%) in cells blocked at the G1/S boundary by RNAi-mediated depletion of Dp, as compared with wild-type cells. Total RNA was extracted and subjected to RNA array analysis from three independent samples per condition. (d) Fold change in mRNA expression in G1/S blocked cells for specific genes as compared with wild-type cells.
to activate SREBP in G1/S arrested cells dysregulates lipid metabolism, and leads to a subsequent loss of membrane homeostasis.

2.2. Insulin stimulation promotes a delay in S/G2-phase progression

Because TORC1 signalling has been described as a key regulator of S/G2 progression kinetics [29], we hypothesized that the AKT–TOR pathway may regulate SREBP-dependent transcriptional output not only by directly promoting SREBP cleavage and nuclear translocation, but also indirectly by promoting cell cycle progression into a phase that is more permissive for SREBP activity. We profiled, using standard cell cytometry procedures, the cell cycle distribution of cells cultured in standard serum-containing growth media, as compared with cells exposed to growth media and insulin (figure 4e, upper panel). In the absence of insulin stimulation, approximately 40% of proliferating S2R+ cells are in G1, approximately 20.5% are in S-phase transition, and approximately 35% are in G2/M. Insulin stimulation leads to an approximate 25% increase in the number of S and G2/M cells, and a decrease in the number of G1 cells (approx. 20%) (figure 4e, lower panel). To determine how insulin stimulation affects cell cycle progression, we briefly pulse-labelled cell populations in S phase with the nucleotide analogue bromodeoxyuridine (BrdU) and estimated their progression time through subsequent stages of the cell cycle by flow cytometry (figure 4f,c) [29]. Untreated S2R+ cells spend approximately 10 h progressing from S through G2/M. However, insulin exposure significantly delayed the progression through these phases of the cell cycle by approximately 6 further hours (figure 4f,d). To determine the effects of insulin stimulation on G2/M progression, we stained normal and insulin-treated S2R+ cells for the early mitotic marker phosphoserine 10 of Histone H3. S2R+ cells, grown in optical 384-well plates, were either left untreated or stimulated for 16 h with 500 nM insulin. pSer10HistH3 signal (normalized to cytoplasmic tubulin signal) was quantified and cells with an intensity greater than or equal to threefold the average background, denoting effective entry into mitosis, were counted from 12 replicate wells, each containing an total average approximately 2500 cells.

Figure 4. Insulin stimulation is associated with a delay in progression through S and G2 phases of the cell cycle. (a) Cell cycle profiles of S2R+ cells grown under either normal culture conditions (upper panel) or stimulated with 500 nM insulin for 16 h (lower panel). Estimated distributions across the cell cycle, according to Dean–Jett–Fox modelling, are shown. (b) Pulse-labelling with and immunostaining for bromodeoxyuridine allows for the profiling of progression through S/G2/M in cells grown under normal conditions (left column) or stimulated with 500 nM insulin approximately 4 h before starting the experiment. Estimated distributions across the cell cycle, according to Dean–Jett–Fox modelling, are shown. (c) The observed changes in cell cycle distribution of unsynchronized cultures is not derived from a delay or blockade in mitotic progression or cytokinesis as assessed by the mitotic marker phosphoserine 10 Histone H3. S2R+ cells, grown in optical 384-well plates, were either left untreated or stimulated for 16 h with 500 nM insulin. pSer10HistH3 signal (normalized to cytoplasmic tubulin signal) was quantified and cells with an intensity greater than or equal to threefold the average background, denoting effective entry into mitosis, were counted from 12 replicate wells, each containing an total average approximately 2500 cells.
We reasoned that if lipid metabolism is indeed a temporally restricted process, we should observe fluctuations in the levels of lipid species in normally proliferating cells in the absence of any chemically or genetically induced cell cycle arrest. Thus, we sorted live cells into G1 versus S/G2 cell cycle fractions by fluorescence-activated cell sorting (FACS) and analysed their relative composition in PC and PE species (electronic supplementary material, table S6) [17]. We also observed very modest, but significant alterations in the composition of lipid precursors towards triacylglyceride synthesis and the formation of lipid droplets, and not, their incorporation into into phospholipids [27].

2.5. Lipidomics profiling reveals cell cycle stage compartmentalization of lipid metabolism in normal proliferating cells

We reasoned that if lipid metabolism is indeed a temporally restricted process, we should observe fluctuations in the levels of lipid species in normally proliferating cells in the absence of any chemically or genetically induced cell cycle arrest. Thus, we sorted live cells into G1 versus S/G2 cell cycle fractions by fluorescence-activated cell sorting (FACS) and analysed their relative composition in PC and PE species. Specifically, insulin leads to an increase in shorter fatty acid chain PC species (12–18C), as well as a substantial relative decrease in a number of longer fatty acid chain species (20–24C), as compared with untreated cells (figure 6a; see also the electronic supplementary material, table S3). We interpret that, in normally proliferating cells, insulin positively regulates the de novo synthesis of specific, shorter fatty acid species that are directly incorporated into PE and PC pools.

Further supporting that G1/S-arrested Drosophila cells are not insulin-resistant, blockade of cell cycle progression at G1/S, either by thymidine or by RNAi-mediated depletion of the essential regulator Dp, did not abolish the increase in total PC levels upon insulin stimulation (electronic supplementary material, figure S3a; see also figure 3e). However, total PC was significantly diminished following insulin treatment, when cells were not allowed to progress through G1/S (electronic supplementary material, figure S3b). Furthermore, G1/S arrest also prevented the insulin-mediated changes in PC species composition that occur when cells are allowed to progress to S phase (figure 6b,c; electronic supplementary material, tables S4 and S5). For example, insulin stimulation in combination with G1/S arrest leads to a relative increase in a number of species of long fatty acid chains, including species bearing C24/C26 acyl chains (figure 6; electronic supplementary material, tables S4 and S5; right-hand arrows). We observed similar changes when profiling PE species from the same samples (electronic supplementary material, figures S3a,b and S4).

To determine whether G1/S arrest in itself results in dysregulation of PC and PE levels, we compared wild-type and G1/S arrested cells in the absence of insulin. Global levels of PC and PE species were significantly diminished across conditions that impaired G1/S progression in the absence of insulin stimulation (electronic supplementary material, figure S5c). In fact, the species that exhibited the largest increase upon insulin stimulation in wild-type cells (26:0/28:1/28:0) were also significantly depleted in unstimulated G1/S-blocked cells as compared with untreated wild-type cells (figure 6d,e). In fact, G1/S-blocked cells exhibit alterations in their profiles of PC and PE species that resemble those observed in SREBP-depleted cells (figure 6d–f; electronic supplementary material, table S6) [17]. We also observed very modest, but significant alterations in the overall degree of acyl chain saturation both in basal culture conditions as well as upon insulin exposure, when comparing wild-type cells with G1/S-arrested cells (electronic supplementary material, figure S3d–f). Altogether, these observations further support the idea that the G1/S transition is an integral component of the homeostatic response to insulin stimulation, and acts by regulating lipid metabolism.
Figure 5. (Caption overleaf.)
composition of the membranes of G1 versus S/G2 cells. Notably, the difference in the lipid profiles between G1 cells versus S/G2 cells resembled the differences observed when comparing mixed populations of cells grown in normal conditions versus cells growing in the presence of insulin (figure 7a,b; see also figure 6a–c; electronic supplementary material, table S7). For example, S/G2-enriched fractions exhibit a higher proportion of short PC/PE species, and reduced levels of longer (24–26C) species, similar to insulin-treated, unsorted cultures (12–18C) (figure 7a,b). We further characterized the relative composition of PC and PE species in sorted G1 versus S/G2 subpopulations from cell cultures exposed for different times to insulin stimulation (figure 7a,b, blue and white bar sets). Of note, relative levels of PC/PE species in G1-sorted cells are indistinguishable from the relative composition of S/G2-sorted cells when derived from cell cultures stimulated for long periods of time with insulin. Because the composition of S/G2 cells did not change to a comparable extent across the three different insulin stimulation time points (electronic supplementary material, table S6), we suggest the residency time in specific stages of the cell cycle is an additional layer in the regulation of complex lipid metabolism.

Although the lipid composition we measure is derived from whole cells, we hypothesized that the architecture and composition of the ER membrane is also regulated by cell cycle progression. To discern how the cell cycle influences the ER membrane, we performed double-labelling experiments in live cells by simultaneously targeting DNA and ER contents with specific probes. As shown in figure 7c, S/G2 cells exhibit a higher average ER membrane content than G1 cells. Strikingly, insulin stimulation does not lead to comparable changes in the average ER content of each subpopulation (figure 7c). In fact, cell cycle distribution alone predicted the overall ER content of a non-segregated cell population (figure 7d,f; see figure 7e for the considered segmentation thresholds). These observations further suggest that lipid metabolism and ER homeostasis are regulated in a manner that is dependent on cell cycle progression.

2.6. P53 is required for the temporal asymmetry of phospholipid metabolism throughout the cell cycle

We sought to identify factors responsible for partitioning of lipid metabolism into cell cycle stages. One candidate for such a factor is the transcriptional master regulator p53, whose activity is controlled in cell cycle dependent fashions and has been previously described to functionally interact in different contexts with SREBP [34–36]. In support of the notion that p53 may regulate lipid metabolism directly, and/or via control of cell cycle progression, we have previously observed that depletion of p53 results in ER stress, but only in cells simultaneously depleted of SREBP (electronic supplementary material, figure S5a,b) [17].

We decided to test whether p53 could be playing a role coupling cell cycle progression with lipid metabolism and ER homeostasis maintenance. Notably, p53 depletion by RNAi did not provoke significant changes in the cell cycle profile of normally cultured cells or insulin-stimulated cells (figure 8a; see also figure 4). Thus, p53 does not function as a cell cycle gatekeeper during proliferation that occurs in the absence of any exogenous stress. However, p53 depletion consistently alleviated the ER stress caused by G1/S block in wild-type cells (figure 8b). Moreover, we observed p53 depletion allowed SREBP target genes to be expressed in G1/S-arrested cells to levels comparable to cycling cells (figure 8c). These effects are unlikely derived from differences in the regulation of the insulin-mediated signalling activity upstream of SREBP, because we did not observe significant changes when comparing wild-type cells with p53-depleted cells across different conditions in terms of AKT phosphorylation or SREBP cleavage (figure 8d).

We further profiled the PC and PE relative composition of cells stimulated to grow but blocked in G1/S, in the presence or the absence of p53 RNAi. p53 depletion completely rescued the alterations in growth-associated phospholipid metabolism associated with G1/S arrest, to the point that the levels of many phospholipid species recovered to levels comparable with those of insulin-stimulated cells that are competent to progress through G1/S (figure 8d; see also the electronic supplementary material, table S8). Taken together, our data suggest that p53 acts to attenuate SREBP-mediated lipid metabolism in G1/S arrested cells, but not during S/G2.

2.7. Endoplasmic reticulum stress results in a delay in progression through S/G2 phase

Because TORC1-driven S/G2 progression kinetics appeared to be a component of the ER homeostatic response in Drosophila cells, we decided to test whether acute ER stress engages these mechanisms. We monitored S/G2 progression in the presence or the absence of the protein glycosylation inhibitor tunicamycin (Tm), which provokes acute ER stress in S2R+ cells in a time-scale of approximately 2 h (electronic supplementary material, figure S6). Acute exposure to Tm leads to an increase in G2/M populations (figure 9a). BrdU pulse-labelling experiments strongly suggested that these changes in cell cycle profile following Tm exposure are due to a delay in progression through S/G2/M phases (figure 9b,c). This cell cycle delay is likely TORC1-dependent because concomitant exposure to rapamycin largely abolished the cell cycle delaying effect
of Tm (figure 9b, leftmost panel column; and figure 9c). We propose that challenges to ER homeostasis delay cell cycle progression in a TORC1-dependent manner in order to regulate lipid metabolism as part of a homeostatic response (figure 10).

3. Discussion

In this study, we show the regulation of PC and PE species, key building blocks of plasma and organelle membranes, are differentially regulated across the cell cycle. Furthermore, our observations support the hypothesis that the ‘residency time’ in specific stages of the cell cycle is an intrinsic mechanism that dictates the appropriate levels of specific lipid species. The underlying mechanisms involve SREBP dependent transcription, because we observe a pronounced attenuation in the transcriptional output of key SREBP targets upon G1/S arrest. SREBP is regulated both by AKT/TORC1-dependent signalling [11,12,14–16,31] as well as structural aspects of nuclear organization and cell cycle progression [15,37,38]. Here we show that both regulatory routes are essentially integrated, as full TORC1-mediated activation of SREBP requires TORC1-driven

![Figure 6](image-url)
G2 entry and progression delay. Finally, we demonstrate that p53 is involved in coupling cell cycle progression to insulin-promoted lipid metabolism. A potential key component of this regulatory action could be an attenuation of SREBP transcriptional activity by p53, preferentially during G1/S stages of the cell cycle (figure 8c). The Drosophila homologue of p53 binds the promoter sequences of several SREBP targets such as Fasn, Skl or Cct1, all of which are important regulators of lipid and phospholipid anabolism [39]. Moreover, p53 has previously been reported as a specific negative regulator of SREBP both in vitro and in vivo [36,40]. The physical and functional interplay between p53 proteins and SREBP is currently a major focus of research.

Figure 7. Population-level changes in phospholipid species following insulin stimulation can be partially explained by changes in cell cycle progression. (a,b) Heatmaps depict percent change in relative amounts of (a) PC species and (b) PE species. Top rows in (a) and (b) show changes resulting from insulin-stimulation in unsynchronized populations stimulated with insulin as compared with control cultures. Next three rows show changes in G2/M versus G1 cells following 0, 8 and 18 h of insulin stimulation. Similarities were assessed by pairwise correlation analysis and ANOVA analysis, across datasets derived from three biological replicates—values are indicated for each condition in the rightmost panels accompanying each graph. Changes in phospholipid levels between insulin stimulated cells and unstimulated cells are similar to the differences between G2/M and G1 (0 h insulin) cells, demonstrating that changes in cell cycle distribution (i.e. an enrichment of G2/M cells) can explain the differences in phospholipid levels following insulin treatment of asynchronous populations. Insulin stimulated cells become dissimilar from G2/M cells as they progress through the cell cycle (8 h and 18 h insulin). (c) ER content from G2/M cells (gated) can explain the differences in phospholipid levels following insulin treatment of asynchronous populations. Insulin stimulated cells become dissimilar to control-treated or insulin-exposed cells. Data are derived from approximately 20 000 cells per condition; error bars report standard deviation. (d–f) ER content from control and insulin-treated unsynchronized populations of cells. (d) ER content as directly measured from ER tracker-counterstained images. (e) A gating comparison for untreated and insulin-treated cells is shown. Data derived from three biological replicates.
attentive in cancer metabolism biology [34,41]. To our knowledge, our observations suggest for the first time that cell cycle stage is a key contextual decision that dictates the outcome of interactions between SREBP and p53.

Dysregulation in the balance of desaturated/saturated fatty acids (and their derivatives) in the ER membrane has been linked with alterations of ER homeostasis—presumably due to changes in the physical properties of the membrane itself [2,8,42–44]. The biological role of different lengths in the acyl chains, and their regulation, are less understood. Acyl chain length can have a profound impact on the curvature, fluidity and fusion rates of biological membranes [7]. Accumulation of longer acyl chain species has been previously linked with environmental or metabolic stress in yeast, and dysregulation of membrane synthesis and integrity maintenance can have a dramatic impact on the process of mitosis and cytokinesis [20,21,24]. Therefore, compartmentalization of lipid metabolism during cell cycle progression may act as a checkpoint strategy that ensures the changes in lipid metabolism required for cytokinesis occur only after successful duplication of genetic material [20,21,23,25,51].

Taken together we have shown there exists systems-coordination of cell growth, cell cycle progression, lipid metabolism and membrane homeostasis. Recent seminal studies suggest that SREBP is a node in metabolic networks where the actions of several oncogenes and tumour suppressors, such as effectors of the Wnt/Hippo pathway and p53,
converge [34,41]. Together with the fact that loss of ER homeostasis has been recursively linked with cancer progression [52–54], this work could lead to a better understanding as to how aberrant metabolism and cell cycle dysregulation are integrated in cancer.

4. Material and methods

4.1. Cell culture and reagents

S2R+ cells were grown in Schneider’s medium (Sigma) supplemented with 10% fetal bovine serum (FBS; Gibco) and 1× penicillin/streptomycin (Gibco) unless stated otherwise, at 25°C. Hoechst 33258 and 33342, bovine insulin, tunicamycin (Tm), thymidine, nocodazole, rapamycin and sodium oleate (Na-C18:1), and anti-bromouridine monoclonal antibodies were purchased from Sigma. Bodipy 493/510, ER Tracker Green, Alexa-488 and Alexa-647 immunoconjugates were purchased from Molecular Probes (Invitrogen). Phospho-histone H3 pSer10 and dAkt pSer505 antibody was purchased from Cell Signaling Technologies. RNAse A was purchased from Ambion. Antibodies against total Drosophila Akt and dSREBP have been developed by the Leevers and Rawson laboratories, respectively [3,17,29]. Calreticulin antibody and α-tubulin antibody were purchased from Abcam and SeroTec, respectively.

4.2. RT, qRT-PCR and protein analysis procedures, and RNA-microarray analysis

Detailed experimental methods have been described elsewhere [17]. The sequences of primers for qRT-PCR analysis can be found in [17]. Microarray analysis of gene expression described in figure 3c,d was performed from total RNA extracted in two consecutive steps of Trizol-chloroform purification. Total RNA was processed and assayed for gene expression in an Affymetrix 2.0 platform (Harvard Medical School) from three biological replicates (3 × 10⁶ cells per replicate).

4.3. dsRNA synthesis, RNAi treatment and siRNA transfection

dsRNA synthesis was carried out using the MEGAScript T7 IVT kit (Ambion-Invitrogen) from T7 promoter-tailed PCR products, and purified using vacuum-driven 96-well filter plates (ThermoScientific). RNAi treatment through ‘bathing’ for RNAi screening was performed as described previously [55]. Batch transfection for dsRNA and DNA was performed using Effectene Reagent (Qiagen) following manufacturer’s protocols. The following amplicons (www.flyrnai.org) were routinely used for validation and biochemical experiments: DRSC18359 (Raptor), DRSC37563 (SREBP), DRSC07402 (Dp), DRSC37618 (dp53), DRSC16665 (dE2f1), DRSC25031 (CycD), DRSC27263 (CDK4), DRSC07601 (dap), DRSC11228 (Myt), DRSC08509 (E(bx)) and DRSC03548 (ial).

4.4. High-throughput sample processing, automated image acquisition and analysis for functional genetic screenings

All automated sample processing and liquid handling was performed on a Cell::Explorer station (PerkinElmer and ThermoScientific). Methodologies and indicated specific procedures for dataset generation for figures 1, 2 and 4 (xbp1-EGFP splicing reporter, ER architecture analysis and normal growth tunicamycin (6 h)) are described in [17].
lipid droplet assessment) have been published elsewhere [17]. Fixation and phospho-histone H3 pSer10 staining was performed as in previous reports [56]. Automated cell segmentation and image analysis were performed using the Acapella 2.5 analysis platform as follows: (i) segmentation of nuclei based on Hoechst 33258 signal; (ii) segmentation of cytoplasm region based on tubulin signal; (iii) filtering of artefacts based on low and high intensity thresholds, nuclear size and roundness, as well as removal of incomplete cell images; (iv) computation of intensities on each channel, normalization of pH3Ser10 signal to tubulin content; and (v) binning or counting of mitotic cells based on manually assessed thresholds.

4.5. Cytometry procedures

All analytic cytometry procedures were performed on an LSRII station (Becton Dickinson). Standard cell cycle profiling using propidium iodide (PI) staining was performed according to standard procedures. Briefly, approximately \(2 \times 10^6\) cells per condition were harvested by gentle scraping and pipetting, washed once in cold Seecof saline buffer (SSB: 6 mM Na₂HPO₄, 3.67 mM KH₂PO₄, 106 mM NaCl, 26.8 mM KCl, 6.4 mM MgCl₂, 2.25 mM CaCl₂, pH 6.8), resuspended in 200 µl of fresh SSB and completed to 1 ml and a final 80% ethanol, and stabilized overnight (O/N) at \(-20^\circ\)C. After two washes in cold SSB, cells were then allowed to progress through cell cycle in the indicated conditions for the indicated times before processing for immunostaining. Cells were pelleted, washed twice in fresh SSB and ethanol-fixed as indicated for propidium staining. Nuclear pellets were then washed twice in fresh SSB, blocked and permeabilized in SSB-B (SSB, 0.5% TX-100, 2% BSA) for 1 h, and then incubated with a 1:20 dilution of anti-BrdU antibody for 2 h at room temperature. After three washes in SSB-T (SSB, 0.1% TX-100) samples were incubated with 1:100 dilution of anti-mouse Alexa488 for 90 min, and then washed thrice in fresh SSB. Stain-positive cells were segmented and analysed for cell cycle progression.

For pulse-labelling of cells entering S phase and immunostaining, we used a modified protocol from Wu et al. [29]. S2R+ cells treated with different conditions were exposed for approximately 10 min to 5 µM BrdU, and then gently washed with 2.5× volumes, two times in sterile SSB supplemented with 1% FBS and five times in fresh medium. Cells were then washed twice in fresh SSB and ethanol-fixed as indicated for propidium staining. Nuclear pellets were then washed twice in fresh SSB, blocked and permeabilized in SSB-B (SSB, 0.5% TX-100, 2% BSA) for 1 h, and then incubated with a 1:20 dilution of anti-BrdU antibody for 2 h at room temperature. After three washes in SSB-T (SSB, 0.1% TX-100) samples were incubated with 1:100 dilution of anti-mouse Alexa488 for 90 min, and then washed thrice in fresh SSB. Stain-positive cells were segmented and analysed for cell cycle progression.

Simultaneous labelling of nuclei and ER and ER-related structures was performed applying a modified protocol [57]. Briefly, live cells corresponding to each treatment were pulse labelled directly in the plate with 0.5 mM Hoechst 33342 and 10 nM ER Tracker Green for 15 min. Cells were then gently scraped and harvested and subjected to a brief step of trypsinization (0.5 U, 2 min), and then washed once in ice-cold complete medium. Cells were spinned and resuspended in ice-cold SSB supplemented with 0.25% BSA, and analysed for DNA and ER content signals.

Sorting of G1 versus S/G2 cells for lipodomics profiling (approx. \(5 \times 10^5\) sorted cells per condition and subpopulation) was performed on a cooled FACS Aria system based on Hoechst 33342 staining after harvesting, brief trypsinization and trypsin inactivation in fresh media on rotation for 30 min. Collection of sorted samples was on ice-cold SSB supplemented with 0.25% BSA before immediate pelleting and snap-freezing.

Figure 10. A model for p53-dependent integration of phospholipid metabolism and ER homeostasis maintenance with TORC1-dependent control of cell cycle progression.

For pulse-labelling of cells entering S phase and immunostaining, we used a modified protocol from Wu et al. [29]. S2R+
4.6. Lipid analysis

All data shown were generated from three independent biological replicates. Equal numbers of cells from each condition (approx. 10^6 cells) were harvested by gentle pipetting, washed twice in fresh Seecof buffer and snap frozen in an ethanol/dry ice bath until further analysis. Upon thawing, cell pellets were subjected to Folch extraction and resuspended in 100 μl ethyl acetate/methanol 1 : 1. After appropriate dilution to work concentration, the lipid extract was analysed by positive ESI-MRM with an AB Sciex 4000 QTRAP station via loop injection with a Shimadzu Prominence HPLC autosampler. Pump A flow rate was set at 0.2 ml min⁻¹ of mixed solvents chloroform/isopropanol/methanol/water 2 : 5 : 2 : 1 (volume ratio). Pump B flow rate was set at 0.05 ml min⁻¹ of isopropanol. The mixed solvents A and B were used for PC and PE ESI ionization in a Turbo Spray ion source before MRM analysis. The operation parameters of the 4000 QTRAP for PC and PE analysis are detailed below.

PC analysis:
- Source/gas parameters: curtain gas (CUR): 25; collision gas (CAD): medium; ion spray voltage (IS): 5500; temperature (TEM): 650; ion source gas 1 (GS1): 35; ion source gas 2 (GS2): 65; interface heater (ihe): on.
- Compound parameters: declustering potential (DP): 140; entrance potential (EP): 10; collision energy (CE): 37; collision cell exit potential (CXP): 11. MRM time: 30 ms. Both Q1 and Q3 mass were set up at unit resolution.

PE analysis:
- Source/gas parameters: curtain gas (CUR): 25; collision gas (CAD): medium; ion spray voltage (IS): 5500; temperature (TEM): 600; ion source gas 1 (GS1): 35; ion source gas 2 (GS2): 60; interface heater (ihe): on.
- Compound parameters: declustering potential (DP): 90; Entrance Potential (EP): 10; collision energy (CE): 31; collision cell exit potential (CXP): 17. MRM time: 20 ms. Both Q1 and Q3 mass were set up at unit resolution.

For the quantitation of the relative PC/PE species shown across figures 6–8, we first calculated a weighted value for each species as compared with total amounts of PC or PE, respectively, and obtained averages of this normalized value across three independent biological replicates. Subsequently, a differential score was calculated for each species as the percentage change from the control average normalized value.

4.7. Data management, statistical analysis and analysis software

Data analysis, presentation and analysis of statistical significance were performed using the GraphPad Prism 6.0 software. For the quantification of XBP1 mRNA unconventional splicing by RT-PCR in the experiments shown in figures 1, 2 and 8, a minimum of two technical replicates, each including two biological replicates (hence, at least four independent runs), were analysed for Student’s t-test for the indicated sample pairs. Cell cycle modelling (Dean–Jett–Fox algorithm) was performed using the FlowJo cytometry package using raw cytometry data. For the focused screens shown in figure 5, robust Z-scores were calculated for each gene using averaged values from replicates, and mean and standard deviation values from control cells. Hierarchical clustering of the dsRNA treatments according to their phenotypic signatures (figure 5a) was based on Euclidean distances.

Authors’ contributions. M.S.-A. and C.B. conceived the study and designed experimental procedures; M.S.-A. performed all experiments and analyses; F.F. assisted on qRT-PCR analyses and microarray data analysis and curation; M.S.-A., Q.Z. and M.J.O.W. carried out lipidomics analyses; M.S.-A. and C.B. wrote the paper.

Competing interests. The authors declare that no conflict of interest exists.

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