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Abstract

This review focuses on recent studies showing that cardiolipin (CL), a unique mitochondrial phospholipid, regulates many cellular functions and signaling pathways, both inside and outside the mitochondria. Inside the mitochondria, CL is a critical target of mitochondrial generated reactive oxygen species (ROS) and regulates signaling events related to apoptosis and aging. CL deficiency causes perturbation of signaling pathways outside the mitochondria, including the PKC-Slt2 cell integrity pathway and the high osmolarity glycerol (HOG) pathway, and is a key player in the cross-talk between the mitochondria and the vacuole. Understanding these connections may shed light on the pathology of Barth syndrome, a disorder of CL remodeling.

Keywords

Cardiolipin • Phosphatidylglycerol • Cellular signaling • Apoptosis • Cell wall biogenesis • Mitophagy • Mitochondria • Vacuolar function • Reactive oxygen species • Anionic phospholipids • Barth syndrome

11.1 Introduction

It is not unusual to find even current depictions of membranes as homogenous lipid matrices that function primarily to support the allegedly *important* protein molecules embedded within. This belies the fascinating discoveries in the past two decades of cellular and organelle-specific

functions attributed to individual membrane lipids, and of the plethora of regulatory and signaling molecules derived from glycerolipids and sphingolipids. In this light, it is essential to elucidate the functions of specific membrane lipids and the cellular consequences of their depletion.

A phospholipid that has been the focus of considerable attention relatively recently – although it was first isolated and purified from beef heart in 1942 [1, 2], is cardiolipin (CL). CL is structurally unique. In contrast to the other membrane phospholipids, in which a single glycerol backbone is acylated to two fatty acid chains, CL contains two phosphatidyl groups (linked to a glycerol

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backbone) and four fatty acyl chains. It is enriched in energy harvesting membranes of mitochondria, chloroplasts, bacterial plasma membranes, and hydrogenosomes, underscoring the importance of this lipid in energy production [3–5]. CL is tightly associated with mitochondrial proteins and respiratory chain complexes and is essential for their optimal activity [6–10]. In the inner membrane, CL provides structural stability to membrane proteins through hydrophobic and electrostatic interactions.

In light of its association with the respiratory apparatus, the role of CL in mitochondrial bioenergetics was not entirely unexpected. Interestingly, however, recent studies carried out primarily in yeast indicate that CL is also required for cellular functions that are not directly associated with oxidative phosphorylation. In accordance with a broad definition of a ‘bioactive lipid’ as one in which changes in levels lead to functional consequences [11], perturbation of CL composition (including CL levels, acyl species, and degree of peroxidation) leads to dramatic cellular consequences: (1) Alterations in CL levels and acyl chain composition increases the recruitment to the mitochondria of cytosolic proteins that trigger apoptosis [12–14]. (2) Perturbation of CL synthesis or remodeling leads to increased production of reactive oxygen species (ROS), which induces aging [15–20]. (3) Blocking CL synthesis in yeast at the first step of the pathway deleteriously affects cell wall biogenesis and alters the response of two signaling pathways, the protein kinase C (PKC)-Slt2 mitogen activated protein kinase (MAPK) and the high osmolarity glycerol (HOG) pathways [21–23]. (4) The inability of yeast cells to synthesize CL leads to decreased vacuolar function and reduced V-ATPase activity, suggesting that CL mediates cross talk between mitochondria and the vacuole [24]. The current review focuses on the role of CL in regulating these cellular functions. We conclude with unanswered questions that remain exciting avenues for future studies, which may have implications for understanding the pathophysiology of Barth syndrome (BTHS), a genetic disorder of CL remodeling.

11.2 CL Biosynthesis and Remodeling

One of the most intriguing aspects of CL biosynthesis is that the lipid that is initially synthesized contains primarily saturated fatty acids, while the mature CL that is essential for normal cellular function contains unsaturated fatty acids. The distinct composition of acyl chains is achieved through a highly conserved pathway of synthesis and remodeling, as shown in Fig. 11.1. The first step is catalyzed by phosphatidylglycerolphosphate (PGP) synthase (Pgs1), which converts CDP-diacylglycerol (DAG) and glycerol-3-phosphate (G-3-P) to PGP [25, 33]. PGP is dephosphorylated to phosphatidylglycerol (PG) by PGP phosphatase (Gep4) [26, 34]. The mammalian homologue of the yeast *GEP4* gene was recently identified as protein tyrosine phosphatase localized in the mitochondrion (PTPMT1) [34]. CL synthase (Crd1) catalyzes an irreversible condensation reaction in which the phosphatidyl group of CDP-DAG is linked to PG via cleavage of a high-energy anhydride bond to form CL [27–30, 35–38]. CL synthase does not show strong preference for specific fatty acyl chains [38–40]. How, then, is acyl specificity achieved? The newly synthesized CL undergoes deacylation by a CL-specific deacylase (Cld1), which is homologous to the mammalian phospholipase A₂ [31, 41, 42]. Cld1 removes one saturated fatty acyl chain from CL to form monolysocardiolipin (MLCL) [31]. The transacylase tafazzin (Taz1) reacylates MLCL with an unsaturated fatty acid to form mature CL [32, 43, 44]. Taz1 carries out exchange of acyl chains between CL and phospholipids that primarily include phosphatidylcholine (PC), to sequentially replace the fatty acyl chains from all four acyl positions of CL [45, 46]. The end result of this exchange is molecular symmetry of CL molecules across the eukaryotic kingdom, from yeast to humans, which is characteristic of the organism and of specific tissues and organs [47]. For example, in yeast, the mature form of CL contains oleic acid, while CL in the normal human heart is primarily tetralinoleoyl-CL (L₄-CL) [47].

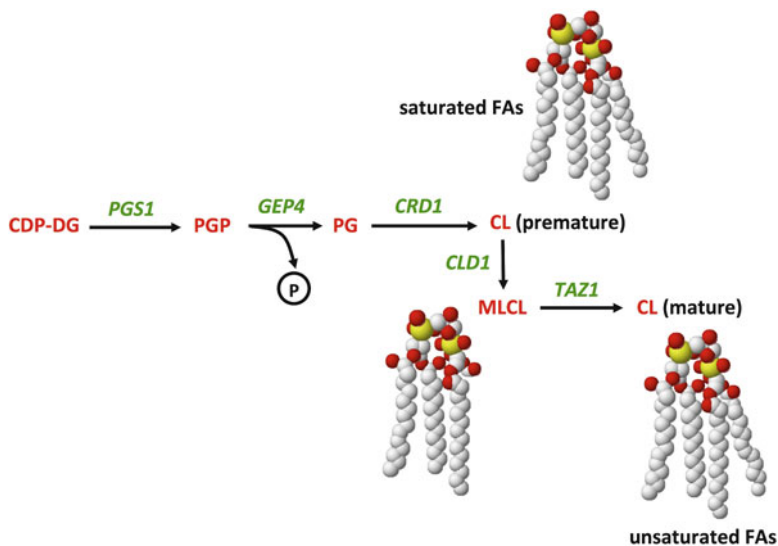


Fig. 11.1 Synthesis and remodeling of CL in yeast. CL synthesis begins with the conversion of CDP-diacylglycerol (CDP-DG) to phosphatidylglycerol phosphate (PGP) by PGP synthase (encoded by *PGS1*) [25]. PGP is dephosphorylated to phosphatidylglycerol (PG) by *GEP4*-encoded PGP phosphatase [26]. CL synthase (encoded by *CRD1*) converts PG to premature CL

containing primarily *saturated* fatty acids (FA) [27–30]. CL is deacylated by CL deacylase (encoded by *CLD1*) to monolysocardiolipin (MLCL) [31], which is reacylated by the *TAZ1*-encoded enzyme tafazzin to mature CL containing *unsaturated* fatty acids [32]. The yeast gene names are depicted in *green*, while phospholipids and their intermediates are shown in *red*

A deficiency of tafazzin in humans leads to a complete absence of L_4 -CL, resulting in the severe cardiomyopathy observed in BTHS.

While tafazzin is the only known yeast enzyme that adds fatty acyl chains to MLCL, two other enzymes in addition to tafazzin remodel CL in mammalian cells. MLCL acyltransferase-1 (MLCLAT1), isolated and purified from pig liver mitochondria, shows specificity for linoleate [48]. Thus, over-expression of MLCLAT1 in tafazzin-deficient BTHS lymphoblasts increased incorporation of linoleic acid into CL, and RNAi knockdown of MLCLAT1 in HeLa cells showed reduced linoleic acid inclusion in CL [49]. The biological function of this enzyme is not clear. A second enzyme, acyl-CoA:lysoCL acyltransferase 1 (ALCAT1), identified in mouse, was initially thought to be located in the endoplasmic reticulum, but was subsequently determined to be present in the mitochondrial-associated membranes, where phospholipid traffic between the endoplasmic reticulum and the mitochondria takes place [17, 50]. In contrast to MLCLAT1,

ALCAT1 shows no specificity for linoleic acid. ALCAT1 was shown to catalyze CL remodeling to incorporate long chain polyunsaturated fatty acyl chains such as docosahexaenoic acid (DHA) [17]. Enhanced incorporation of polyunsaturated fatty acyl chains in CL makes it more susceptible to oxidative damage by ROS, causing early peroxidation [51–53]. ALCAT1 null mutant mice exhibit elevated CL levels along with increased L_4 -CL [16, 17], whereas overexpression of ALCAT1 has been shown to decrease total CL levels and increase incorporation of long chain polyunsaturated fatty acyl chains [54]. These findings suggest that ALCAT1 may negatively regulate CL biosynthesis.

In light of the importance of CL in cellular function, it is not surprising that perturbation of CL synthesis leads to serious illness. The most direct example of this link is seen in BTHS, a life-threatening illness characterized by dilated cardiomyopathy and sudden death from arrhythmia [55, 56]. BTHS results from mutation in the CL remodeling enzyme tafazzin [44, 57].

This leads to an abnormal CL profile characterized by decreased total CL, increased MLCL, and aberrant CL acylation, most notably the loss of the predominant CL species in normal myocardium, L₄-CL [58]. How these abnormalities cause the associated pathology in BTHS is not known [59].

CL abnormalities have also been observed in heart failure [60, 61]. Heart failure due to dilated cardiomyopathy is the primary cause of death in diabetic patients [62, 63]. Metabolic perturbations observed in diabetic cardiomyopathy include increased utilization of fatty acid substrates, decreased utilization of glucose, and mitochondrial dysfunction [64–66]. However, the molecular mechanism that leads to heart failure in diabetic patients is not known. Interestingly, a decrease in CL levels and alterations in CL acyl species were found in early stages of diabetes induced by streptozotocin in mice, suggesting that mitochondrial dysfunction and cardiomyopathy may be due to alterations in CL metabolism [67, 68]. The decrease in CL levels may result from remodeling of CL fatty acyl species with DHA, which is known to cause CL peroxidation by ROS [51–53]. In summary, depletion of CL content and alterations in CL fatty acyl species lead to BTHS, and may also contribute to pathological conditions and metabolic perturbations in other human disorders.

11.3 CL and Apoptosis

Perturbations in CL levels and acyl composition play a crucial role in regulating apoptosis, the complex process leading to programmed cell death. The role of CL in apoptosis derives from its interactions with cytochrome c (Cyt c) and with apoptotic proteins (Fig. 11.2).

11.3.1 CL and Cyt c

Interactions between CL and Cyt c are an important determinant of apoptosis. Cyt c, which transfers electrons from complex III to complex IV, is bound to the outer leaflet of the mitochondrion inner

membrane through interactions with CL [69, 70]. The binding of Cyt c to CL is essential to anchor it to the inner membrane, and release of Cyt c to the cytosol serves as a signal to recruit apoptotic proteins to the mitochondria to initiate apoptosis [74, 75, 79, 80]. CL binds Cyt c in two different conformations – a loosely bound state that is facilitated by means of electrostatic interactions, and a tightly bound state that is mediated by hydrophobic interactions in which Cyt c is partially embedded in the inner membrane [69, 70]. Release of Cyt c from CL requires dissociation of both electrostatic and hydrophobic interactions [81]. The production of ROS may alter the CL-Cyt c association [80–82]. Alternatively, the peroxidation of CL by hydrogen peroxide generated in the mitochondria leads to the release of Cyt c from the tightly bound state into the intermembrane space [12, 76].

11.3.2 Recruitment of Apoptotic Proteins

An early trigger of apoptosis is the change in CL composition in the mitochondrial inner and outer membranes, followed by dissipation of the membrane potential and flipping of phosphatidylserine (PS) to the external surface of the plasma membrane [83, 84]. A diverse set of apoptotic proteins such as t-Bid, Bax, Bak, and caspase-8 are recruited to the mitochondrial surface of cells undergoing apoptosis in a CL-dependent manner [71–73]. Upon activation, caspase-8 migrates to the mitochondrial outer membrane in regions where CL is present. Caspase-8 is said to cleave Bid to its active form, tBid (truncated Bid). A significant amount of CL is translocated from the inner to the outer mitochondrial membrane, which likely serves as a signal for binding of the apoptotic proteins [14, 85, 86]. The binding of t-Bid to CL is thought to further increase CL transfer to the outer membranes. Alternatively, apoptotic proteins may be guided to the mitochondria by means of altering the outer membrane charge [87]. By increasing the CL content, the mitochondrial outer membrane may accrue a more

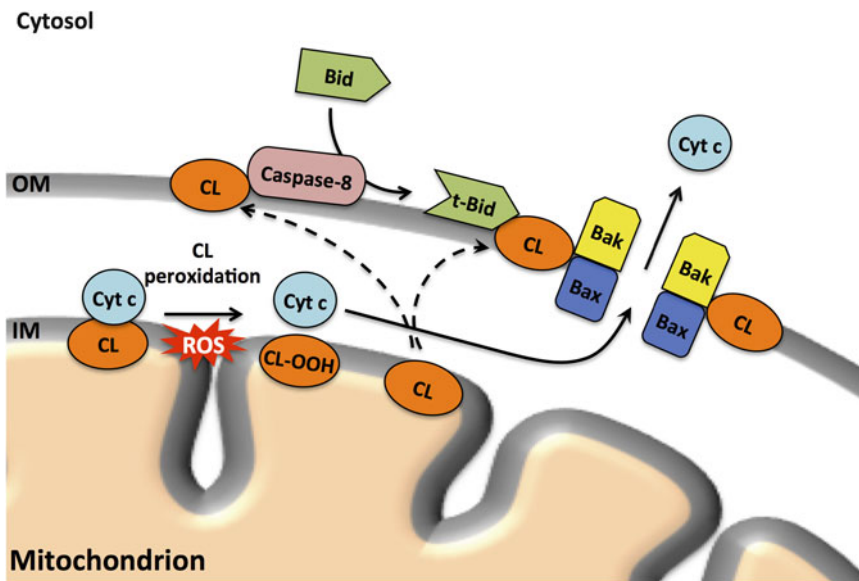


Fig. 11.2 Perturbation of CL metabolism triggers apoptosis. The binding of cytochrome c (Cyt c) to CL is essential to anchor it to the inner mitochondrial membrane, facing the intermembrane space [69, 70]. Peroxidation of CL (CL-OOH) by reactive oxygen species (ROS) leads to release of Cyt c to the cytosol, which

serves as a signal to initiate apoptosis [71–73]. Caspase-8 cleaves Bid protein to its active form, truncated Bid (t-Bid) [74–76]. Binding of t-Bid to CL enhances translocation of CL to the outer mitochondrial membrane, which facilitates targeting of apoptotic proteins (Bak and Bax) to the outer membrane [77, 78]

negative charge, which serves as a targeting signal for recruiting polycationic apoptotic proteins to the mitochondria [77, 85]. Consistent with this, ectopic overexpression of a CL-binding protein masked the negative charge on the membrane and inhibited apoptosis [87]. The recruitment to and oligomerization of Bak-Bax in the outer mitochondrial membrane is a CL dependent process, which permeabilizes the outer mitochondria to trigger Cyt c release and progression of apoptosis [88, 89]. This suggests that CL-rich regions in the outer membrane serve as a key signal for targeting pro-apoptotic proteins of the Bcl2 family to bring about apoptosis [78, 85].

11.3.3 Translocation of CL

Early in apoptosis, CL translocation from the inner to the outer mitochondrial membrane may be carried out through several transport modes. First, the inner and outer membrane contact

sites, which are enriched in CL through interactions with mitochondrial creatine kinase (MtCK), could facilitate the transfer of CL from the inner to outer membrane [90–95]. Second, phospholipid scramblase-3 (PLS-3) has been shown to translocate CL from the inner membrane to the outer membrane during the onset of apoptosis [96–98]. Consistent with this, cells overexpressing PLS-3 exhibit increased apoptosis, while inactivation of PLS-3 leads to increased resistance to UV-induced apoptosis [97]. CL and Bid interactions have been shown at the contact sites, which likely contribute to mitochondrial permeabilization to induce apoptosis [99]. Changes in CL content in the membrane may be mediated by Bid, as evidence suggests that Bid exhibits lipid transfer activity [100, 101]. Lymphoblastoid cells derived from BTHS and TAZ knockdown HeLa cells were more resistant to Fas-induced apoptosis [72]. Specifically, reduction of mature CL caused defective activation of caspase-8, suggesting that processing of caspase-8 on the mitochondrial membranes is

CL-dependent. To summarize, CL in the mitochondria is an important mediator of apoptosis, and apoptotic proteins are directed to the mitochondria in a CL-dependent manner.

11.4 CL in Bioenergetics and Mitochondrial Dysfunction

The relationship between CL and ROS is complex. CL physically interacts with proteins of the mitochondrial respiratory chain complexes and other components of the membrane and forms lipid scaffolds for tethering and stabilizing mitochondrial membrane proteins to enhance their enzymatic activities [7, 8, 102–105]. Consistent with the role of CL in bioenergetics, mitochondria deficient in CL exhibit decreased activity of respiratory complexes and carrier proteins [106]. The generation of ROS in mitochondria, which is a byproduct of oxidative phosphorylation [107–109], is enhanced upon CL deficiency [20]. ROS, in turn, damages CL by peroxidation of the unsaturated fatty acids.

11.4.1 CL and Supercomplexes

For efficient substrate channeling between the individual complexes, the mitochondrial respiratory chain components are organized in supra-molecular structures called supercomplexes [110]. In mammalian cells, complex I is associated with two units of complex III and multiple units of complex IV. In *S. cerevisiae*, which lacks complex I, two copies of complex III are bound to either one or two units of complex IV. CL deficiency in yeast leads to destabilization of the respiratory supercomplexes, indicating that CL functions to stabilize these complexes [10, 111, 112]. Similarly, tafazzin deficient human fibroblasts exhibit destabilization of the supercomplexes [113]. For efficient ADP/ATP exchange, CL is also required for the association of the ADP/ATP carrier protein with the supercomplexes [114].

11.4.2 CL Deficiency and ROS Generation

The role of CL in the supercomplexes may be that of a proton trap, to avoid leakage of protons and enhance the membrane potential for efficient oxidative phosphorylation [115–117]. Not surprisingly, defective supercomplex formation and CL deficiency lead to increased ROS production [20, 118].

Among the respiratory chain complexes, complexes I and III are prime sites for ROS generation [119–122]. Because of the proximity of CL to these ROS generating centers, the unsaturated fatty acyl chains of CL are susceptible to damage by peroxidation. Superoxide generated by respiratory complex III causes peroxidation of CL and alters the activity of Cyt c oxidase [123–125]. Optimal function of Cyt c oxidase, the terminal enzyme complex of the respiratory chain, is dependent on CL [6, 126–128]. Reduced activity of Cyt c oxidase from reperfused heart was restored specifically by exogenous supplementation of CL, but not by peroxidized CL or other phospholipids [129]. In addition, reduced activity and increased ROS generation by complexes I and III were also rescued by CL supplementation [125, 130]. These studies indicate that peroxidized CL cannot effectively carry out mitochondrial functions that are dependent on normal CL.

Peroxidation of CL by ROS is seen as the primary cause of CL mobilization to the outer leaflet of the inner membrane. Human leukemia cells treated with the apoptosis-inducing drug staurosporine rapidly underwent apoptosis along with an increase in CL content in the outer mitochondrial membrane [83]. However, the change in CL content was preceded by increased ROS production and CL peroxidation, suggesting that perturbation of CL metabolism could be an early step in mitochondria-induced apoptosis. Due to the high content of unsaturated fatty acyl chains, CL is particularly susceptible to peroxidation [131, 132]. Peroxidation of CL alters the molecular conformation leading to formation of non-bilayer hexagonal structures, which could serve as a

marker for targeting the cytosolic apoptotic machinery to the mitochondria [77].

11.4.3 CL in Mitochondrial Dysfunction and Aging

Under normal physiological conditions, the damaged fatty acyl chains of CL may be replaced through the remodeling process [45]. Pathological remodeling of CL has been linked to mitochondrial dysfunction in human diseases [17, 18, 61, 67]. Recent studies have shown that *ALCAT1* may be involved in the pathological remodeling of CL in cells undergoing oxidative stress. As mentioned earlier, *ALCAT1* overexpression leads to a decrease in CL levels and aberrant remodeling of CL with long chain polyunsaturated acyl chains such as DHA, which are highly susceptible to oxidation by ROS [17, 52, 53]. The close proximity of CL to respiratory complexes in the inner membrane where ROS is generated increases exposure of these long chain unsaturated fatty acyl chains to ROS. Aberrant CL remodeling resulting from increased *ALCAT1* expression leads to the mitochondrial dysfunction seen in pathological conditions such as hyperthyroid cardiomyopathy, diabetes, and diet-induced obesity in mice [15–17, 133]. *ALCAT1* null mice exhibit increased expression of *MLCAT1* along with elevated levels of CL containing linoleic acid. These findings underscore the significance of CL remodeling and the impact of this process on mitochondrial function and ROS generation.

A decline in CL levels appears to be a primary feature of aging [134–139]. In aging cells, CL is pathologically remodeled with polyunsaturated fatty acyl chains such as arachidonic and docosahexaenoic acids, which are more susceptible to peroxidation than linoleic acid in normal CL [18, 54]. Mitochondrial CL levels, along with oxidative capacity and ATP synthesis, decrease significantly with age [134, 140–143].

CL is required for the optimal function of several mitochondrial carrier proteins involved in the transport of essential metabolites into mitochondria [106]. In the heart, oxidation of pyruvate and β -oxidation of fatty acids are

two major sources of ATP generation [144–146]. The transport of pyruvate into mitochondria by the pyruvate carrier and the exchange of carnitine esters by the carnitine:acylcarnitine translocase are, therefore, critical for energy metabolism. Studies have demonstrated that enzymatic activities of both the mitochondrial pyruvate carrier and carnitine:acylcarnitine translocase, which are dependent on CL [147, 148], are decreased in aging heart muscle [149, 150]. Interestingly, administration of acetyl-L-carnitine in aged rats restored decreased CL levels and the activities of the mitochondrial pyruvate carrier and carnitine:acylcarnitine translocase to levels found in young rats [149, 150]. Dietary supplementation of acetyl-L-carnitine also showed similar beneficial effects, increasing mitochondria membrane potential and, in turn, improving physical mobility in aged rats [141, 151]. These findings suggest that the supply of carnitine to the mitochondria may become limited during aging, hindering energy production through β -oxidation [150, 152]. Although acetyl-L-carnitine supplementation restored CL levels and improved mitochondrial metabolic functions in aged animals, the underlying molecular mechanism remains unresolved.

11.5 CL and the PKC-Slt2 Cell Integrity Pathway

Null mutants in yeast have been characterized for each step of the CL biosynthetic pathway, and mutants blocked earlier in the pathway have more severe phenotypes. Thus, the *pgs1* Δ mutant, which cannot synthesize CL or the precursor PG (Fig. 11.1), exhibits severe growth defects not only in non-fermentable carbon sources, which are metabolized by respiration, but also in fermentable carbon sources, in which respiration is not required [25, 153]. This observation indicated that PG and/or CL are required for cellular functions apart from mitochondrial bioenergetics [154]. Genetic studies to isolate spontaneous suppressors of the *pgs1* Δ mutant growth defect identified a loss of function mutation of *KRE5*, a gene involved in cell wall biogenesis [21].

Consistent with defective cell wall biogenesis, the *pgs1Δ* mutant exhibited enlarged cell size characteristic of cell wall mutants, reduced levels of β-1,3-glucan as a result of decreased activity of glucan synthase, and sensitivity to cell wall perturbing agents [155–157]. These defects were restored by disruption of *KRE5* in *pgs1Δ*, which increased expression of the genes *FKS1* and *FKS2* encoding glucan synthase [22]. These findings were in agreement with the identification of *PGS1* in a screen to identify genes involved in cell wall biogenesis [158].

Studies to gain insight into the mechanism linking CL to the cell wall focused on the PKC-Slt2 cell integrity pathway. Activation of the cell integrity pathway is triggered by signals generated from cell wall sensor proteins to Rom2, which, in turn, activates formation of the GTP-bound form of Rho1p. The activated Rho1 protein transmits a signal to Pkc1 to trigger the Mpk1/Slt2 MAPK signaling cascade, which results in dual phosphorylation of Slt2 [159, 160]. The dual phosphorylation of Slt2 is essential to activate transcription factors that up-regulate genes involved in cell wall remodeling, particularly in response to heat stress [156, 161, 162]. The *pgs1Δ* mutant exhibited defective activation of the PKC-Slt2 cell-integrity signaling cascade, indicated by decreased Slt2 phosphorylation levels [22]. Consistent with this, overexpression of individual genes in the PKC-Slt2 pathway rescued the growth defect of *pgs1Δ* at elevated temperature and improved resistance to the cell wall perturbing chemicals calcofluor white and caffeine. Interestingly, deletion of *KRE5* in *pgs1Δ* also led to increased activation of the PKC-Slt2 cell-integrity pathway.

A mitochondrial connection to the cell wall is not new. Genome-wide screens have identified several yeast genes required for mitochondrial function that, when mutated, affect chemical components of the cell wall [158, 163, 164]. Furthermore, mitochondrial respiratory defects negatively impact the synthesis of cell wall components [158, 164]. The underlying mechanism whereby CL regulates cell wall remodeling is not known. One possibility is that CL is required for activity of one or more proteins that exhibit dual

localization in the cell wall/plasma membrane and mitochondria [165]. Interesting possibilities include three proteins of the PKC-Slt2 cell integrity pathway, Fks1, Zeo1 and Rho1, which are found both in the mitochondria and the plasma membrane [166–168]. Mitochondrial targeting of these proteins may be CL-dependent. Alternatively, their stability in the mitochondrial membrane may be decreased in the absence of CL.

The yeast cell wall also plays an important role in regulating replicative life span [169]. Consistent with this, the *pgs1Δ* mutant, which exhibits cell wall defects, also has a decreased replicative life span [21, 23]. Intriguingly, experiments to elucidate the mechanism linking PG/CL to defects in the cell wall, PKC/Slt2 signaling and aging led to another signaling pathway – the HOG stress response pathway.

11.6 CL and the HOG Stress Response Pathway

In response to stress, cells are regulated by the opposing actions of the PKC-Slt2 and HOG signaling pathways [170–172]. Heat or low osmolarity stress leads to activation of the PKC-Slt2 pathway, resulting in increased expression of the cell wall remodeling genes leading to a decrease in turgor pressure [173–175]. In contrast, activation of the HOG signaling pathway causes an increase in turgor pressure [175, 176]. Because the *pgs1Δ* mutant exhibited defective activation of the PKC-Slt2 signaling cascade, it was hypothesized that growth defects of the mutant resulted from increased turgor pressure, which may be rescued by down-regulation of the HOG pathway (Fig. 11.3) [23]. This hypothesis was supported by the finding that deletion of *SHO1*, an upstream activator of HOG signaling, rescued growth defects, increased the replicative life span, and alleviated sensitivity to cell wall perturbing agents in *pgs1Δ* [23]. Interestingly, the mutant did not exhibit increased activation of the HOG pathway. It is possible that, in the absence of PKC-Slt2 activation, even wild type levels of HOG activation lead to turgor pressure levels that affect growth. These findings suggest that homeostasis achieved

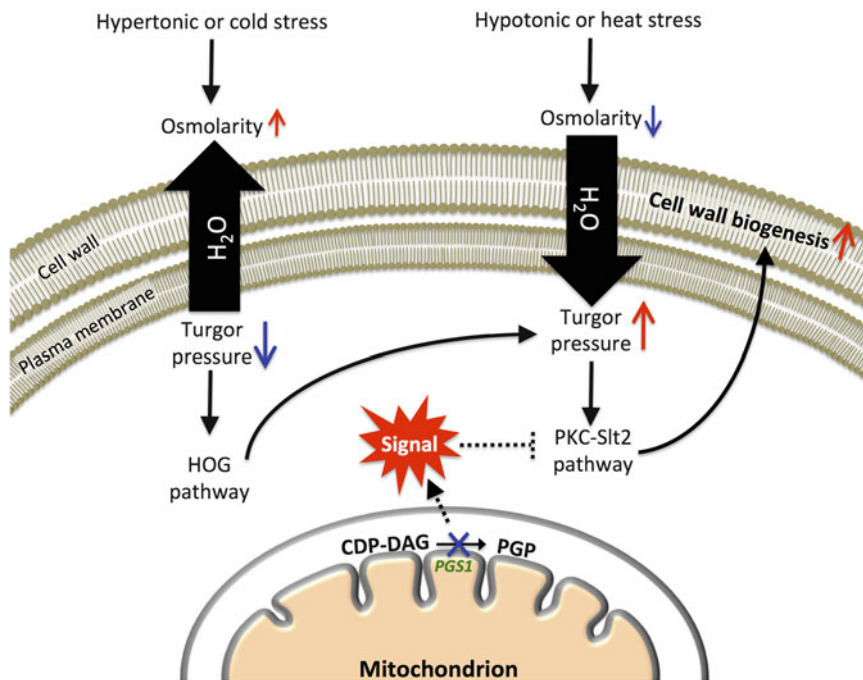


Fig. 11.3 CL deficiency leads to perturbation of PKC-Slt2 and HOG signaling pathways. The PKC-Slt2 and HOG signaling pathways coordinately regulate cell wall biogenesis and intracellular turgor pressure, respectively [173, 175]. Under hypertonic or cold stress conditions, extracellular osmolarity is increased, causing an efflux of intracellular water to reduce the turgor pressure on the cell wall. To counteract augmented extracellular osmolarity, the HOG pathway is activated, which leads to an increase in intracellular turgor pressure [170, 177]. In contrast, under heat or hypotonic stress, extracellular osmolarity

is decreased, which causes an influx of water inside the cell to increase intracellular turgor pressure. To counteract the increased turgor pressure, the activated PKC-Slt2 pathway induces cell wall synthesis [172, 173]. We hypothesize that disruption of the CL pathway by mutation of *PGS1* generates a signal that is detected by regulators or components of the PKC-Slt2 pathway, which, in turn, down-regulates the pathway [21, 22]. Under these conditions, an increase in intracellular turgor pressure by activation of the HOG pathway is deleterious in *pgs1Δ* cells [23]

by these two signaling pathways is perturbed upon CL deficiency (Fig. 11.3).

11.7 CL Mediates Cross-Talk Between Mitochondria and Vacuole

The yeast *crd1Δ* mutant, which lacks CL, was shown to have defective vacuolar function [24]. CL deficiency caused decreased V-ATPase activity and proton pumping, reduced vacuolar acidification, and enlargement of the vacuole. The yeast vacuole plays a crucial role in adjusting to high external osmolarity and decreased turgor pressure, and in maintaining cytosolic ion concentrations [178, 179]. Consistent with

perturbation of intracellular osmotic balance in the *crd1Δ* mutant, growth and vacuolar defects were rescued by supplementation of sorbitol [24].

In some genetic backgrounds, the *crd1Δ* mutant exhibits increased expression of *RTG2*, a critical sensor of mitochondrial dysfunction that relays metabolic defects to the nucleus via the retrograde signaling pathway [180, 181]. Consistent with overactivation of Rtg2, deletion of the *RTG2* gene restored vacuolar acidification and V-ATPase activity and rescued the growth defect of the *crd1Δ* mutant at elevated temperature. However, deletion of the retrograde pathway activator *RTG3* did not rescue the mutant, suggesting that the defects observed in *crd1Δ* resulted from Rtg2 functions unrelated to retrograde activation.

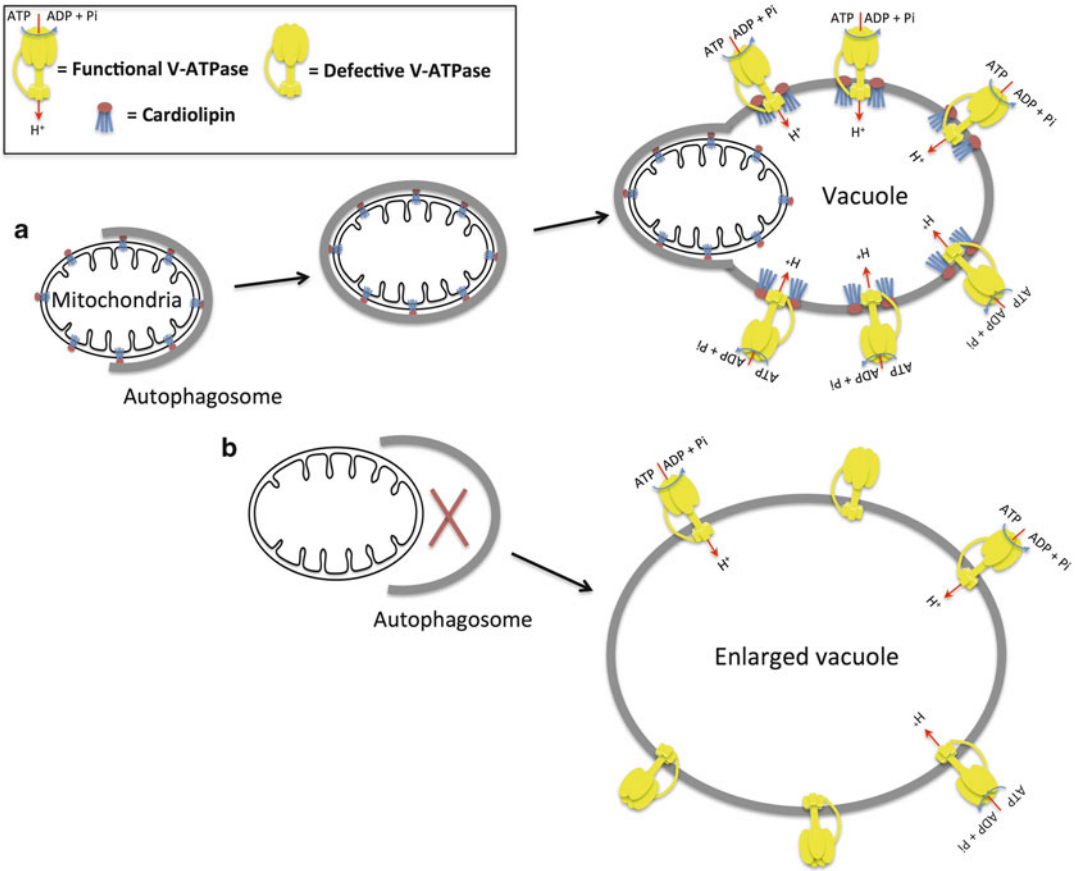


Fig. 11.4 Proposed models to explain the role of CL in vacuolar function. It is likely that CL is transported to the vacuole through mitophagy, the selective degradation of mitochondria via the autophagosome, which delivers its cargo to the vacuole. (a) Under normal physiological conditions, CL may provide stability to the

V-ATPase, which is essential to maintain its activity [24]. (b) CL deficiency may lead to perturbation of mitophagy, which results in decreased delivery of CL to the vacuole and, subsequently, to destabilization of the V-ATPase, decreased ATPase activity, and enlargement of the vacuole

One possible explanation for the vacuolar defects in *crd1Δ* is that the loss of CL leads to intracellular osmotic imbalance, as suggested by the enlarged cell size of the mutant (Fig. 11.4). Consistent with this, deletion of the *NHX1* gene (but not any of the other vacuole ion transporters) in *crd1Δ* restored vacuolar morphology to wild type levels [24]. Nhx1 is the Na^+/H^+ exchanger located in late endosomal/prevacuolar membranes, and is involved in the export of protons in exchange for cytosolic Na^+ or K^+ [182, 183].

Another possibility is that CL may regulate vacuolar function by directly activating the V-ATPase (Fig. 11.4). While CL is predominantly found in the mitochondrial membranes, significant

amounts are also detected in the vacuolar membrane, and the levels vary depending on the carbon source of the growth media [184]. How does CL, which is synthesized in the mitochondria, get to the vacuole? The most likely mechanism is via selective degradation of the mitochondria by the autophagic process known as mitophagy, which is strongly induced in yeast by nutrient starvation and during the stationary growth phase [185–190]. CL that has integrated into the vacuolar membrane as a result of mitophagy may directly activate the V-ATPase and/or stabilize the protein. This possibility is highly speculative at this stage, as such interactions have not yet been reported.

Cross-talk between mitochondria and vacuole is further supported by a recent finding, which showed that the vacuolar pH is a determinant of mitochondrial function and aging in yeast cells [191]. Aging yeast cells exhibit a decline in vacuolar acidity, which causes mitochondrial dysfunction and a decrease in replicative life-span [191]. Consistent with this, enhancing vacuolar acidity by overexpressing *VMA1* or *VPH2*, which encode proteins that regulate V-ATPase activity, suppressed mitochondrial dysfunction. The mechanisms underlying the interplay between vacuole and mitochondria, and the role of CL in this process, remain to be elucidated.

11.8 Unanswered Questions and Future Directions

The studies discussed here show that changes in the levels and species of CL affect not only mitochondrial function but also signaling pathways and other organelles. Elucidating the mechanisms whereby CL mediates these activities remains an exciting area for future investigation. In this regard, we pose the following questions.

During apoptosis, the CL content of the outer mitochondrial membrane increases [83, 87]. How is CL transferred from its site of synthesis in the inner mitochondrial membrane to the outer membrane?

Peroxidation of CL has been shown to be a major mechanism of free radical toxicity resulting from ischemia-reperfusion injury to cardiac myocytes [129, 192–194]. The degree of peroxidation is dependent upon the acyl composition of the lipid. What regulates the fatty acyl chain composition of CL? Is this regulation age dependent?

What is the mechanism whereby CL regulates vacuolar function and V-ATPase activity? Interestingly, enlargement of the lysosome (mammalian equivalent of the vacuole) was also observed in the mouse model of BTHS, suggesting that the role of CL in vacuole/lysosome function is highly conserved [195]. Are the vacuole/lysosome defects due to CL deficiency? Alternatively, are the defects an indirect consequence of perturbation of mitophagy?

How does CL regulate the PKC-Slt2 and HOG signaling pathways? The mammalian homolog of HOG1, p38, is also a signal relay protein that responds to osmotic stress. p38 is involved in the cardiac expression of proinflammatory cytokines and in the development of cardiac dysfunction relative to the inflammatory response [196]. A role for p38 in cardiomyopathy is suggested by the finding that depletion of p38 α alleviates cardiomyopathy induced by overexpression of the α -adrenergic receptor [197]. However, the link between CL and p38 is speculative, as the effects of CL deficiency on mammalian p38 have not been studied. In addition to p38, members of the PKC family are also involved in maintaining cardiac structure and function [198, 199]. A recent study showed that PKC θ is expressed at significant levels in neonatal mouse ventricular myocytes and is specifically activated during stress [200]. Furthermore, PKC θ deficiency leads to dilation of heart muscle cells and decreased viability. Similarly, PKC ϵ migrates to the mitochondria and plays a cardio-protective role in injuries arising from ischemia and reperfusion [201–203]. However, it should be noted that expression of only a few PKC isoforms exhibit beneficial effects in cardiac injury [204–206]. It would be interesting to determine if CL is involved in the modulation of PKC function in heart muscle.

Answering these questions will have important implications for understanding the pathophysiology of BTHS and other disorders in which CL deficiency plays a role. Although BTHS is a monogenic disorder, the clinical presentation is highly variable, even among patients with the same mutation, ranging from death in the newborn period to asymptomatic. This suggests that physiological modifiers may contribute to the clinical symptoms observed in BTHS patients. It is likely that additional deficiencies in cellular functions that require CL may exacerbate the symptoms of tafazzin deficiency in BTHS.

In conclusion, our understanding of the role of CL in essential cell functions and signaling networks has increased dramatically in recent years. However, it is probably safe to assume that we have only scratched the surface of this expanding field.

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