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Rapid phosphatidic acid accumulation in response to low temperature stress in *Arabidopsis* is generated through diacylglycerol kinase

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Phosphatidic acid (PtdOH) is emerging as an important signaling lipid in abiotic stress responses in plants. The effect of cold stress was monitored using 32P-labeled seedlings and leaf discs of *Arabidopsis thaliana*. Low, non-freezing temperatures were found to trigger a very rapid 32P-PtdOH increase, peaking within 2 and 5 min, respectively. In principle, PtdOH can be generated through three different pathways, i.e., (1) via de novo phospholipid biosynthesis (through acylation of lyso-PtdOH), (2) via phospholipase D hydrolysis of structural phospholipids, or (3) via phosphorylation of diacylglycerol (DAG) by DAG kinase (DGK). Using a differential 32P-labeling protocol and a PLD-transphosphatidylation assay, evidence is provided that the rapid 32P-PtdOH response was primarily generated through DGK. A simultaneous decrease in the levels of 32P-PtdInsP, correlating in time, temperature dependency, and magnitude with the increase in 32P-PtdOH, suggested that a PtdInsP-hydrolyzing PLC generated the DAG in this reaction. Testing T-DNA insertion lines available for the seven DGK genes, revealed no clear changes in 32P-PtdOH responses, suggesting functional redundancy. Similarly, known cold-stress mutants were analyzed to investigate whether the PtdOH response acted downstream of the respective gene products. The hos1, los1, and fry1 mutants were found to exhibit normal PtdOH responses. Slight changes were found for icle1, snow1, and the overexpression line SuperICE1, however, this was not cold-specific and likely due to pleiotropic effects. A tentative model illustrating direct cold effects on phospholipid metabolism is presented.

Keywords: abiotic stress, cold stress, diacylglycerol kinase, lipid signaling, phosphatidic acid, phosphoinositide, phospholipase, plant signaling

**INTRODUCTION**

The potential to survive low temperatures is one of the factors that determine the geographical distribution of plants. Moreover, freezing and cold stress restrict the arable land and yield of crops. Therefore, much effort is made to understand the mechanisms that make plants more tolerant to low temperatures. One of the most popular plant models in these studies is *Arabidopsis thaliana* (Van Buskirk and Thomashow, 2006).

Like many temperate plants, *Arabidopsis* is capable of cold acclimation, i.e., during a period of cold, non-freezing temperatures, its tolerance for freezing temperatures increases. This process, also referred to as cold hardening, involves a myriad of metabolic and developmental changes, accompanied by accumulation of proteins and compatible solutes, and alterations in membrane composition (Umura et al., 1995; Thomashow, 1999; Cook et al., 2004; Chinnusamy et al., 2007).

Transcriptome profiling and mutant screens have resulted in the characterization of multiple genes involved in the initiation of cold acclimation and freezing tolerance. These include the conserved CBF/DREB1 transcription factors that are responsible for activating the expression of many cold response (COR) genes via conserved C-repeat elements in their promoters. Zhu and coworkers have used *Arabidopsis* plants transfected with the *RD29A-LUC* construct to select for mutants with altered responses to cold treatment ("cold response mutants"), resulting in the identification of several genes. Enhanced cold-induced expression was found in the *fry1* (Xiong et al., 2001) and *hos1* (Ishitani et al., 1998) mutants, whereas *los1* (Guo et al., 2002) showed decreased expression. Moreover, the dominant negative *icle1* (Chinnusamy et al., 2003) mutation has been demonstrated to negatively affect cold-induced gene transcription by interfering with the function of *AtICE1*, a myc-type transcription factor which functions in CBF transcription in cold signaling. The *myb*-type transcription factor SNOW1/MYB15, also binds to the CBF promoter region, interacting with ICE1 (Agarwal et al., 2006). Upon exposure to cold stress (4°C), the transcript levels of CBF/DREB1 genes increase within 15–30 min, followed by the accumulation of COR gene transcripts after about 2 h (Thomashow, 1999).
Much less is known about the signal transduction pathway that precedes the gene expression changes. Nonetheless, there is mounting evidence that Ca$^{2+}$ functions as a second messenger (Knight et al., 1996; Knight and Knight, 2000; Carpaneto et al., 2007) and that part of the pathway involves activation of a MAP kinase cascade (Jonak et al., 1996; Mizoguchi et al., 1996; Teige et al., 2004). One of the latest additions to the field of cold signaling is the formation of the lipid second messenger, phosphatidic acid (PtdOH). In suspension-cultured cells, this phospholipid was shown to accumulate within minutes of cold stress (Gawer et al., 1999; Rueillard et al., 2002; Cantrel et al., 2011). Like Ca$^{2+}$ and MAP kinases, PtdOH is involved in the signal transduction pathways of several other plant stress responses, including drought, wounding, and pathogen infection (Li et al., 2009; Testerink and Munnik, 2011), and it is not unlikely that these pathways strongly overlap.

In stress-induced signal transduction, PtdOH responses have been mainly attributed to two pathways. It is the direct product of phospholipase D (PLD), which hydrolyses structural phospholipids like phosphatidylcholine (PtdCho) and phosphatidylethanolamine (PtdEtn), and a secondary product of the phospholipase C (PLC) pathway, which first hydrolyzes polyphosphoinositides (PPIs) to diacylglycerol (DAG), that is subsequently phosphorylated to PtdOH by diacylglycerol kinase (DGK). However, metabolism of DAG and PtdOH is more complex, since multiple sources have now been demonstrated, and PtdOH is formed de novo via acylation of glycerolphosphate (Gro3P) as a common intermediate in glycerolipid biosynthesis, both in the plastid and the ER. Thus, PtdOH is precursor to all phosphoglycerolipids as well as triacylglycerols and galactolipids, and its turnover is crucial in determining lipid metabolic fluxes and membrane compositions.

The Arabidopsis genome is predicted to encode 12 PLDs, 9 PLCs, and 7 DGKs (Gomez-Merino et al., 2004; Testerink and Munnik, 2005, 2011; Tasma et al., 2008; Arisz et al., 2009; Li et al., 2009; Munnik and Testerink, 2009). Their genetic abundance and specific gene expression patterns suggest that some of these enzymes are specific to certain locations in specific organs and/or involved in distinct processes. The PLC/DGK and PLD pathways have been implicated in the transcriptional induction of an array of cold-induced genes in Arabidopsis (Vergnolle et al., 2005). PLD8 has been shown to be important in the generation of freezing tolerance during acclimation (Li et al., 2004) in contrast to PLDα1 which negatively influenced survival of freezing, both in cold-acclimated and in non-acclimated plants (Rajashekar et al., 2006; Chen et al., 2008; Du et al., 2010). In suspension-cultured cells, biochemical evidence was found that cold shock activated both PLC/DGK and PLD pathways (Rueillard et al., 2002). Moreover, several genes have been shown to be upregulated in response to cold stress, including PLDα1, PLDβ, PLC1, PLC4, PLC5, DGK1, and DGK2 (Hirayama et al., 1995; Gomez-Merino et al., 2004; Li et al., 2004; Lee et al., 2005). Also, in maize roots and leaves several genes encoding DGK, PLC, and PLD were upregulated within 30 min of cold stress (Sui et al., 2008).

In this study we show that Arabidopsis seedlings and leaf disks exposed to low temperatures accumulate PtdOH within minutes. Using a differential 32P-labeling strategy (Munnik et al., 1998b; Arisz et al., 2009) and PLD’s ability to transphosphatidylate n-butanol to PtdBut (Munnik et al., 1995, 1998b), we provide evidence that the rapid PtdOH response does not originate from PLD but from DGK. The simultaneous decrease in the level of phosphatidylinositolphosphate (PtdInsP) suggests the involvement of a PtdInsP-hydrolyzing PLC. T-DNA insertion lines were used to address the question which DGK and PLC were involved, while the COR mutants hos1, los1, fry1, icel1, and snow1 were analyzed to see whether PtdOH acts up- or down-stream of these genes in the COR.

**MATERIALS AND METHODS**

**PLANT MATERIAL**

*A. thaliana* seeds were sterilized in 70% EtOH (1 min) and 25% bleach (20 min), and sown on media in Petri dishes. For 32P-radiolabeling experiments, seedlings were grown on ½ x Murashige and Skoog (MS) basal medium at pH 5.7 (KOH), solidified with 1.0% bacto-agar. The icel, snow1, los1, hos1, fry1 mutants, and their WT’s were grown on 1 x MS medium supplemented with 1% sucrose. A 16 h light/8 h dark regime (150 umol quanta m$^{-2}$s$^{-1}$) at 21°C was set. To promote uniform germination, plates were kept in the dark at 4°C for 2 days before transfer to a climate room.

**RT-PCR EXPRESSION ANALYSES OF DGK T-DNA INSERTION LINES**

Homozygous T-DNA insertion lines of the DGK genes were genotyped using primer sequences found in Table A1 (Figure A3). Wild type A. thaliana Col-0 or lines containing T-DNA insertions in DGK1, -3, -5, -7 genes were grown on ½ x Murashige and Skoog (MS) basal medium supplemented with 1% w/v sucrose at pH 4.6, solidified with 1% w/v daishin agar. To promote uniform germination, plates were kept in the dark at 4°C for 2 days before transfer to a climate room. Seedlings were harvested for RNA isolation after 9 days in a climate room with light regime set at 16 h light/8 h dark at 21°C and Relative Humidity 70%. Additionally, flowers of A. thaliana lines containing T-DNA insertions in DGK2, -4, -6 genes, and wild type Col-0 were collected from plants grown in a greenhouse under the same environmental conditions. RNA was isolated using Tri Reagens LS (Sigma) and treated with Turbo RNAse free DNase (Ambion) for removal of genomic DNA. The RNA concentration and integrity was analyzed using a Nanodrop ND-1000 spectrophotometer.

cDNA was synthesized from 2 μg total RNA using ReverAid H Minus Reverse Transcriptase (Fermentas) according to the manufacturers protocol. RT-PCR was performed using Accuprime Taq DNA polymerase (Invitrogen). Table A2 contains the primer sequences used to amplify the different Arabidopsis DGK genes and the At2g28390 (SAND family) reference gene (Figure A4; Hong et al., 2010). Thermal cycling was done according to the following profile; 94°C for 2 min, followed by 40 cycles of 94°C for 30 s, 50°C for 30 s, 68°C for 2 min and 1 cycle of 68°C for 6 min.

**32P-ORTHOPHOSPHATE RADIOLABELING in vivo AND ANALYSIS OF PHOSPHOLIPIDS**

Five-days-old seedlings or leaf disks (5 mm θ) of 3-weeks-old plants were transferred to a 2.0 ml Eppendorf tube, containing
MES (2-[N-morpholino]ethane sulfonic acid)-based buffer of 2.56 mM MES (pH 5.7) and 1 mM KCl. To label phospholipids, 10 μCi carrier-free 32P-orthophosphate per tube was added for 16 h, unless indicated otherwise. Cold shock treatments were executed by transferring tubes to ice water. Incubations were stopped by the addition of HClO4 (final concentration 5%, w/v), and 10 min of subsequent shaking.

The total solvent was removed and 375 μl CHCl3/MeOH/HCl (50:100:1, by vol.) was added to extract the lipids. After 10 min of vigourous shaking, two phases were induced by adding 375 μl CHCl3 and 200 μl 0.9% (w/v) NaCl. The organic lower phase was then transferred to a tube containing 375 μl CHCl3/MeOH/1M HCl (3:48:47, by vol.). Shaking, spinning, and removing the upper phase yielded a purified organic phase, which was dried down in a vacuum centrifuge at 50°C. The residue was resuspended in 50 μl CHCl3 and sampled for lipid analysis.

Phospholipids were analyzed by thin-layer chromatography (TLC) on heat-activated silica gel 60 plates (Merck, 20 × 20 cm) using one of the following solvent systems (ratios by vol.): (A) CHCl3/MeOH/NH4OH (25%)/H2O (90:70:4:16); or (B) ethylacetate/iso-octane/formic acid/H2O (13:2:3:10), of which the organic phase was used for TLC. Solvent A was used for total phospholipid analysis, while B was used to quantitate PtdOH and PtdBut. Radiolabeled phospholipids were visualized and quantified by phosphoimaging (Molecular Dynamics, Sunnyvale CA, USA).

RESULTS

COLD STRESS RAPIDLY TRIGGERS A PtdOH RESPONSE

PtdOH levels in plants are approximately 2 mol% of total phospholipids (Welti et al., 2002) which likely represents ER- and plastid-localized PtdOH as precursor and turnover product of structural glycerolipids. To be able to see PtdOH increases during stress-signaling, plants can be metabolically radiolabeled with carrier-free 32P-phosphate (32P). To study phospholipid metabolism during cold shock in Arabidopsis, we radiolabeled 5-days-old seedlings for 16 h with 32P and subsequently incubated them for 5 min at 0°C. Phospholipids were then extracted, separated by TLC and analyzed by autoradiography. A typical 32P-labeling pattern is shown in Figure 1, revealing a PtdOH increase in response to cold.

To test the temperature dependency of this response, 32P-prelabeled seedlings were exposed to different temperatures for 5 min. As shown in Figures 2A,B, a temperature-dependent PtdOH response was found. Concomitantly, a decrease in 32P-PtdInsP was observed (Figure 2A). To investigate whether leaves of adult plants responded similarly, leaf disks of 3-weeks-old plants were subjected to the same labeling procedure whether leaves of adult plants responded similarly, leaf disks of vigorous shaking, two phases were induced by adding 375 μl CHCl3 and 200 μl 0.9% (w/v) NaCl. The organic lower phase was then transferred to a tube containing 375 μl CHCl3/MeOH/1M HCl (3:48:47, by vol.). Shaking, spinning, and removing the upper phase yielded a purified organic phase, which was dried down in a vacuum centrifuge at 50°C. The residue was resuspended in 50 μl CHCl3 and sampled for lipid analysis.

Next, we focused on the metabolic origin of the cold-induced PtdOH response. Previous studies in suspension-cultured Arabidopsis cells indicated that part of the cold shock-induced PtdOH response was generated by PLD activity (Ruelland et al., 2002). To investigate PLD’s contribution a transphosphatidylation assay was performed, i.e., in the presence of a low concentration of a primary alcohol, such as n-ButOH, this serves as a substrate in a PLD-catalyzed reaction generating PtdBut, at the cost of PLD-catalyzed production of PtdOH (Munnik et al., 1995). The accumulation of PtdBut is a measure of PLD activity.

Thus, seedlings were prelabeled for 16 h with 32P, then n-ButOH (0.5% final conc.) was added, and 30 min later the seedlings were transferred to 0°C for 5 min or kept at room temperature. As shown in Figure 4A, cold stress did not affect 32P-PtdBut levels, while 32P-PtdOH levels increased. These data indicate that PLD is not responsible for the initial PtdOH response.

To investigate the potential involvement of DGK, a differential radiolabeling protocol was applied (Munnik, 2001; Arisz et al., 2009). In short, when cells are metabolically labeled with 32P, the phospholipid classes are labeled with different kinetics, depending on the labeling of their precursors, their rates of synthesis, turnover, and pool size. Thus, DGK-derived PtdOH is labeled after relatively short labeling times because it acquires its 32P-phosphate directly from ATP molecules, which are rapidly labeled. This is in contrast to PtdOH arising from PLD activity, which are not labeled until the pool of its precursor, i.e., PtdEtn. at 5 min after the onset of incubation after which it leveled off, approaching control levels after 2 h (Figure 3B).
FIGURE 2 | Temperature-dependent accumulation of $^{32}$P-PtdOH in Arabidopsis leaves and seedlings. (A) O/N $^{32}$P-prelabeled seedlings were incubated for 5 min at the indicated temperatures. Lipids were then extracted, separated by TLC, and visualized by autoradiography. (B) Quantitation by phosphoimaging of $^{32}$P-PtdOH formed at different temperatures in seedlings. (C) Formation of $^{32}$P-PtdOH in leaf disks at different temperatures. Values are means of triplicates ± SD. Asterisks indicate highest temperatures giving rise to a significant ($p < 0.05$) increase in $^{32}$P-PtdOH.

PtdCho, or PtdGro, is sufficiently labeled, which is typically O/N (Munnik et al., 1998b; Arisz and Munnik, 2011).

Thus, seedlings were $^{32}$P$_7$-prelabeled for different periods of time (20, 60, and 180 min) after which they were subjected for 5 min to 0°C. As shown in Figures 4B,C, cold stress triggered a marked increase in $^{32}$P-PtdOH in seedlings prelabeled for only 20 min. Under these conditions, structural phospholipids like PC and PE were hardly labeled excluding them as precursors to $^{32}$P-PtdOH in a PLD-catalyzed reaction. This is in agreement with the results of the transphosphatidylation assay (Figure 4A). Hence, the increase in $^{32}$P-PtdOH is unlikely to reflect a PLD activity, and is consistent with a DGK activity. At longer prelabeling time points, the relative increases in $^{32}$P-PtdOH gradually diminished (Figure 4C), due to the decrease in the specific radioactivity of the ATP pool and the general increase in structural phospholipid labeling.

Two of the most abundant PLD isoforms in Arabidopsis, $\text{PLD}\alpha_1$ and $\text{PLD}\delta$, have been implicated in cold stress tolerance (Ruelland et al., 2002; Li et al., 2004; Rajashekar et al., 2006). To test their contribution to the early PtdOH response to cold stress, both single and double KO-mutants were analyzed (Bargmann et al., 2009a,b). As shown in Figure 4D, all mutants exhibited a normal PtdOH response upon cold stress.

Together, these results argue against the involvement of PLD in the acute cold-shock-induced PtdOH response and strongly point to a role for DGK.

The implication of DGK in the early COR raised the question of DAG’s metabolic origin. One possible source of DAG is the induced PLC hydrolysis of the polyphosphoinositides, PtdInsP and/or PtdInsP$_2$, a well-defined plant stress response, which was supported by the observation that $^{32}$P-PtdInsP decreased in response to cold (Figure 2A). Moreover, this decrease correlated closely with an equivalent increase in $^{32}$P-PtdOH, in a temperature- and time-dependent fashion (Figure 5). These results strongly argue for the scenario that cold stress activates
PLC hydrolysis of PtdInsP to form DAG, which is subsequently phosphorylated to PtdOH by DGK.

**PtdOH RESPONSES IN ARABIDOPSIS dgk- AND COLD STRESS MUTANTS**

*Arabidopsis* contains 7 DGK encoding genes. In an attempt to identify the isozyme involved in the cold-induced PtdOH response, a reversed genetic approach was used, screening a series of T-DNA insertion lines (Tables 1, 2). These lines carry insertions in or near the DGK encoding regions, although not all of the lines were established as knockout or knockdown mutants (Table 1; Figure A4). Seedlings of these lines were
Phosphoimaging. PtdOH levels are expressed as a percentage of the total each (* increases were found in cold-stressed ice1, whilst slight larger PtdOH normal control PtdOH levels, neither showed significant defects sure their PtdOH response. Surprisingly, among the lines with 2 dgk4-2 dgk4-1 1 dgk2-2 dgk2-1 dgk1-1 2 Col-0 at 0°C for 5 min. Lipids were then extracted separated by TLC and quantified by phosphoimaging. PtdOH levels are expressed as a percentage of the total 32P-labeled lipids and values represent averages of multiple samples containing 2 seedlings each (± SD).

<table>
<thead>
<tr>
<th>Gene</th>
<th>AGI ID</th>
<th>Line</th>
<th>Status*</th>
<th>Control</th>
<th>Cold</th>
<th>Fold increase</th>
<th>Replicates</th>
</tr>
</thead>
<tbody>
<tr>
<td>AtDGK1</td>
<td>At5g07920</td>
<td>wt</td>
<td>Col-0</td>
<td>0.98 ± 0.07</td>
<td>3.00 ± 0.20</td>
<td>3.1</td>
<td>6</td>
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<tr>
<td>AtDGK2</td>
<td>At5g63770</td>
<td>SALK 053412</td>
<td>dgk-1</td>
<td>0.93 ± 0.07</td>
<td>3.11 ± 0.31</td>
<td>3.4</td>
<td>6</td>
</tr>
<tr>
<td>AtDGK4</td>
<td>At2g20900</td>
<td>SAIL 71_003</td>
<td>dgk-2</td>
<td>1.00 ± 0.06</td>
<td>2.70 ± 0.48</td>
<td>2.7</td>
<td>6</td>
</tr>
<tr>
<td>AtDGK5</td>
<td>At2g20900</td>
<td>SAIL 339_C01</td>
<td>dgk-4</td>
<td>0.96 ± 0.10</td>
<td>3.19 ± 0.40</td>
<td>3.3</td>
<td>6</td>
</tr>
<tr>
<td>AtDGK6</td>
<td>At4g28130</td>
<td>SAIL 069158</td>
<td>dgk-4</td>
<td>1.22 ± 0.08</td>
<td>3.73 ± 0.26</td>
<td>3.1</td>
<td>3</td>
</tr>
<tr>
<td>AtDGK7</td>
<td>At4g30340</td>
<td>SAIL 51_E04</td>
<td>no KO</td>
<td>0.83 ± 0.08</td>
<td>3.65 ± 0.50</td>
<td>4.4</td>
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</tr>
<tr>
<td></td>
<td>SALK 059060</td>
<td>dgk-7</td>
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<td>4.4</td>
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<tr>
<td></td>
<td>SALK 007896</td>
<td>dgk-7-3</td>
<td>no KO</td>
<td>0.91 ± 0.14</td>
<td>3.24 ± 0.15**</td>
<td>3.6</td>
<td>8</td>
</tr>
</tbody>
</table>

5-days-old Arabidopsis seedlings were labeled O/N with 32P, and incubated at 0°C for 5 min. Lipids were then extracted separated by TLC and quantified by phosphoimaging. PtdOH levels are expressed as a percentage of the total 32P-labeled lipids and values represent averages of multiple samples containing 2 seedlings each (± SD).

* Transcript analysis by RT-PCR confirmed knock-down (KD) or knock-out (KO) status. Expression of DGK6 was too low for detection hence the status of dgk6-1 could not be determined.

** Reproducibly statistically significant difference of T-DNA line compared with wild type (Tukey HSD test, P < 0.05) within the wild type control homogeneous subset.

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**DISCUSSION**

While, in Arabidopsis seedlings and leaves, the acclimation process in response to low temperatures is rapidly initiated, it takes 6–7 days to achieve maximal freezing tolerance (Uemura et al., 1995; Peng et al., 2002). The formation of PtdOH has been speculated to function in the regulation of this response (Ruelland et al., 2002; Xiong et al., 2002; Gomez-Merino et al., 2004; Li et al.,...
DGK RATHER THAN PLD ACTIVITY GENERATES EARLY, COLD-INDUCED PtdOH

Two routes have been found to generate PtdOH under conditions of environmental stress in plants, i.e., PLD hydrolysis of strucural phospholipids (i.e., PtdCho/PtdEtn/PtdGro) and phosphorylation of DAG by DGK (Arisz et al., 2009; Testerink and Munnik, 2011). Using transphosphatidylation assays, the absence of a 32P-PtdBut increase under chilling conditions that triggered massive 32P-PtdOH responses indicate that PLD is not involved (Figure 4A). Using a differential 32P1-labeling assay, 32P-PtdOH demonstrated to be rapidly labeled, in agreement with a DGK involvement, and in contrast to the labeling of structural phospholipids PtdEtn, PtdCho, and PtdGro, which required long labeling times, again suggesting a PLD-independent pathway (Figure 4B).

Although this seemed at variance with studies of suspension-cultured cells, which suggested a cold-activated PLD activity (Ruelland et al., 2002; Cantrel et al., 2011), it is well-possible that PLD plays a role at a later phase of the COR. This is for example supported by (1) the induced membrane localization of PLDδ after 1 day at 2°C (Kawamura and Uemura, 2003), (2) its importance in freezing tolerance (Li et al., 2004; Chen et al., 2008; Du et al., 2010) and (3) the transcriptional regulation of Arabidopsis PLDδ and PLDα1 (Welti et al., 2002; Li et al., 2004) and two PLDα homologs from cotton (Kargiotidou et al., 2010) during cold acclimation. Nevertheless, consistent with the present data, we have found pldδ1/pldδ seedlings to display a normal 32P-PtdOH response after 5 min at 0°C (Figure 4D).

THE SUBSTRATE FOR DGK MAY BE GENERATED BY A PtdInsP-HYDROLYZING PLC

Since DGK was implicated, the question was raised how the substrate DAG was formed. Several pathways could account for this. A clue was provided by the concomitant decreases of 32P-PtdInsP, equivalent to the increase of 32P-PtdOH, suggesting the former to be precursor to DAG and PtdOH via PLC and DGK, respectively (Figures 5 and 8, reactions 1 and 3). Previously, cold stress in Arabidopsis cells has been shown to trigger decreases in both PtdInsP2 and PtdInsP (Ruelland et al., 2002). While PtdInsP2 is usually considered as the substrate for
In contrast, in both systems a knock-down allele of DGK7, was associated with an increased accumulation of PtdOH. Knockdown of DGK7, did not result in significantly reduced PtdOH levels, perhaps as a consequence of the activity of the structurally similar DGK1 (Gomez-Merino et al., 2004; Arisz et al., 2009). These results may indicate a functional redundancy among Arabidopsis DGKs, such that deficient gene functions are compensated for by related isozymes. The PtdOH “overshoot” in the dkg7-2 KD line could reflect such a mechanism. This experimental problem will be precluded by generating multigene KO lines, e.g., dkg1/dkg2.

In young seedlings, but also in rosette leaves, DGK7 is more abundantly expressed than DGK1 and DGK2 (Arisz et al., 2009), but its transcript levels have not been found to increase upon cold stress. Transgenically expressed DGK7 protein has been shown to have in vitro DGK activity despite the lack of a C1 domain, which is thought to function in the regulation of kinase activity in cluster-I DGKs, DGK1 and DGK2 (Gomez-Merino et al., 2004, 2005; Arisz et al., 2009). DGK7 belongs to cluster II, together with DGK3 and DGK4 whose activity may be responsible for the enhanced PtdOH production in dkg7-2 seedlings.

OTHER POTENTIAL SOURCES OF DAG AND PtdOH

Although biochemical evidence strongly suggested a PLC-DGK route, two alternative enzymes might be considered as contributors to the cold-induced PtdOH accumulation as well. Inositolphosphorylceramide synthase (IPCS) transfers the inositol phosphate group from PtdIns to ceramide to generate inositolphosphorylceramide (IPC) and DAG (Figure A1). In yeast, the PtdIns substrate in this reaction is supplied by repeated methylations of EtnP, catalyzed by phosphatidic acid phosphatase (PAP) to generate DAG as substrate in a reaction by which phosphoethanolamine (EtNp) is transferred from cytidine diphosphate-ethanolamine (CDP-Etn) to the lipid moiety, yielding PtdEtn. Cold does not seem to cause a general inhibition in the uptake of 32P or its incorporation into the Kennedy pathway of glycerolipid de novo synthesis, since labeling of other structural phospholipids was not affected by cold stress (Figure A2). Therefore, the cause of decreased 32P-PtdOH accumulation was achieved at 0°C (Figure A2).

Glycerolipid de novo synthesis starts with two acylations of Gro3P to generate PtdOH (Figure 8). For the synthesis of PtdIns (PtdGro), PtdOH is converted to cytidine diphosphate-diacylglycerol (CDP-DAG), the substrate for phosphatidylinositol synthase (PIS). Alternatively, PtdOH is dephosphorylated by phosphatidic acid phosphatase (PAP) to generate DAG as substrate in a reaction by which phosphoethanolamine (EtNp) is transferred from cytidine diphosphate-ethanolamine (CDP-Etn) to the lipid moiety, yielding PtdEtn. Cold does not seem to cause a general inhibition in the uptake of 32P or its incorporation into the Kennedy pathway of glycerolipid de novo synthesis, since labeling of other structural phospholipids was not affected by cold stress (Figure A2). Therefore, the cause of decreased 32P-PtdEtn labeling is most likely in the synthesis or supply of its headgroup.

The precursor CDP-Etn is generated through the cytidylation of EtNp by phosphoethanolamine cytidylyl transferase (PECT), analogous to the PtdCho headgroup precursor CDP-Chol, being the product of phosphocholine cytidylyl transferase (CCT) using ChoP as substrate. The latter is produced by repeated methylation of EtNp, catalyzed by phosphoethanolaminemethyltransferase (PEAMT). This activity, which is considered rate-limiting for PtdCho synthesis, likely accounts for the different labeling kinetics of PtdCho and PtdEtn, only the latter being radioactively detected after 30 min of 32P labeling.
FIGURE 8 | Model illustrating potential early effects of cold stress on phospholipid metabolism and de novo synthesis in Arabidopsis. The main route to rapid cold-induced PtdOH formation is suggested to be based on the phosphorylation of PLC-generated DAG from PtdInsP (reactions 1/3). The activity of PECT, which produces the precursor of the polar head of PtdEtn, CDP-Etn, is proposed to be down regulated by low ambient temperature (2). This would lead to reduced PtdEtn formation, and potentially, to DAG accumulation, which might cause PtdOH to accumulate as a result from phosphorylation of DAG by a DGK (3), or due to product inhibition of PAP by DAG (4). The major pathway of PtdCho synthesis depends on methylation of EtnP by PEAMT, which could be inhibited by PtdOH (5). Note that the model only highlights immediate effects of cold temperature; longer exposure to cold induces a myriad of metabolic changes which impact lipid biosynthesis in different ways. Abbreviations: Acyl-CoA, acyl-coenzyme A; CDS, CDP-DAG synthase; EK, ethanolamine kinase; EPT, CDP-ethanolamine phosphotransferase; GPAT, glycerol 3-phosphate acyltransferase; LPAAT, lysophosphatidic acid acyltransferase; lyso-PtdOH, lysophosphatidic acid.

As previous studies have shown that low temperatures can inhibit the in vitro activity of recombinant CCT (Inatsugi et al., 2002), PECT activity is speculated to be similarly downregulated by cold (Figure 8, designated by “2”), resulting in a limited availability of CDP-Etn for PtdEtn synthesis. This would form a bottleneck leading to the accumulation of DAG as precursor for PtdEtn synthesis. Notably, this DAG could be an additional source for cold-induced PtdOH through DGK activity (Figure 8, reaction 3), which has been shown to be partly localized at the ER in Arabidopsis (Vaultier et al., 2008). Alternatively, accumulated DAG may block its own formation through feedback inhibition of PtdOH phosphatase (Figure 8, reaction 4), again promoting PtdOH accumulation. Similar regulation of PAP activity by product inhibition has been demonstrated in chloroplast envelope membranes from spinach (Malherbe et al., 1992).

In summary, we have shown a very fast (in minutes) accumulation of PtdOH in response to cold temperatures in Arabidopsis seedlings and leaf discs, which was not due to PLD activity. Instead, $^{32}$P-radiolabeling studies indicated a dominant role of DGK under these conditions. Using single T-DNA insertion lines, we were unable to pinpoint the DGK gene(s) involved but do propose that DGK acts in tandem with a PtdInsP-hydrolyzing PLC, based on the close correlation between the increase in $^{32}$P-PtdOH and the decrease in $^{32}$P-PtdInsP.

PtdOH accumulation was not affected by the fry1, hos1, and los1 mutations, consistent with an independent, upstream position in cold signaling. Although the snow1 and ice1 mutants displayed decreased PtdOH levels they likely reflected pleiotropic effects of the mutations.

Apart from the PLC/DGK route, additional, hypothetical sources of DAG and PtdOH were discussed, viz. via IPCS (Figure A1), NPC, GGGT and lipid de novo synthesis (Figure 8). Although for neither of these pathways there is sufficient evidence at present, they should not be ignored when studying PtdOH responses to cold or other environmental stresses.


**Conflict of Interest Statement:** The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.
## APPENDIX

Table A1 | Primers used for genotyping the DGK T-DNA insertion lines.

<table>
<thead>
<tr>
<th>Genotype</th>
<th>LP</th>
<th>PR</th>
<th>Border primer</th>
<th>Sequence</th>
<th>Wild type</th>
<th>Insertion</th>
<th>LP/PR</th>
<th>RP/LB</th>
<th>Insertion</th>
</tr>
</thead>
<tbody>
<tr>
<td>dgk1-1</td>
<td>SALK_053412</td>
<td>GGA TTC TCC TTC CGT AGA TTG</td>
<td>TCA TGC CGT ACT GGA AAA TTC</td>
<td>LBb1.3</td>
<td>ATTTTGGGATTTTGGGAGA</td>
<td>LP/PR</td>
<td>RP/LBb1.3</td>
<td>1205 bp</td>
<td>588–888 bp</td>
</tr>
<tr>
<td>dgk2-1</td>
<td>SAIL_718_G03</td>
<td>GCA AAG AAC AAA AAG GCA CAG</td>
<td>CAG ATG CAA GAC CGC TCT TAT</td>
<td>LB3</td>
<td>TAGCATCTGAGATTTCATAAC</td>
<td>LP/PR</td>
<td>RP/LB3</td>
<td>1106 bp</td>
<td>439–739 bp</td>
</tr>
<tr>
<td>dgk2-2</td>
<td>SAIL_71_B03</td>
<td>TGT TAAC TGG ATC TGT TGG CC</td>
<td>CTA AAA GGC GTC TTT GAT CTT</td>
<td>LB3</td>
<td>TAGCATCTGAGATTTCATAAC</td>
<td>LP/PR</td>
<td>RP/LB3</td>
<td>957 bp</td>
<td>432–732 bp</td>
</tr>
<tr>
<td>dgk3-1</td>
<td>SALK_082600</td>
<td>TGC TCT CAG TGG GAA GAG ATC</td>
<td>CCG GAA AAT TAT CCG GAA TAC</td>
<td>LBb1.3</td>
<td>ATTTTGGGATTTTGGGAGA</td>
<td>LP/PR</td>
<td>RP/LBb1.3</td>
<td>1179 bp</td>
<td>539–839 bp</td>
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<td>dgk4-1</td>
<td>SAIL_339_C01</td>
<td>AAA GCG AAG CCC ATA TAA AGC</td>
<td>GTC TTT GGC AAA TGG TCT TAC</td>
<td>LB3</td>
<td>TAGCATCTGAGATTTCATAAC</td>
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<td>RP/LB3</td>
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<td>dgk4-2</td>
<td>SALK_069158</td>
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<td>GCC GAT GAT GGA CTG TTA GAG</td>
<td>LBb1.3</td>
<td>ATTTTGGGATTTTGGGAGA</td>
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<td>RP/LBb1.3</td>
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<td>dgk4-3</td>
<td>SALK_151239</td>
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<td>GAA TCA TCC TCG CGG TCA AGT</td>
<td>LBb1.3</td>
<td>ATTTTGGGATTTTGGGAGA</td>
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<td>RP/LBb1.3</td>
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<td>dgk5-1</td>
<td>SAIL_1212_E10</td>
<td>TTC AGA GCA CAT GGG ACC AAC</td>
<td>TCC AAT TCG GAC ATT TTT TTC</td>
<td>LB3</td>
<td>TAGCATCTGAGATTTCATAAC</td>
<td>LP/PR</td>
<td>RP/LB3</td>
<td>1163 bp</td>
<td>505–805 bp</td>
</tr>
<tr>
<td>dgk5-2</td>
<td>SAIL_253_E12</td>
<td>TTT GAT CCC ATC GAA ACT CAC</td>
<td>GCC GAT GAT GGA CTG TTA GAG</td>
<td>LB3</td>
<td>TAGCATCTGAGATTTCATAAC</td>
<td>LP/PR</td>
<td>RP/LB3</td>
<td>1164 bp</td>
<td>536–836 bp</td>
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<tr>
<td>dgk6-1</td>
<td>SALK_016285</td>
<td>TGG GTA AAG TGA TCA ATG CAA AAG A</td>
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<td>LBb1.3</td>
<td>ATTTTGGGATTTTGGGAGA</td>
<td>LP/PR</td>
<td>RP/LBb1.3</td>
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<tr>
<td>dgk6-2</td>
<td>SALK_054320</td>
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<td>CCT CCA GAT CAA AAA CCT GAG</td>
<td>LBb1.3</td>
<td>ATTTTGGGATTTTGGGAGA</td>
<td>LP/PR</td>
<td>RP/LBb1.3</td>
<td>1265 bp</td>
<td>606–906 bp</td>
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<tr>
<td>dgk7-1</td>
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<td>TTT GCA AGA ATG TAT TGA TTC</td>
<td>TGG TGA TGG AGA TGG ACC TCC</td>
<td>LB3</td>
<td>TAGCATCTGAGATTTCATAAC</td>
<td>LP/PR</td>
<td>RP/LB3</td>
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<td>dgk7-2</td>
<td>SALK_059060</td>
<td>CAA CAT AAT ACA ACC CAC ACC C</td>
<td>AC TGG ACC ACT TGT CAT GAG</td>
<td>LBb1.3</td>
<td>ATTTTGGGATTTTGGGAGA</td>
<td>LP/PR</td>
<td>RP/LBb1.3</td>
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<td>CCG AAC ACG TTC TGT TAA ACG</td>
<td>LBb1.3</td>
<td>ATTTTGGGATTTTGGGAGA</td>
<td>LP/PR</td>
<td>RP/LBb1.3</td>
<td>1056 bp</td>
<td>457–757 bp</td>
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Table A2 | Primers used for RT-PCR expression analyses of DGK T-DNA insertion lines.

<table>
<thead>
<tr>
<th>Gene</th>
<th>Direction</th>
<th>Primername</th>
<th>Sequence</th>
</tr>
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<tbody>
<tr>
<td>DGK1</td>
<td>sense</td>
<td>SALK_053412_LP</td>
<td>GGAATTCTCCTCCCGTAGATTG</td>
</tr>
<tr>
<td></td>
<td>antisense</td>
<td>SALK_053412_RP</td>
<td>TCATGCGATCTCGGAAATCTC</td>
</tr>
<tr>
<td>DGK2</td>
<td>sense</td>
<td>dgk2 fw</td>
<td>GACTGAGATTCCACCATTC</td>
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<td></td>
<td>antisense</td>
<td>dgk2 rv</td>
<td>GATCTACTCCACCCATAGC</td>
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<tr>
<td>DGK3</td>
<td>sense</td>
<td>SALK_082600_LP (dgk3-1)</td>
<td>TGCCTCTACAGTGGAAGAGATC</td>
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<tr>
<td></td>
<td>antisense</td>
<td>dgk3 rv</td>
<td>CAAACCTCTACCTCCACAAC</td>
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<td>DGK4</td>
<td>sense</td>
<td>dgk4 fw</td>
<td>GCAGTGTTGTGATTGAATCTAC</td>
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<td></td>
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<td>dgk4 rv (A)</td>
<td>CCAAGAAGTGAGGGGACTC</td>
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<td></td>
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<td>dgk4 r3 (B)</td>
<td>CGCATCTTTCCAGTCTTC</td>
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<tr>
<td>DGK5</td>
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<td>dgk5 rv</td>
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<td>sense</td>
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<td>CAGACAGGGGATGCG</td>
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<tr>
<td></td>
<td>antisense</td>
<td>At2g28390-Q-rv</td>
<td>GCCTTCTCAAGGTTCTG</td>
</tr>
</tbody>
</table>

Sequences of the different primer pairs used to measure the expression of the various DGK genes used in this study. SAND (At2g28390) expression was used as the reference gene (Hong et al., 2010).

FIGURE A1 | Two pathways with the potential to generate DAG and PtdOH at the expense of PtdIns4P. PtdIns4P is suggested to be the substrate of cold-induced PLC activity which not only generates DAG, but at the same time releases InsP2 that can be converted to InsP6 and/or Ins. The latter products may have a functional relevance in the stress response because InsP6 is a signaling compound in plants, and Ins is a precursor to compatible solutes (Vermeer and Munnik, 2010). Alternatively, inositolphosphorylceramide synthase (IPCS) generates DAG while transferring the InsP headgroup from PtdIns to ceramide (Cer), generating inositolphosphorylceramide (IPC). The PtdIns substrate in this conversion can be derived from PtdIns4P dephosphorylation, as, in yeast, through Sac1 activity. DAG generated via either of these pathways may subsequently be phosphorylated by DGK to generate PtdOH.

FIGURE A2 | Cold temperatures suppress 32P-PtdEtn accumulation in Arabidopsis leaf disks. After 30 min 32P-labeling and 5 min incubation at the indicated temperatures, phospholipids were quantitatively analyzed by phosphoimaging. Values are in arbitrary units (AU) representing means (±SD) of the radioactivity levels.
FIGURE A3 | Genotyping of the Arabidopsis dgk T-DNA insertion lines. DNA was isolated from leaf discs from 3 to 4 independent plants and zygosity determined by PCR using specific wt- and mutant-primer sets as listed in Table A1. Gel sample order (from left to right): Size marker; Col-0 (wt), with first primer set, LP/RP (= wt band) and second primer set, RP/LB (= insertion band); Three (or four) independent dgk plants, with first primer set, LP/RP (= wt band) and second primer set RP/LB (= insertion band); Last lane, primer control (−). Some gels end with the size marker. Results clearly show that all lines used are homozygous T-DNA insertion lines since Col-0 was the only line giving wt bands and all insertion lines gave only bands with the second primer set. For the SALK lines LBb1.3 was used as LB primer, for the SAIL lines LB3 was used as LB primer (see primer list, Table A1).
FIGURE A4 | Determination of DGK KO/KD-expression in Arabidopsis T-DNA insertion mutants by RT-PCR. RNA was isolated from 9-days old roots (DGK1,−3,−5,−7) or flowers (DGK2,−4,−6) since the latter genes did not reveal expression in the root (not shown). Predicted band Sizes: DGK1, 702 bp; DGK3, 592 bp; DGK5, 534 bp; DGK8, 434 bp; DGK7, 791 bp; SAND (reference gene), 244 bp. Abbreviations: ND, not detectable; NAC, non-amplification control (test for genomic DNA contamination), i.e., RT reaction without RT enzyme on Col-0 RNA; NTC, no target control (test for contamination + primer dimers), i.e., RT reaction with water sample.

=> Summary:
dgk1-1 -> KD (exon)
dgk2-1 -> KO (exon)
dgk2-2 -> KO (exon)
dgk3-1 -> KO/KD (3’UTR)
dgk4-1 -> no KD (3’UTR)
dgk4-2 -> KO (exon)
dgk4-3 -> no KD (promotor)
dgk5-1 -> KO/KD intron)
dgk5-2 -> no KD (intron 5’UTR)
DGK6 -> ND
dgk6-1 -> possible KO/KD (exon)
dgk6-2 -> OE (exon, 40bp after ATG)
dgk7-1 -> strong KD (exon)
dgk7-2 -> weak KD (promotor)
dgk7-3 -> no KD (intron)