A Small Phospholipase A<sub>2</sub>-α from Castor Catalyzes the Removal of Hydroxy Fatty Acids from Phosphatidylcholine in Transgenic Arabidopsis Seeds<sup>1[OPEN]</sup>

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Ricinoleic acid, an industrially useful hydroxy fatty acid (HFA), only accumulates to high levels in the triacylglycerol fraction of castor (Ricinus communis) endosperm, even though it is synthesized on the membrane lipid phosphatidylcholine (PC) from an oleoyl ester. The acyl chains of PC undergo intense remodeling through the process of acyl editing. The identities of the proteins involved in this process, however, are unknown. A phospholipase A<sub>2</sub> (PLA<sub>2</sub>) is thought to be involved in the acyl-editing process. We show here a role for RcsPLA<sub>2</sub> in the acyl editing of HFA esterified to PC. RcsPLA<sub>2</sub> was identified by its high relative expression in the castor endosperm transcriptome. Coexpression in Arabidopsis (Arabidopsis thaliana) seeds of RcsPLA<sub>2</sub> with the castor fatty acid hydroxylase RcFAH12 led to a dramatic decrease in seed HFA content when compared with RcFAH12 expression alone in both PC and the neutral lipid fraction. The low-HFA trait was heritable and gene dosage dependent, with hemizygous lines showing intermediate HFA levels. The low seed HFA levels suggested that RcsPLA<sub>2</sub> functions in vivo as a PLA<sub>2</sub> with HFA specificity. Activity assays with yeast (Saccharomyces cerevisiae) microsomes showed a high specificity of RcsPLA<sub>2</sub> for ricinoleic acid, superior to that of the endogenous Arabidopsis PLA<sub>2</sub>s. These results point to RcsPLA<sub>2</sub> as a phospholipase involved in acyl editing, adapted to specifically removing HFA from membrane lipids in seeds.

Phospholipase A enzymes (PLAs) catalyze the hydrolysis of either the sn-1 (PLA<sub>1</sub>) or the sn-2 (PLA<sub>2</sub>) ester bond of phospholipids to produce lysophospholipids and free fatty acids (FAs). They are involved in several biological processes in both animals and plants (Chen et al., 2011): (1) as a component of the acylation/hydrolysis of phospholipids in the so-called Lands cycle involved in primary lipid metabolism in animals (Lands, 1960; Balsinde and Dennis, 1997; Imae et al., 2010) and plants (Li et al., 2013); (2) in membrane architecture and trafficking (Lee et al., 2010; Kim et al., 2011); (3) in the production of bioactive compounds involved in signaling, pathogen defense, and programmed cell death (Munnik and Testerink, 2009; Canonne et al., 2011); (4) in catalyzing the hydrolysis of oxidized lipids (van Kuijk et al., 1987; Banaś et al., 1992); (5) in seed storage lipid mobilization (Rudolph et al., 2011); and (6) in uncommon and modified FA production in seeds (Bafor et al., 1991; Ståhl et al., 1995; Bates and Browse, 2011).

With recent developments in the understanding of lipid biosynthesis, focusing on FA incorporation and turnover in phosphatidylcholine (PC), attention is moving from the traditional Kennedy pathway of lipid synthesis to that of acyl editing (Bates et al., 2012; Wang et al., 2012; Xu et al., 2012), with the relative importance of each pathway in lipid synthesis depending on the plant species (Bates and Browse, 2012). Acyl turnover in membrane lipids, through a cycle of deacylation/acylation of PC to lysophosphatidylcholine (LPC), was first described by Lands (1958). Substantial progress has been made in the understanding of the acylation mechanism of LPC, involving lysophosphatidylcholine acyltransferases (LPCAT; Ståhl et al., 2008; Bates et al., 2012; Wang et al., 2012; Xu et al., 2012). As suggested by Lands (1960), PC deacylation was initially thought to result from the activity of a phospholipase. Until now, in plants, however, evidence suggested that LPC production comes from the action of phospholipid:diacylglycerol acyltransferase (PDAT; Zhang et al., 2009; van Erp et al., 2011; Xu et al., 2012) and through the reverse activity of LPCAT (Stymne and Stobart, 1984; Yurchenko et al., 2009; Bates et al., 2012; Lager et al., 2013).

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<sup>1</sup>This work was supported by the U.S. National Science Foundation (grant nos. DBI-0701919 and IOS-1339385), by the Agricultural Research Center at Washington State University (to J.B.), and by Alberta Innovates Bio Solutions, AVAC, Ltd., and the Canada Research Chairs Program (to R.J.W.).

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acyl editing includes a broader set of enzymatic activities than originally envisioned by Lands (1960). Despite the recent description of a patatin-related phospholipase, pPLAIIb, contributing to acyl turnover in PC (Li et al., 2013), phospholipase involvement in acyl editing in plants remains largely to be determined.

In contrast to common FAs, FAs with unusual functional groups only accumulate to relatively high levels in seed triacylglycerol (TAG) and are excluded from membrane lipids (Millar et al., 2000). Phospholipase activity also has been shown to be involved in the metabolism of the uncommon FAs ricinoleate (12-OH 18:1, et al., 1995). In castor (Ricinus communis), ricinoleate is synthesized from oleate (18:1) and laurate in plant seeds (Bafor et al., 1991; Ståhl et al., 1992) esterified to the sn-2 position of PC, and the activity of a ricinoleate-specific phospholipase is involved in liberating the newly formed hydroxy fatty acid (HFA) for further incorporation into TAG (Bafor et al., 1991). Phospholipases also may be involved in maintaining cellular membrane integrity through the hydrolysis of oxidized lipid. Banaś et al. (1992) showed in a variety of plants that both lipid peroxides and lipid hydroxides were preferentially hydrolyzed over nonoxidized lipids.

In plants, three major groups of PLAs have been identified: the patatin-related pPLAs, the Delayed Anthér Dehiscencel (DAD1)-like PLA, and the secretory/ small sPLA,S (Matos and Pham-Thi, 2009; Chen et al., 2011). In the first group, pPLA proteins show homology to patatin, a storage glycoprotein with lipase activity present in potato (Solanum tuberosum) tubers, and have been associated with signaling, pathogen defense, and lipid mobilization during seed germination (Scherer et al., 2010). In the second group of PLAs, DAD1 and DONGLE are clearly involved in signaling and jasmonate production (Ishiguro et al., 2001; Seo et al., 2009). The third group contains four paralogous genes coding for low-molecular-mass PLAs of around 14 kD, sPLA,α, sPLA,β, sPLA,γ, and sPLA,δ (Lee et al., 2005; Matos and Pham-Thi, 2009). Evidence for the involvement of sPLA,α in signaling and pathogen defense is more limited (Munnik and Testerink, 2009; Canonne et al., 2011). Their involvement in membrane trafficking, however, is emerging: reductions in sPLA,α expression in Arabidopsis (Arabidopsis thaliana) plants led to Golgi disruption and the inhibition of PIN auxin efflux transporter traffic to the plasma membrane in roots (Lee et al., 2010) and also to membrane disruption in pollen (Kim et al., 2011). Two other proteins, SOBER1 (Kirik and Mudgett, 2009) and Lecithin Cholesterol Acyltransferase (LCAT)-like4 (Chen et al., 2012), unrelated to these three main families, also have been identified as sPLA,S.

With the aim of gaining more insights into the involvement and identities of PLAs in acyl editing and HFA metabolism, with potential downstream industrial applications, we made use of the available castor endosperm transcriptome database (Troncoso-Ponce et al., 2011) and the transgenic Arabidopsis seed line CL37 expressing the castor fatty acid hydroxylase FAH12 (Lu et al., 2006). Among the PLA genes examined from the castor endosperm transcriptome, RcsPLAα was the most highly expressed, indicating possible involvement in ricinoleate metabolism in castor. The expression of RcsPLAα in CL37 seeds led to a drastic reduction in HFA levels in both TAG and PC fractions. Also, microsomal fractions from yeast (Saccharomyces cerevisiae) expressing RcsPLAα showed strong activity with sn-2-ricinoleoyl-PC as a substrate. Our results suggest roles for RcsPLAα in (1) acyl editing to generate LPC for reacylation through LPCAT activity, (2) freeing HFAs for activation to acyl-CoA and incorporation into TAG, and (3) contributing to membrane integrity through the removal of potentially deleterious ricinoleate from membrane lipids.

RESULTS

PLA,α Is the Most Highly Expressed PLA in Developing Castor Endosperm

To identify which of the PLA genes are potentially involved in castor lipid metabolism, protein sequences of Arabidopsis PLAs were used in a BLASTP search against the 4x draft castor genome accessible from the J. Craig Venter Institute (JCVI; http://www.jcvi.org). The gene sequences identified were then used in a BLASTN search against the Michigan State University castor EST database (http://glbrc.bch.msu.edu/castor/; Troncoso-Ponce et al., 2011) to determine gene expression levels. The 13 PLA genes found to be expressed in castor endosperm are listed in Table I. Information about 38 known or putative PLA isoforms in castor and Arabidopsis is included in Supplemental Table S1. Twelve PC-PLAα, one phosphatidic acid (PA)-PLAα, one LCAT-like3, 12 pPLA, two sPLA, one SOBER1, and one LCAT-like4 were identified in the castor genome. Four PLAs were found to have substantial expression in developing castor endosperm, the highest being sPLA,α (12.1 ESTs per 105), followed by LCAT-like4 (7.7 ESTs per 105), pPLA (4.6 ESTs per 105), and sPLA,β (3.2 ESTs per 105). By combining expression data with the knowledge available about the substrate specificity of PL A enzymes, it appears that the castor phospholipases most likely involved in catalyzing HFA hydrolysis from PC are RcsPLA,α and RcsPLA,β. Both Arabidopsis homologs, AtsPLA α and AtsPLA,β, have been shown to catalyze the hydrolysis of FAs specifically from the sn-2 position of PC and phosphatidylethanolamine (Lee et al., 2003; Ryu et al., 2005; Mansfeld and Ulbrich-Hofmann, 2007), whereas AtpPLAI is selective for galactolipid acyl chains at both sn-1 and sn-2 positions (Yang et al., 2007) and the PLA2 AtLCAT-like4 displays the acyl preference oleoyl > linoleoyl > ricinoleoyl and is mostly cytosolic (Chen et al., 2012).

Phylogenetic and Sequence Analyses of sPLA2

Phylogenetic analysis shows the evolutionary relatedness of sPLA2 protein sequences from castor, Arabidopsis,
and rice (*Oryza sativa*; Fig. 1). Both castor RcsPLA$_{\alpha}$ and RcsPLA$_{\beta}$, identified by BLAST search in The Institute for Genomic Research, show a close relatedness with Arabidopsis AtsPLA$_{\alpha}$ and AtsPLA$_{\beta}$, with a degree of identity at the amino acid level of 73.5% and 52.9%, respectively. No castor homologs were identified for AtsPLA$_{\gamma}$ or AtsPLA$_{\delta}$. Multiple sequence alignment analysis confirmed, in both RcsPLA$_{\alpha}$ and RcsPLA$_{\beta}$, the presence of highly conserved regulatory and catalytically important motifs characteristic of sPLA$_2$ proteins. Both RcsPLA$_{\alpha}$ and RcsPLA$_{\beta}$ harbor a defined PA$_2$C (SMART accession no. SM00085) domain with a conserved Ca$^{2+}$-binding loop denoted by the YGKYCGxxxxGC motif and the catalytic site LDACCxxHDxCV, with His/Asp residues participating in catalysis (Fig. 2). Twelve Cys residues are completely conserved in the different sPLA$_2$ proteins and are potentially involved in intramolecular disulfide bridges, stabilizing the protein structure (Fig. 2). In relation to subcellular localization, both Arabidopsis homologs AtsPLA$_{\alpha}$ and AtsPLA$_{\beta}$ and the rice homolog OssPLA$_{\alpha}$ possess signal sequences as predicted by PSORT (http://psort.hgc.jp) and have been localized previously to the endoplasmic reticulum (ER) or Golgi (Seo et al., 2008; Matos and Pham-Thi, 2009; Lee et al., 2010; Singh et al., 2012). A common motif (-LHKP) is found at the C terminus of both the rice and castor sPLA$_{\alpha}$ sequences, constituting a putative ER retention signal (Singh et al., 2012).

### RcsPLA$_{\alpha}$ Expression Leads to a Dramatic Reduction of HFA Levels in CL37 Seeds

RcsPLA$_{\alpha}$ and RcsPLA$_{\beta}$ were cloned from a castor endosperm complementary DNA (cDNA) library, introduced into the expression vector pGate-DsRed-Phas (Lu et al., 2006), and expressed under the control of the seed-specific phaseolin promoter (Slighlom et al., 1983) in the Arabidopsis CL37 line. CL37 is an Arabidopsis line expressing RcFAH12 and accumulating 17% HFAs, including ricinoleic acid and dicosyl acid (12-hydroxy-octadec-cis-9,15-enoic acid [18:2-OH]; Lu et al., 2006). CL37 also is mutated in its fatty acid elongase (*fie1*) gene (Kunst et al., 1992) and thus is devoid of the very-long-chain HFAs lesquerolic acid (20:1-OH) and auricolic acid (20:2-OH), simplifying the FA profile analysis by gas chromatography (GC). The marker geneDsRed allows the identification of transgenic seeds (Stuitje et al., 2003).

To obtain an initial estimate of the effect of each enzyme on HFA metabolism in transgenic Arabidopsis seeds, we analyzed samples (30 seeds each) of red and brown T1 seeds. Thus, each sample of red seed was hemizygous for 30 distinct phaseolin:RcsPLA$_{\alpha}$ or phaseolin:RcsPLA$_{\beta}$ transgenes.

### Table 1. Expression Data for 13 Genes Encoding Phospholipase Isozymes in Developing Castor Endosperm

<table>
<thead>
<tr>
<th>Castor Name</th>
<th>Gene Identifier</th>
<th>Arabidopsis Homolog</th>
<th>Amino Acid Identity</th>
<th>Total ESTs</th>
<th>Stage III</th>
<th>Stage IVa</th>
<th>Stage VI</th>
<th>Stages VII + VIII</th>
</tr>
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<td>RcPLA1-β2</td>
<td>28192.m000243</td>
<td>At4g16820</td>
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<td>0</td>
<td>0.4</td>
<td>0</td>
<td>0</td>
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<td>RcPLA1-1y1</td>
<td>29883.m001996</td>
<td>At1g06800</td>
<td>53.7</td>
<td>5</td>
<td>2.1</td>
<td>0.4</td>
<td>0</td>
<td>0</td>
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<tr>
<td>RcPA-PLA1</td>
<td>29757.m000745</td>
<td>At3g14800</td>
<td>65.3</td>
<td>10</td>
<td>1.4</td>
<td>0.4</td>
<td>1.3</td>
<td>1</td>
</tr>
<tr>
<td>RcLCAT3</td>
<td>29929.m004538</td>
<td>At3g33310</td>
<td>69.2</td>
<td>7</td>
<td>0.7</td>
<td>1.2</td>
<td>0.7</td>
<td>1</td>
</tr>
<tr>
<td>RcpPLA1</td>
<td>29842.m003623</td>
<td>At1g1850</td>
<td>69.6</td>
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<td>7</td>
<td>5.6</td>
<td>1.3</td>
<td>5</td>
</tr>
<tr>
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<td>1.4</td>
<td>0.7</td>
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<td>RcpPLAl</td>
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<td>At4g29800</td>
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<td>0.7</td>
<td>0.4</td>
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<td>0</td>
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<td>RcpPLAlβ</td>
<td>29647.m002082</td>
<td>At3g63200</td>
<td>72.8</td>
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<td>2.8</td>
<td>1.9</td>
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<td>29912.m005406</td>
<td>At2g19690</td>
<td>54.1</td>
<td>38</td>
<td>2.8</td>
<td>7.9</td>
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<td>0</td>
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<tr>
<td>RcsPLAl</td>
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<td>At4g19860</td>
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<td>98</td>
<td>4.9</td>
<td>8.6</td>
<td>3.3</td>
<td>14</td>
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</tbody>
</table>

Figure 1. Phylogenetic relationship of the sPLA$_2$ family in castor (Rc), Arabidopsis (At), and rice (Os). The sequence alignment was produced with ClustalX 2.0, and the rectangular cladogram was generated using TreeView. The percentage amino acid pairwise identity between the different protein sequences and RcsPLA$_{\alpha}$ is indicated in parentheses. The scale bar represents 0.1 amino acid substitutions per site.
oleic acid. Our results are consistent with the RcsPLA2 increase in linoleic acid (18:2 Δ9Δ12) CL37 controls. In all plants of each line are shown in Table II. HFA content of seed samples collected from homozygous lines expressing the RcsPLA2 construct showed no change in HFA content compared with CL37 control samples, and subsequent analysis of T2 seeds from 30 additional T1 plants also failed to provide any evidence that expression of RcsPLA2 altered HFA accumulation or other aspects of TAG metabolism in seeds. T1 seed samples expressing RcsPLA2, however, exhibited an average 20% reduction in HFA relative to segregating and control CL37 samples (14.8% ± 0.1% versus 18.8% ± 0.3%). Therefore, we grew 75 T1 plants to maturity and analyzed the FA composition of a sample of T2 (segregating) seeds from each plant. Twenty-four of the 75 plants yielded seeds with a greater than 25% reduction in HFA relative to three CL37 controls, with several lines having approximately 5% HFA.

Segregation of the DsRed marker indicated that both single-insert (75% red seeds) and multiple-insert (more than 90% red seeds) lines were present. By genetic analysis in the T2 and subsequent generations, we identified five homozygous, single-insert lines (designated RcsPLA2–CL37 line 1–RcsPLA2–CL37 line 5) for further characterization, along with null-segregant lines that were analyzed and confirmed to have seed FA compositions similar to CL37. The fatty acid compositions of seed samples collected from homozygous plants of each line are shown in Table II. HFA content was decreased by 64% (line 4) to 94% (line 5) relative to CL37 controls. In all five lines, we noted substantial increases in α-linolenic acid (18:3Δ9Δ12), linoleic acid (18:2Δ9Δ12), and a modest decrease in oleic acid. Our results are consistent with the RcsPLA2 enzyme acting to selectively remove HFA from the pathway of TAG synthesis, possibly through the hydrolysis of HFA from the pathway intermediate, PC. Our analyses of seed lipids did not indicate a decrease in PC content or any substantial increase in free fatty acids or LPC. These two products of PLA2 enzymes presumably are rapidly metabolized, since their accumulation can disrupt membrane and cell function.

Figure 2. Alignment of amino acid sequences of seven sPLA2s from castor (Rc), Arabidopsis (At), and rice (Os). The conserved domains, Ca2+-binding loop (RYGKYCxxxxGC) and active site (LDACCxxHDxC) motifs, are boxed. Each of the 12 conserved Cys residues is indicated by an asterisk. The putative signal sequences as predicted by the PSORT prediction program (http://psort.hgc.jp) are underlined. The arrow marks the conserved His/Asp dyad of the active site.

phospholipase (RcsPLA2β) transformation events. Samples of seeds expressing the RcsPLA2β construct showed no change in HFA content compared with CL37 control samples, and subsequent analysis of T2 seeds from 30 additional T1 plants also failed to provide any evidence that expression of RcsPLA2β altered HFA accumulation or other aspects of TAG metabolism in seeds. T1 seed samples expressing RcsPLA2α, however, exhibited an average 20% reduction in HFA relative to segregating and control CL37 samples (14.8% ± 0.1% versus 18.8% ± 0.3%). Therefore, we grew 75 T1 plants to maturity and analyzed the FA composition of a sample of T2 (segregating) seeds from each plant. Twenty-four of the 75 plants yielded seeds with a greater than 25% reduction in HFA relative to three CL37 controls, with several lines having approximately 5% HFA.

Segregation of the DsRed marker indicated that both single-insert (75% red seeds) and multiple-insert (more than 90% red seeds) lines were present. By genetic analysis in the T2 and subsequent generations, we identified five homozygous, single-insert lines (designated RcsPLA2α–CL37 line 1–RcsPLA2α–CL37 line 5) for further characterization, along with null-segregant lines that were analyzed and confirmed to have seed FA compositions similar to CL37. The fatty acid compositions of seed samples collected from homozygous plants of each line are shown in Table II. HFA content was decreased by 64% (line 4) to 94% (line 5) relative to CL37 controls. In all five lines, we noted substantial increases in α-linolenic acid (18:3Δ9Δ12), linoleic acid (18:2Δ9Δ12), and a modest decrease in oleic acid. Our results are consistent with the RcsPLA2α enzyme acting to selectively remove HFA from the pathway of TAG synthesis, possibly through the hydrolysis of HFA from the pathway intermediate, PC. Our analyses of seed lipids did not indicate a decrease in PC content or any substantial increase in free fatty acids or LPC. These two products of PLA2 enzymes presumably are rapidly metabolized, since their accumulation can disrupt membrane and cell function.

Overexpression of the Arabidopsis sPLA2α Homolog Does Not Alter HFA Levels in CL37 Seeds

To ascertain whether the reduction in HFA in RcsPLA2α–CL37 lines was not due simply to increased nonspecific PLA2 activity but is indeed due to RcsPLA2α having specificity for HFAs, the endogenous Arabidopsis gene AtsPLA2α was cloned into the pGate-DsRed-Phas vector and used to transform CL37 plants. Samples of T2 seeds from 24 independent T1 transformants were analyzed for FA composition. None of the samples had HFA content beyond 2 SD of 12 CL37 control samples (low, 16.4% HFA; high, 20.3% HFA), and the mean value of all 24 plants, 18.7% ± 0.2% (SE), was indistinguishable from that of the controls at 18.5% ± 0.3% (SE). The proportions of other FAs in the AtsPLA2α transgenics also were very similar to the CL37 controls (Supplemental Table S2). We also overexpressed RcsPLA2β in CL37 using the same pGate-DsRed-Phas vector and observed a similar lack of impact on the HFA content of the resulting transgenic seeds (Supplemental Table S2). The absence of modification in the lipid profile in AtsPLA2α–CL37 seeds may indicate a lack of specificity of AtsPLA2α for HFA or possibly a low degree of activity of the AtsPLA2α isozyme in the seed tissues. We also cannot exclude the possibility that, for some reason, our transgene failed to express high amounts of the protein. In any case, our results indicate that the castor sPLA2α enzyme likely possesses specificity for HFA above that of AtsPLA2α and that the HFA reductions observed are not due solely to a general increase in PLA2 activity.

RcsPLA2α Is More Efficient than AtsPLA2α in Catalyzing the Liberation of Ricinoleate from Ricinoleoyl-PC

To further investigate the castor and Arabidopsis sPLA2α isozymes, we cloned cDNAs encoding RcsPLA2α and AtsPLA2α into a pYES2 vector to allow strong inducible expression in yeast. An empty-vector construct

Table II. FA composition of T3 and T4 homozygous seeds coexpressing castor Rspla2α with castor hydroxylase (CL37 background)

All samples were derived from lines with a single transgenic insert, as determined by pedigree analysis. Data are means ± s for three to six samples of 30 seeds each. –, Not detected.

<table>
<thead>
<tr>
<th>Line</th>
<th>16:0</th>
<th>18:0</th>
<th>18:1</th>
<th>18:2</th>
<th>18:3</th>
<th>18:1-OH</th>
<th>18:2-OH</th>
<th>Sum of HFAs</th>
</tr>
</thead>
<tbody>
<tr>
<td>fae1</td>
<td>9.7 ± 0.1</td>
<td>3.5 ± 0.1</td>
<td>27.3 ± 0.5</td>
<td>36.0 ± 0.1</td>
<td>23.2 ± 0.5</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>CL37</td>
<td>12.6 ± 0.3</td>
<td>6.0 ± 0.2</td>
<td>37.4 ± 0.4</td>
<td>20.0 ± 0.5</td>
<td>6.2 ± 0.1</td>
<td>14.3 ± 0.5</td>
<td>3.6 ± 0.1</td>
<td>17.9 ± 0.5</td>
</tr>
<tr>
<td>Line 1</td>
<td>10.0 ± 0.1</td>
<td>2.6 ± 0.1</td>
<td>33.6 ± 0.5</td>
<td>32.5 ± 0.3</td>
<td>17.8 ± 0.4</td>
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<td>1.3 ± 0.1</td>
<td>3.5 ± 0.2</td>
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<tr>
<td>Line 2</td>
<td>9.9 ± 0.1</td>
<td>3.3 ± 0.0</td>
<td>35.7 ± 0.3</td>
<td>28.5 ± 0.1</td>
<td>18.1 ± 0.2</td>
<td>2.8 ± 0.0</td>
<td>1.7 ± 0.0</td>
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<td>Line 3</td>
<td>11.7 ± 1.3</td>
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<td>34.7 ± 0.5</td>
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<td>Line 4</td>
<td>10.1 ± 0.1</td>
<td>4.1 ± 0.1</td>
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<td>1.8 ± 0.5</td>
<td>6.5 ± 1.6</td>
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<tr>
<td>Line 5</td>
<td>10.1 ± 0.1</td>
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<td>29.5 ± 0.4</td>
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<td>0.7 ± 0.1</td>
<td>0.4 ± 0.2</td>
<td>1.1 ± 0.2</td>
</tr>
</tbody>
</table>

Changes in the FA Composition of TAG and PC during Seed Development of Rspla2α-CL37 Lines

Total lipids were extracted from CL37 and Rspla2α-CL37 seeds at different stages of development from 7 to 18 d after flowering. Total lipid fractions were separated into neutral lipids (mostly TAG) and PC (Fig. 3) by thin-layer chromatography (TLC). The neutral lipid fraction from CL37 seeds showed an increase in HFAs, which rose from 0% to 20% of total FAs in mid development (Fig. 4A). Developing Rspla2α-CL37 seed TAG also showed an increase in HFAs during development, but the maximum of less than 5% of total FAs was much lower than that in CL37 seeds (Fig. 4C). The approximately 80% HFA reduction in Rspla2α-CL37 seed TAG relative to CL37 was not confined to mature seeds but was evident throughout development (Fig. 4E). Relative amounts of 18:3 and 18:2 also showed significant increases during development, with 18:3 increasing by 160% and 18:2 increasing by almost 50% due to the expression of the Rspla2α transgene (Fig. 4E).

In the PC fraction derived from CL37 developing seeds, HFA levels increased up to 9.5% in the mid development stage, whereas 16:0 and 18:0 were relatively constant throughout seed development (Fig. 4B). 18:1 showed an increase correlating with a large decrease in 18:2 before stabilizing at mid development. A similar pattern occurred in PC derived from Rspla2α-CL37 seeds, but HFA increased only marginally during development to 2.9% (Fig. 4D). When comparing differences in PC FA composition between CL37 and Rspla2α-CL37 seeds, the reduction in HFA observed in PC (approximately 70%) was similar to the reduction observed in TAG (approximately 80%) and was constant throughout development (Fig. 4F). The changes in other FAs were modest throughout seed development, with the exception of 18:3, which showed large differences (up to 70%) during early to mid development stages before being reduced to 20% at a later stage of development.
(Fig. 4F). 18:1 and 18:2 both showed slight increases of approximately 15% during later stages of development, whereas 18:0 and 16:0 were reduced by approximately 50% and approximately 30%, respectively, during seed development. The differences in FA composition in PC between the two lines can be considered mostly constant after the mid development stage (Fig. 4F).

**Total Fatty Acid Content Is Increased Slightly and Germination Rate Is Restored in RcsPLA2-α-CL37 Seeds**

The total FA content of homozygote seeds from five RcsPLA2-α-CL37 lines was compared with that of the brown null-segregant seeds from the same lines and that of fae1 seeds (Fig. 5). Previous analyses by Bates and Browse (2011) and van Erp et al. (2011) showed reductions in seed total FA content of 30% and 20%, respectively, in CL37 plants expressing RcFAH12, compared with parental fae1, and the difference between fae1 and the CL37 null segregants in Figure 5 (25.6%) is in this range. The expression of RcsPLA2-α in CL37 seed increased the total average FA content in homozygote seeds up to 5.63 μg per seed, compared with brown null-segregating CL37 seeds (5.05 μg per seed). This represents a significant increase of 11.5% (P = 0.024); however, oil content remained substantially below that of the fae1 controls (6.79 μg per seed). Seed germination rates also were restored to nearly wild-type levels, from an average of 24% for cosegregating T2 CL37 seeds to 95% for the transgenic T2 RcsPLA2-α-CL37 seeds from three different lines.

**DISCUSSION**

The castor hydroxylase RcFAH12 is an ER enzyme that converts 18:1 to 18:1-OH esterified at the sn-2 position of PC (Bafor et al., 1991; Broun and Somerville, 1997). When RcFAH12 is expressed in Arabidopsis seeds (in lines CL7 and CL37), 18:1-OH and 18:2-OH HFA accumulate to 10% to 11% of the FA in PC and produce a bottleneck in lipid metabolism that reduces FA synthesis and TAG accumulation through feedback inhibition of acetyl-CoA carboxylase (Bates and Browse, 2011; Bates et al., 2014). Expression of castor Diacylglycerol Acyltransferase2 or RcPDAT1A reduced PC HFA levels (van Erp et al., 2011) and substantially alleviated the reductions in FA synthesis and TAG accumulation (Bates et al., 2014). In castor endosperm, it is likely that PLA2 plays a major role in removing newly synthesized HFA from PC (Bafor et al., 1991). Therefore, we sought to identify a suitable PLA2 gene in castor and test its effectiveness in supporting metabolism and the accumulation of HFA when coexpressed with RcFAH12 in transgenic Arabidopsis.

RNA sequencing results (Table I) indicate that the RcsPLA2 gene is the most highly expressed PLA2 isoform throughout the stages of oil accumulation in developing castor endosperm (Troncoso-Ponce et al., 2011). This gene encodes an enzyme of the small PLA2 family, RcsPLA2-α. sPLA2-α homologs have been identified in Arabidopsis, rice, and several other plant species (Ståhl et al., 1999; Lee et al., 2005; Singh et al., 2012). The rice sPLA2-α is strongly expressed in seeds and other tissues (Singh et al., 2012), while the Arabidopsis homolog is not highly expressed in developing seeds (Supplemental Table S1). AtPLA2-α is expressed in vegetative tissues, and the encoded enzyme likely acts in lipid signaling (Lee et al., 2005). In contrast to the very low expression of AtPLA2-α in developing Arabidopsis seeds, the high expression of RcsPLA2-α in developing castor endosperm suggests that it may encode an enzyme responsible for the efficient removal of HFA.
of HFA from sn-2 of PC following its synthesis catalyzed by the hydroxylase during TAG accumulation and seed development in castor. Release of HFA from PC in castor endosperm is thought to allow conversion to the CoA thioester and incorporation into TAG by the three acyltransferases of the Kennedy pathway, sn-glycerol-3-phosphate acyltransferase, lysophosphatidic acid acyltransferase, and diacylglycerol acyltransferase (Bafor et al., 1991).

The rice sPLA₂α protein fused to GFP was shown to colocalize with an ER marker (Singh et al., 2012). This result is consistent with our finding that recombinant RcsPLA₂α produced in yeast showed high activity in the microsomal fraction of cell homogenates (Supplemental Fig. S1), but the activity in the high-speed supernatant also was high. The RcsPLA₂α protein has a C-terminal sequence, -LHKP, that is identical to the sequence in the rice protein (Singh et al., 2012), and this may constitute the ER retention signal. Alternatively, protein acylation has been suggested as a potential mechanism for localization to the ER (Ståhl et al., 1999).

The enzymatic properties of the Arabidopsis family of sPLA₂s have been well characterized, with a regiospecificity for sn-2 acyl chains and with a head group selectivity for PC and phosphatidylethanolamine over other phospholipids (Chen et al., 2011). In this study, the in vitro assays using yeast microsomes show that both castor and Arabidopsis sPLA₂α are active in the picomolar range against [14C]18:1-PC, demonstrating the sn-2 regiospecificity of PLA₂. Enzymes from both castor and Arabidopsis displayed higher specificity for [14C]18:1-PC than for [13C]Ric-PC (Fig. 3A). However, this loss of oleate from PC through the preferential hydrolysis of 18:1-PC over sn-1-palmitoyl-sn-2-ricinoleoylphosphatidylcholine (Ric-PC) may be mitigated to some extent through the selective reacylation of LPC by the endogenous Arabidopsis LPCATs (Lager et al., 2013). The newly liberated oleic acid would have to be reactivated to its CoA-thioester, prior to transfer catalyzed by LPCAT into PC, via the catalytic action of long-chain acyl-coenzyme A synthetase (LACS; Shockey et al., 2002). Both specificity and selectivity assays showed that RcsPLA₂α was a more efficient enzyme than AtsPLA₂α in catalyzing the hydrolysis of [14C]Ric-PC. Assuming comparable levels of protein expression in the yeast, the specific activity of RcsPLA₂α was 9 times that of AtsPLA₂α (32.7 ± 0.1 versus 3.4 ± 0.1 pmol min⁻¹ mg⁻¹ protein) with [14C]Ric-PC as sole substrate, and RcsPLA₂α was twice as efficient as...
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Figure 5. Partial recovery of seed oil content in CL37 lines expressing RcsPLA₂α. Five plants from each of the homozygous lines 1 to 5 were sampled (Homo), together with 11 CL37 segregants (Null-seg) and three fae1 plants. Data are means ± st for total fatty acids for five transgenic and five null-segregant lines.

AtsPLA₂α in a selectivity assay with the presence of an equimolar mixture of [14C]18:1-PC and [14C]Ric-PC (Fig. 3).

Consistent with the high activity of recombinant RcsPLA₂α on Ric-PC, developing CL37 seeds expressing RcsPLA₂α showed a dramatic decrease in HFA in PC to less than 3% of total FAs during the period of oil accumulation, compared with 10% in CL37 controls (Fig. 4). In mature CL37 seeds, approximately 70% of HFA in TAG is esterified to the sn-2 position of the glycerol backbone and is produced from PC via PC-derived diacylglycerol (DAG; Bates and Browse, 2011). Thus, the activity of the castor lipase in RcsPLA₂α-derived diacylglycerol (DAG; Bates and Browse, 2011).

The expression of RcsPLA₂α in CL37 also resulted in substantial changes in the proportions of other FAs in the seed. Compared with the fae1 parental line, CL37 seeds had a 66% decrease in 18:2 + 18:3 fatty acids (from 59.2% to 26.2%; Table II). Coexpression of the sPLA₂ α in our RcsPLA₂α-CL37 lines reduces this change, especially in line 5 with the lowest HFA level, which had an FA composition similar to that of fae1. It has been proposed that HFA-CoA is not synthesized or, possibly, be expected to be available for TAG synthesis catalyzed by the acyltransferases of the Kennedy pathway as well as for the reincorporation into PC catalyzed by LPCAT. The very low levels of HFA in both PC and TAG of RcsPLA₂α-CL37 seeds indicate that these routes of HFA reincorporation are substantially unused either because HFA-CoA is not synthesized or, possibly, because the three acyltransferases of the Kennedy pathway (glycerol-3-phosphate acyltransferase, lysophosphatidic acid acyltransferase, and diacylglycerol acyltransferase) have low activity with HFA-CoA and preferentially select other 16- and 18-carbon acyl-CoAs for incorporation into glycerolipids. We have considered the possibility that Arabidopsis ER (or cytoplasm) LACS isozymes are not able to efficiently convert HFA to HFA-CoA. In attempting to overcome this potential barrier to the

and Browse, 2011), this shift also would contribute to explaining the FA composition observed in CL37 seeds. The reverse changes in FA composition in RcsPLA₂α-CL37 seeds suggest that the bottleneck may be substantially alleviated. We did observe an increase in total FA accumulation in lines expressing RcsPLA₂α, but this was relatively small compared with the difference between CL37 (RcsPLA₂α-null) segregants and the fae1 parental line (Fig. 5).

Following the removal of HFA from sn-2 of PC catalyzed by RcsPLA₂α, the expected route of HFA breakdown is via β-oxidation in the peroxisome. The current view of β-oxidation would anticipate the conversion of HFA to the HFA-CoA thioester via the activity of a LACS (Shockey et al., 2002), subsequent hydrolysis of the HFA-CoA during transport into the peroxisome through the Peroxisomal ABC transporter1 ATP-binding cassette transporter (De Marcos Lousa et al., 2013), and the resynthesis of HFA-CoA inside the peroxisome catalyzed by the LACS6 and LACS7 isozymes (Fulda et al., 2004). While acyl-CoAs are known to be substrates for the PXA1 transporter, it is not definitively known whether the plant PXA1 also can accept free FAs for transport into the peroxisome and activation catalyzed by LACS6 and LACS7. It may be that HFA released by RcsPLA₂α is transported directly into the peroxisome for degradation. Moire et al. (2004) used a transgene encoding polyhydroxyalkanoate synthase to capture β-oxidation intermediates and allow the assessment of the relative flux of HFA and other fatty acids through the β-oxidation pathway. The expression of polyhydroxyalkanoate synthase in CL37 and RcsPLA₂α-CL37 plants could be used to confirm our expectation that HFA degradation occurs through β-oxidation. Interestingly, while this technique indicated increased rates of β-oxidation in seeds of Arabidopsis lines producing HFA or other unusual fatty acids, there was no increase in transcript levels of genes encoding enzymes of the β-oxidation pathway (Moire et al., 2004).

The question of whether HFAs released by RcsPLA₂α are direct substrates of the peroxisomal PXA1 transporter is potentially important, because if HFA-CoA were synthesized in the ER (or cytoplasm), it would be expected to be available for TAG synthesis catalyzed by the acyltransferases of the Kennedy pathway as well as for the reincorporation into PC catalyzed by LPCAT. The very low levels of HFA in both PC and TAG of RcsPLA₂α-CL37 seeds indicate that these routes of HFA reincorporation are substantially unused either because HFA-CoA is not synthesized or, possibly, because the three acyltransferases of the Kennedy pathway (glycerol-3-phosphate acyltransferase, lysophosphatidic acid acyltransferase, and diacylglycerol acyltransferase) have low activity with HFA-CoA and preferentially select other 16- and 18-carbon acyl-CoAs for incorporation into glycerolipids. We have considered the possibility that Arabidopsis ER (or cytoplasm) LACS isozymes are not able to efficiently convert HFA to HFA-CoA. In attempting to overcome this potential barrier to the
We coexpressed each of these isoforms in RcsPLA2 sperm tissue (Troncoso-Ponce et al., 2011). However, when genes (homologs of Arabidopsis
vested pathway (Bafor et al., 1991). Our goal in this in-
 Pyrosequencing of Castor Endosperm

MATERIALS AND METHODS

Isolation and Cloning of RcsPLA2

The protein sequences corresponding to the RcsPLA2 (NP_00252659) open reading frame obtained after translation using the Expasy translate tool (http://web.expasy.org/translate) of DNA sequences identified from the castor database at the JCVI (http://www.jcvi.org; GI: 29840.m001629), the National Center for Biotechnology Information GenBank (http://www.ncbi.nlm.nih.gov/genbank/; XM_00252613), and the Michigan State University castor database (http://gbrch.cbs.edu/castor/; MI010002005) are identical at the amino acid level and show a high degree of identity (73.5%) with AtsPLA2 (At4g37050) and RcPLA21/r (XP_002523613), and the percentage identity; if there was more than one homolog, the castor gene name was appended with a letter with decreasing levels of homology. The castor protein sequence was then used in a TBLASTN at the JCVI to obtain the nucleotide sequence. The castor nucleotide sequence was subsequently used to perform a BLASTN at the Michigan State University Castor 454 expression database (approximately 70,000 contigs assembled from approximately 1,060,000 ESTs; http://glbrc.plantbiology.msu.edu/castor). The expression data of the stages were obtained from castor seeds that were harvested from stage III to stage VIII, based on embryo length and testa (seed coat) color, as defined anatomically by Greenwood and Bewley (1982). In the 454 database, the total number of contigs is 69,194, stage III contains 141,964 ESTs, stage IV contains 267,141 ESTs, stage V contains 152,462 ESTs, and stages VII and VIII contain 151,964 ESTs. With only 77,518 and 84,170 ESTs, respectively, stages V and IV were ignored, as were stages III to V with 184,642 ESTs. Data containing the contig number, the number of ESTs per contig, the best Arabidopsis homolog, and the number of ESTs per 100,000 per embryo stage are compiled in Table I. Table I also includes the gene family, the Arabidopsis gene identifier, the Arabidopsis gene name, the name of the castor homolog, the castor gene model accession from the JCVI, and the percentage homology as measured by the percentage of pairwise identical amino acids in the aligned sequences. Additional methodology is available from Troncoso-Ponce et al. (2011).

Isolation and Cloning of RcsPLA2

The corresponding Arabidopsis (Arabidopsis thaliana) protein sequences were obtained from The Arabidopsis Information Resource (http://www.arabidopsis.org/), and the castor (Ricinus communis) homologs were obtained by performing a protein BLAST against the 4x draft castor protein database hosted by the JCVI (http://www.jcvi.org). The castor gene model identities were identified using a cutoff score of 1,000. The protein sequences of the castor genes and their Arabidopsis homologs used as queries were then aligned using the ClustalW2 algorithm (Larkin et al., 2007) and visualized as a homology tree with TreeView (http://taxonomy.zoology.gla.ac.uk/rod/treeview.html). Analysis of the tree allowed the identification of castor homologs of the Arabidopsis homologs. The high degree of homology (greater than 60% pairwise identity) was confirmed by aligning the castor protein sequence with that of its homolog using the alignment function in Geneious (www.geneious.com). (Only 12% of selected protein sequences had a pairwise identity of less than 50%) Castor genes were named after their closest Arabidopsis homolog based on percentage identity; if there was more than one homolog, the castor gene name was appended with a letter with decreasing levels of homology. The castor protein sequence was then used in a TBLASTN at the JCVI to obtain the nucleotide sequence. The castor nucleotide sequence was subsequently used to perform a BLASTN at the Michigan State University Castor 454 expression database (approximately 70,000 contigs assembled from approximately 1,060,000 ESTs; http://glbrc.plantbiology.msu.edu/castor). The expression data of the stages were obtained from castor seeds that were harvested from stage III to stage VIII, based on embryo length and testa (seed coat) color, as defined anatomically by Greenwood and Bewley (1982). In the 454 database, the total number of contigs is 69,194, stage III contains 141,964 ESTs, stage IV contains 267,141 ESTs, stage V contains 152,462 ESTs, and stages VII and VIII contain 151,964 ESTs. With only 77,518 and 84,170 ESTs, respectively, stages V and IV were ignored, as were stages III to V with 184,642 ESTs. Data containing the contig number, the number of ESTs per contig, the best Arabidopsis homolog, and the number of ESTs per 100,000 per embryo stage are compiled in Table I. Table I also includes the gene family, the Arabidopsis gene identifier, the Arabidopsis gene name, the name of the castor homolog, the castor gene model accession from the JCVI, and the percentage homology as measured by the percentage of pairwise identical amino acids in the aligned sequences. Additional methodology is available from Troncoso-Ponce et al. (2011).
Plant Growth and Selection of Transgenic Plants

The different Arabidopsis lines used in the experiments are f0, a fatty acid elongase mutant line (AC56) of Arabidopsis ecotype Columbia (Kunst et al., 1992), and CL37, which is derived from f0, expresses RfH2, and accumulates approximately 17% (w/w) HFA (Lu et al., 2006). Plants were grown in growth chambers under continuous fluorescent light (100-200 μmol m−2 s−1) at 22°C. Seeds were sterilized following 5 min of incubation in sterilization solution (0.5% [w/v] NaOCl [bleach], 30% [v/v] ethanol, and 1 g L−1 SDS), followed by five washes with sterile water and 24 h of stratification at 4°C. Seeds were germinated on one-half-strength Murashige and Skoog medium (4.4 g L−1), 1% (w/v) agar plates containing 1% (w/v) Suc and then transplanted to soil. Transgenic seeds expressing the marker DiRed protein were identified by illumination with green light and a hand-held magnifying glass or microscope equipped with a red laser. DNA was isolated from T2 leaf material by PCR using the gene-specific primers. The presence of the transgene in T2 plants was performed by screening DNA obtained from T2 leaf material by PCR using the gene-specific primers. DNA was obtained by using Whatman FTA Classic Cards. Leaf discs crushed onto Whatman FTA cards were incubated in 10 L was used for PCR amplification (30 cycles; melting temperature of 60°C) using the KOD polymerase.

Preparation of Fatty Acid Methyl Esters and Gas Chromatography Analysis

Fatty acid methyl esters (FAMEs) were isolated from 30 whole seeds by derivatizing the seed lipid in 1 mL of 2.5% (v/v) sulfuric acid in methanol for 1 h, 30 min at 80°C. After cooling, 200 μL of hexane and 1.5 mL of water were added and vortexed, spun down at 2,000 g, and 100 μL was transferred to a GC vial. For total seed FA quantification, 10 μL of glycerol triheptadecanoate (3 μg L−1) was added prior to derivatization. FAMEs were quantified by GC with flame ionization detection on a wax column (EC Wax, 30 m × 0.53-mm i.d. × 1.20 μm; Alltech). GC parameters were as follows: 220°C for 2 min, followed by a ramp (10°C min−1) up to 245°C, with a 6-min final temperature hold. The significance of difference between FA content from transgenic seeds and cosegregating seeds was determined by Student’s t test.

Developmental Time Course and Seed Lipid Extraction

Flowers and siliques from lines CL37 and RcsPLA2 CL37 line 3 were counted as they appeared on a daily basis to determine silique age. After 20 d, siliques were harvested according to their age, frozen with liquid N2, and counted as they appeared on a daily basis to determine silique age. After 20 d, flowers and siliques were harvested and frozen with liquid N2, and stored at −80°C. Lipid extraction followed the protocol from the Kansas Lipidomics Center (http://www.k-state.edu/lipid/lipidomics/AT-seed-extraction.html). Triplet samples of 10 siliques were harvested at each time point. Prior to TLC, lipid content was determined by GC analysis using glyceryl triheptadecanoate standard (3 μg L−1). Lipids were separated on Whatman Partisol K6 silica gel 60-Ä 20 × 20-cm glass plates with mobile phase CHCl3/methanol/acidic acid (75/25:1, v/v/v). Plates were dried in a vacuum for 20 min prior to staining with 0.005% (w/v) primulin in acetonitrile/water/acetic acid (80:20:2, v/v/v). Lipid bands were visualized by UV light, and bands corresponding to neutral TAG fraction and PC fraction were scraped into 8-mL vials and used to generate FAMEs for GC analysis as described above.

Heterologous Expression of RcsPLAα and AtsPLAα in Yeast, Yeast Cultivation, and Protein Preparation

The open reading frame of AtsPLAα was amplified with the cDNA in the Gateway pENTR/D-TOPO entry vector as the template using primers GC164 (5’-ACTATGCGGCCCTCCGATATTTTCTC-3’) and GC165 (5’-TAGGTTTCTTGATCACGTTCGCGCC-3’). Similarly, RcsPLAα was amplified using primers GC166 (5’-ACAATGCGACCATATTTTGCAG-3’) and GC167 (5’-CATGTTTCTAGGACCTCTACG-3’). The PCR products were individually subcloned into the yeast (Saccharomyces cerevisiae) expression vector pYES2.1/V5-His-TOPO (Invitrogen). The plasmids were then transformed into wild-type yeast (Inv Sc 1 strain; Invitrogen). A yeast strain transformed with a null pYES2.1/V5-His-TOPO vector was used as a negative control.

Transformed yeast cells were grown at 30°C and 200 rpm in synthetic uracil dropout medium containing 1% (w/v) raffinose and 2% (w/v) Gal for 20 h. Yeast cells were then harvested, washed with 50 mM Tris·HCl, pH 7.6, and suspended in 1 mL of breaking buffer (50 mM Tris·HCl, pH 7.6, 600 mM sorbitol, and 1 mM EDTA) containing protease inhibitor (Complete; Roche). The cells were then broken with a Mini-Beadbeater (BioSpec Products), and the crude homogenates were centrifuged at 12,000 g for 10 min to remove the cell debris. The supernatant was further centrifuged at 100,000 g for 70 min to separate microsomal and cytosolic fractions. The microsomal pellets were washed and resuspended in breaking buffer. Protein concentration was determined using the Bradford method (Bradford, 1976). The protein samples were flash frozen with liquid nitrogen and stored at −80°C until used in the assays (Chen et al., 2012).

Enzyme Assays

For PLA enzyme assays, sn-1-palmitoyl-sn-2-[14C]oleoyl-PC was purchased from American Radiolabeled Chemicals, and sn-1-palmitoyl-sn-2-[14C]linoleoyl-PC was synthesized according to Banas et al. (1992). The PLA enzyme assay was performed at 30°C with agitation at 750 rpm in a 200-μL reaction mixture containing 50 mM Tris·HCl, 10 mM CaCl2, 0.05% (v/v) Triton X-100, 9 mM of substrate, and 100 μg of protein at pH 8 with the incubation times indicated in the figures. The reaction was terminated by the addition of 1 mL of chloroform: methanol (1:1, v/v) and 200 μL of 0.15 M acetic acid and vortexed. After centrifugation, the chloroform phase (lower phase) was dried under nitrogen, dissolved in 40 μL of chloroform, and applied to a TLC plate with standards (0.25-mm Silica gel; DC-Fertigplatten). The plate was developed in the polar solvent chloroform:methanol:water:acetic acid (65:25:4:1, v/v/v/v). The products were visualized by phosphor imaging (Typhoon Trio Variable Mode Imager; GE Healthcare). Spots corresponding to free FA were scraped and analyzed for radioactivity by scintillation counting. For the substrate selectivity experiment, equal amounts of 18:1-PC and Ric-PC (4.5 mmol each) were mixed. The spots corresponding to free FAs were scraped from TLC plates, extracted with chloroform (Bigh and Dyer, 1999), and loaded onto TLC plates. The plates were developed in the neutral solvent hexane:ethyl ester:acetic acid (50:50:1, v/v/v) to separate oleic acid and ricinoleic acid. The corresponding spots were then scraped for scintillation counting. All assays were repeated in triplicate, and the results are represented as means ± SE.

Sequence data from this article can be found in the GenBank/EMBL data libraries under the following accession numbers: At1g06925 (AtsPLAα), At2g19300 (AtsPLAβ), At4g29460 (AtPLAγ), At4g29470 (AtPLAδ), XM_002523613 (RcsPLAα), XM_002514118 (RcsPLAβ), NM_001057569 (OsPLAα), XM_002528081 (RfH2), XM_00251598 (RcLACS7), XM_002509911 (RcLACS4), and XM_00252166 (RcLACS8).

Supplemental Data

The following supplemental materials are available.

Supplemental Figure S1. Enzyme reaction progress curve.

Supplemental Table S1. Expression levels of PLA genes in castor endosperm stages III to VIII (number of ESTs per 107) and expression levels from the Bio-Analytical Resource expression browser (http://www.bar.utoronto.ca) of Arabidopsis Columbia-0 seeds and siliques.

Supplemental Table S2. FA composition of seeds from the CL37 control line and T1 CL37 lines expressing Arabidopsis genes AtsPLAα and AtsPLAβ.

Acknowledgments

We thank all members of the Browse laboratory who contributed to this article and the greenhouse staff for help with growing the plants.

Received November 12, 2014; accepted February 4, 2015; published February 9, 2015.

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