

Table S1. Primers used for quantitative real-time PCR analyses. F—forward; R—reverse.

<i>Gene Name</i>	<i>Primers for qRT-PCR (5'–3')</i>
<i>GmDGK1</i>	F: CTGGCACATTCTTATGCGGATGAG R: CCATCCTTGTGTGCATCCAAGC
<i>GmDGK2</i>	F: CGGGGATCCATGTGTGACAGTTTGG R: GCTCTAGATTATGAAAGATTGATGGCCA
<i>GmDGK3</i>	F: CTTATGCGGATGAGGGCTCC R: CAGTTGGTCAATCAGAGTAC
<i>GmDGK4</i>	F: GAAAATGTCGGTGACGTGCC R: CGGGTTATCAGTTTGCTGA
<i>GmDGK5</i>	F: GATCGTGGAGTCGTTGCC R: CACTCATTAGATGTTGAAGCCTC
<i>GmDGK6</i>	F: CATCAACAACCTGGAGACACGAGC R: GCTTTGTGGTCGTCTTTGCTAC
<i>GmDGK7</i>	F: GGTCTCGTTCGTGGAATCG R: CTCAGCGCGGCTAATGTAGC
<i>GmDGK8</i>	F: GTAAAAGGGGCAAGGGAAATG R: CCCC CGGTAAGTGTGGT
<i>GmDGK9</i>	F: GCTACTGTGCCATTGGGGAC R: CTCAAGGGGTGCAATAGGGT
<i>GmDGK10</i>	F: CCACGGGTGACACGAACAAG R: CTCGGCACGGTTGATGTAGC
<i>GmDGK11</i>	F: TCAAACCCTTGGGCCTATAGTA R: ATCCAACGAACAGTCCATTGGT
<i>GmDGK12</i>	F: CTCTAGGACCTATTGTAGCTCTG R: GGTCAGCTACATCTGTCCAACA

Table S2. The accession numbers of all the DGKs are listed. *Glycine max* (Gm), *Arabidopsis thaliana* (At), *Oryza sativa* (Os), and *Malus domestica* (Md) DGKs.

<i>Gene Name</i>	<i>Gene Locus</i>	<i>GenBank or UniProtKB Accession</i>	<i>Length (aa)</i>	<i>Molecular Mass (kDa)</i>	<i>cDNA/EST</i>
<i>AtDGK1</i>	AT5G07920	NP_196409	728	80.0	BT004148
<i>AtDGK2</i>	AT5G63770	NP_201182	712	79.4	AY380783
<i>AtDGK3</i>	AT2G18730	NP_849980	488	53.9	AY141990
<i>AtDGK4</i>	AT5G57690	NP_200577	487	55.5	DQ447086
<i>AtDGK5a</i>	AT2G20900	AAM62810	491	55.3	AY085589
<i>AtDGK5b</i>	AT2G20900	NP_850007	509	57.4	AC006234
<i>AtDGK6</i>	AT4G28130	NP_194542	466	52.5	AL035524
<i>AtDGK7</i>	AT4G30340	NP_567845	492	54.6	AF360174
<i>GmDGK1</i>	Glyma.13G302200	XP_003541921.1	430	48.62	XM_003541873.1
<i>GmDGK2</i>	Glyma.05G196100	XP_006580353.1	725	78.6	XM_006580290.2
<i>GmDGK3</i>	Glyma.12G200100	XP_014632628	480	53.7	XM_014777142
<i>GmDGK4</i>	Glyma.06G299200	XP_003526295	484	54.29	XM_003526247
<i>GmDGK5</i>	Glyma.06G223900	XP_014632628	480	53.76	XM_014777142
<i>GmDGK6</i>	Glyma.04G143000	XP_003552048	485	54.2	XM_003552000
<i>GmDGK7</i>	Glyma.13G093100	XP_003542286	480	53.54	XM_003542238
<i>GmDGK8</i>	Glyma.06G2549001	XP_014632201	504	56.32	XM_014776715
<i>GmDGK9</i>	Glyma.12G146700	XP_006592585	485	54.35	XM_006592522
<i>GmDGK10</i>	Glyma.17G067400	XP_014625529.3	480	53.56	XM_014770043
<i>GmDGK11</i>	Glyma.17G077100	XP_014625346.1	727	80.97	XM_014769860
<i>GmDGK12</i>	Glyma.05G022500	XP_006579516	727	80.93	XM_006579453
<i>OsDGK1</i>	OS04G54200	EAZ32109	541	60.3	CM000141
<i>OsDGK2</i>	OS08G08110	NP_001061130	502	55.8	AP008214
<i>OsDGK3</i>	OS02G54650	NP_001048345	488	53.9	AP005535
<i>OsDGK4</i>	OS12G38780	NP_001067111	705	78.7	DP000011
<i>OsDGK5</i>	OS03G31180	ABF96709	616	68.1	DP000009
<i>OsDGK6</i>	OS08G15090	BAD05689	527	57.1	AP005495
<i>OsDGK7</i>	OS01G57420	EEE55501	499	55.9	CM000138
<i>OsDGK8</i>	OS12G12260	ABG21922	663	72.8	DP000011

<i>MdDGK1</i>	MDP0000900186	KM099881	707	79.3	CN874967
<i>MdDGK2</i>	MDP0000246501	KM099882	489	54.6	CN890995
<i>MdDGK3</i>	MDP0000276007	EB177954	724	80.2	EB177954
<i>MdDGK4</i>	MDP0000139683	GO512216	502	54.5	GO512216
<i>MdDGK5</i>	MDP0000401076	KM099880	522	58.5	CN892391
<i>MdDGK6</i>	MDP0000237723	GO552958	488	54.5	GO552958
<i>MdDGK7</i>	MDP0000286961	KM099883	737	81.6	EB110199
<i>MdDGK8</i>	MDP0000171640	DR992213	538	60.2	DR992213

Table S3. Subcellular localization data found on **DeepLoc-1.0**; the uncolored cases represent the highest values for each gene in different parts of the cell. From top to bottom, the values in the table are colored differently according to clusters I, II, and III.

Genes	Nucleus	Cytoplasm	Peroxisome	Cell Membrane	Mitochondrion	Lysosome	Golgi Apparatus	Endoplasmic Reticulum	Extra Cellular	Platid
<i>GmDGK2</i>	0.0002	0	0.0001	0.7858	0.0008	0.0152	0.0935	0.1044	0	0
<i>GmDGK11</i>	0.0046	0.0004	0.0112	0.4733	0.0278	0.0728	0.1536	0.2536	0.001	0.0017
<i>GmDGK12</i>	0.0013	0.0003	0.0013	0.6059	0.0041	0.0395	0.1734	0.1736	0.0001	0.0006
<i>AtDGK1</i>	0.0003	0	0.0002	0.8015	0.0004	0.0044	0.1111	0.0821	0.0001	0
<i>AtDGK2</i>	0.0001	0	0	0.7834	0.0001	0.0007	0.1733	0.0422	0	0
<i>GmDGK5</i>	0.0781	0.5242	0.1985	0.0734	0.0589	0.0187	0.0095	0.0266	0.0055	0.0066
<i>GmDGK6</i>	0.2288	0.6091	0.0339	0.0066	0.0414	0.0133	0.0105	0.0124	0.0088	0.0351
<i>GmDGK7</i>	0.2419	0.4886	0.034	0.0586	0.092	0.0273	0.0196	0.0254	0.0053	0.0072
<i>GmDGK10</i>	0.463	0.3372	0.0123	0.0482	0.0688	0.0125	0.0087	0.0046	0.0067	0.0379
<i>AtDGK3</i>	0.4414	0.2774	0.1085	0.0666	0.0377	0.0174	0.0164	0.0151	0.0105	0.009
<i>AtDGK4</i>	0.3848	0.3591	0.0154	0.1309	0.008	0.043	0.0172	0.0117	0.0279	0.0021
<i>AtDGK7</i>	0.5091	0.3567	0.0071	0.0567	0.0048	0.0175	0.0139	0.0112	0.0222	0.0001
<i>GmDGK1</i>	0.227	0.4039	0.1129	0.0527	0.1044	0.0145	0.0408	0.0241	0.0071	0.0126
<i>GmDGK3</i>	0.2122	0.3607	0.2087	0.0677	0.0782	0.0097	0.0187	0.0174	0.0091	0.0187
<i>GmDGK4</i>	0.212	0.49	0.112	0.0663	0.0553	0.0173	0.014	0.0114	0.0109	0.0108
<i>GmDGK8</i>	0.2563	0.5964	0.0152	0.0569	0.021	0.0169	0.0117	0.0089	0.013	0.0036
<i>GmDGK9</i>	0.2012	0.5483	0.0758	0.0989	0.0142	0.0202	0.0154	0.0096	0.0141	0.0022
<i>AtDGK5</i>	0.1692	0.6145	0.0836	0.0434	0.0313	0.0186	0.0154	0.0112	0.0087	0.004
<i>AtDGK6</i>	0.287	0.6074	0.0077	0.0558	0.0059	0.0143	0.0076	0.0043	0.0081	0.00019

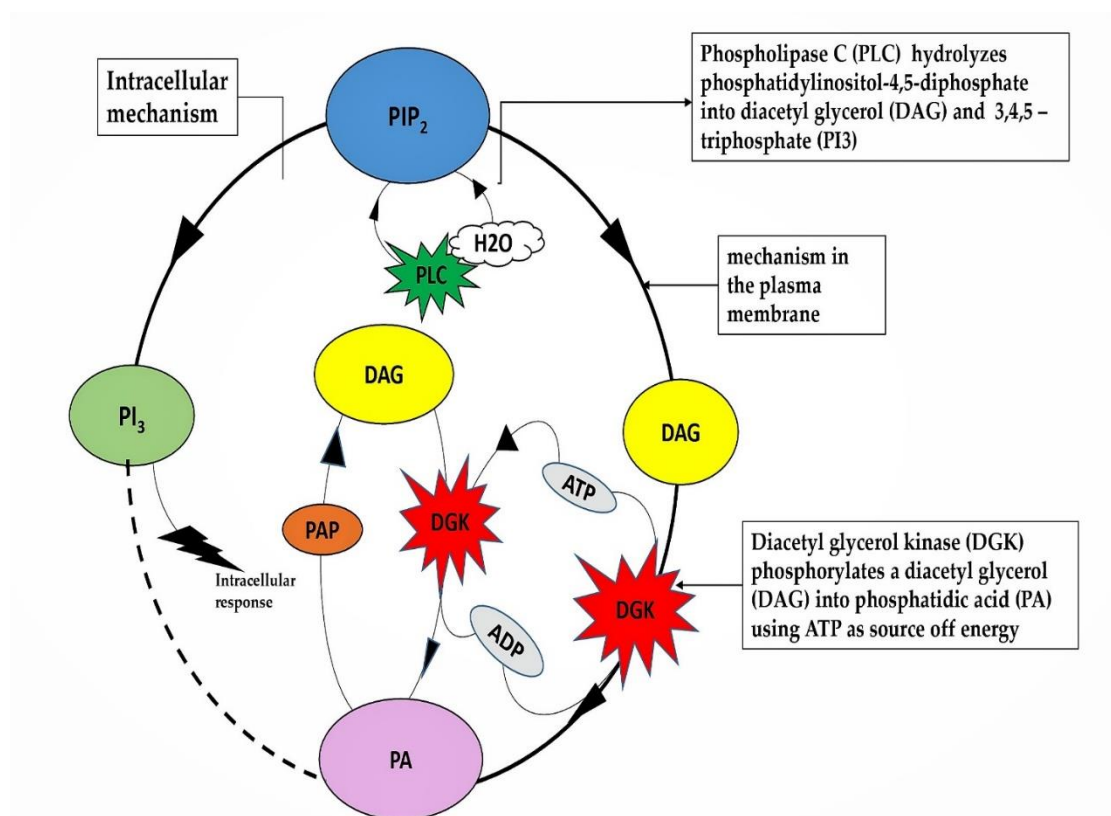


Figure S1. The general function of DGKs in eukaryotic cells, i.e., phosphate acid (PA) production via the coupled action of phospholipase C and diacylglycerol kinase.