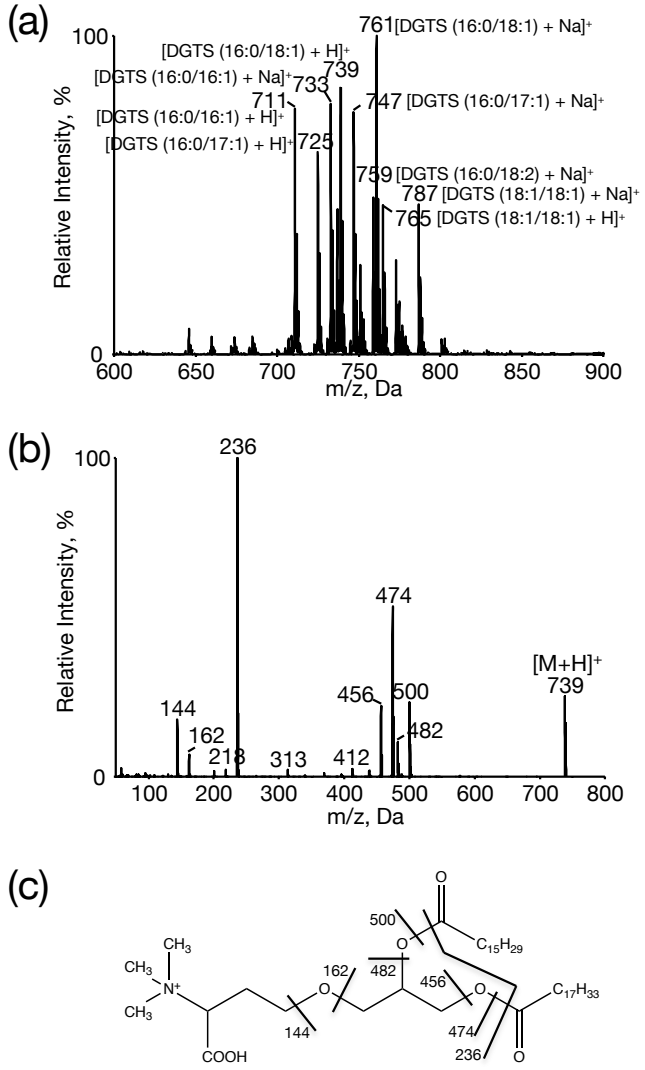
Supplementary Table 1 Primer set

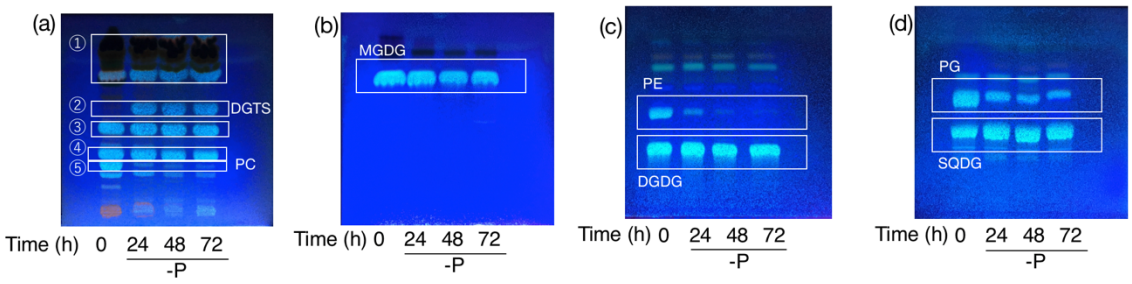
set	gene	Forward	Reverse	Query
1	*5′ race cDNA*	ctaatacgactcactatagggcaagcagtggtatcaacgcagag	gattacgccaagcttcagtcactgggtcctcccacgact	
2	*3′ race cDNA*	gattacgccaagctttcttcccgcccaccttcctgtac	ctaatacgactcactatagggcaagcagtggtatcaacgcagag	
3	*CkBTA1*	gcgcagactaattcgatgggacgcggtggagat	tgttgttgttgttcgtcagtgggccttcttgcc	
4	*BTA1*	atgtgattgcatccccatc	ccaatgtcgatgttgtctgtg	Cre.07.g324200.t1.2
5	*PLCC1*	gctctcatggtagccgactc	tttagctccttcgaccctga	Cre03.g203600.t1.2
6	*PLCC2*	catcttccctgaccacac	ccgttgaatgcctggttg	Cre16.g683850.t1.3
7	*PLP*	cacccctaccatgagtgcag	gccagcacaacgtcttgc	AT1G17710
8	*ACT*	agaaggacacttacattggc	cagagtcaagcacaataccg	AB046457.1

Supplementary Table 2 BtaA, BtaB, and BTA1 homologs

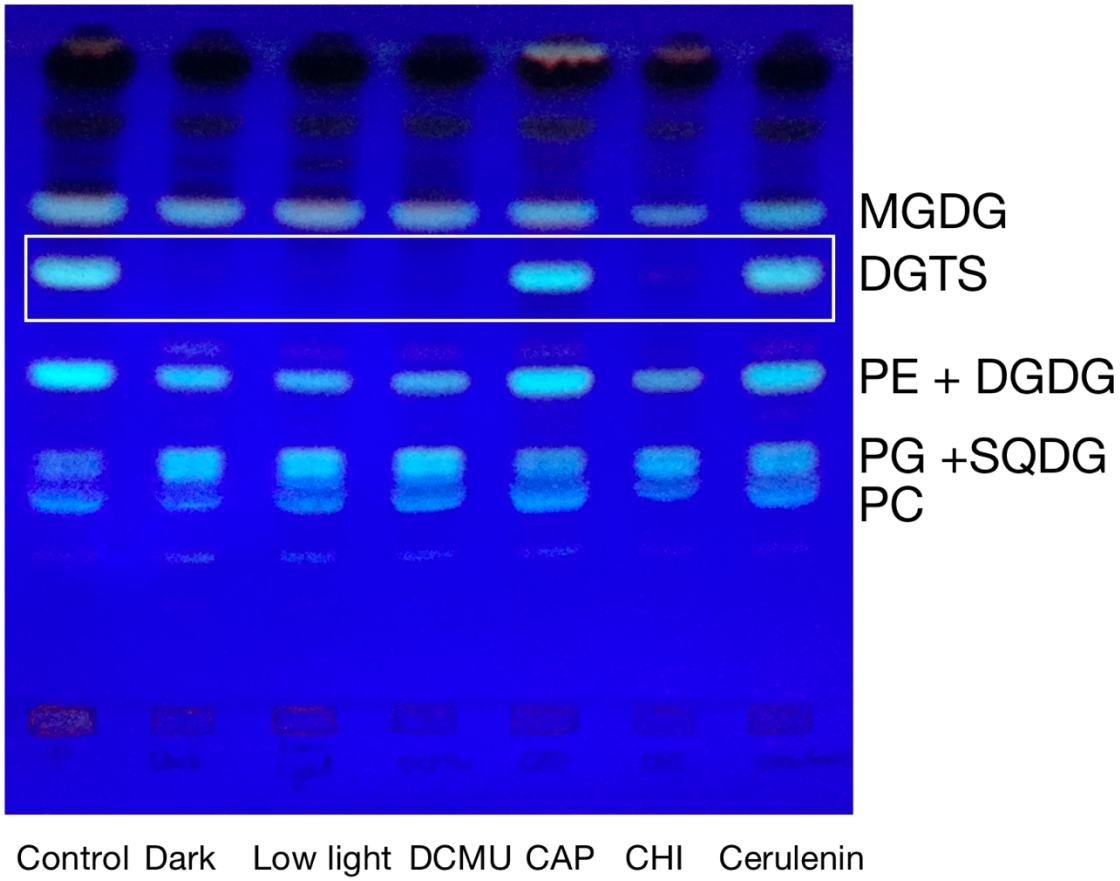
	Organisms	gene ID
BtaA	**Bacteria**	
	Rhodobacter sphaeroides ATCC 17029	*Rsph17029_2516*
	Rhodobacter sphaeroides ATCC 17025	*Rsph17025_3616*
	Rhizobium sp S41	BA939_05055
	Rhizobium leguminosarum bv. trifolii WSM2304	Rleg2_2613
	Rhizobium jaguaris	CCGE525_12990
	Rhizobium tropici	RTCIAT899_CH11455
	Rhizobium etli bv. mimosae Mim1	REMIM1_CH02915
	Sinorhizobium meliloti 2011	NP_386300
BtaB	**Bacteria**	
	Rhodobacter sphaeroides ATCC 17029	Rsph17029_2515
	Rhodobacter sphaeroides ATCC 17025	Rsph17025_3617
	Rhizobium-sp NT-26	NT26_2169
	Rhizobium leguminosarum bv. trifolii WSM2304	*Rleg2_2614*
	Rhizobium jaguaris	CCGE525_12995
	Rhizobium etli by phaseoli	IE4803_CH03093
BTA1	**Green algae**	
	Chlamydomonas reinhardtii	CHLREDRAFT_77062
	Coccomyxa subellipsoidea	COCSUDRAFT_28345
	Auxenochlorella protothecoides	F751_5248
	Volvox carteri f. nagariensis	VOLCADRAFT_83033
	Ostreococcus lucimarinus	OSTLU_27669
	Ostreococcus tauri	OT_ostta15g02860
	Micromonas pusilla	MICPUCDRAFT_48920
	Bathycoccus prasinos	Bathy08g00260
	Monoraphidium neglectum	MNEG_12083
	Fern	
	Selaginella moellendorffii	SELMODRAFT_429378
	Moss	
	Physcomitrella patens subsp. Patens	112274025
	Secondary endosymbiotic algae	
	Emiliania huxleyi	EMIHUDRAFT_105120
	Nannochloropsis oceanica	LC375792
	Fungi	
	Metarhizium robertsii	MAA_07461
	Purpureocillium lilacinum	VFPFJ_09846
	Colletotrichum fioriniae	CFIO01_08357
	Nectria haematococc a	NECHADRAFT_31251
	Fusarium graminearum	FGSG_00742
	Flammulina velutipes	KM668875
	Neurospora crassa	NCU03032



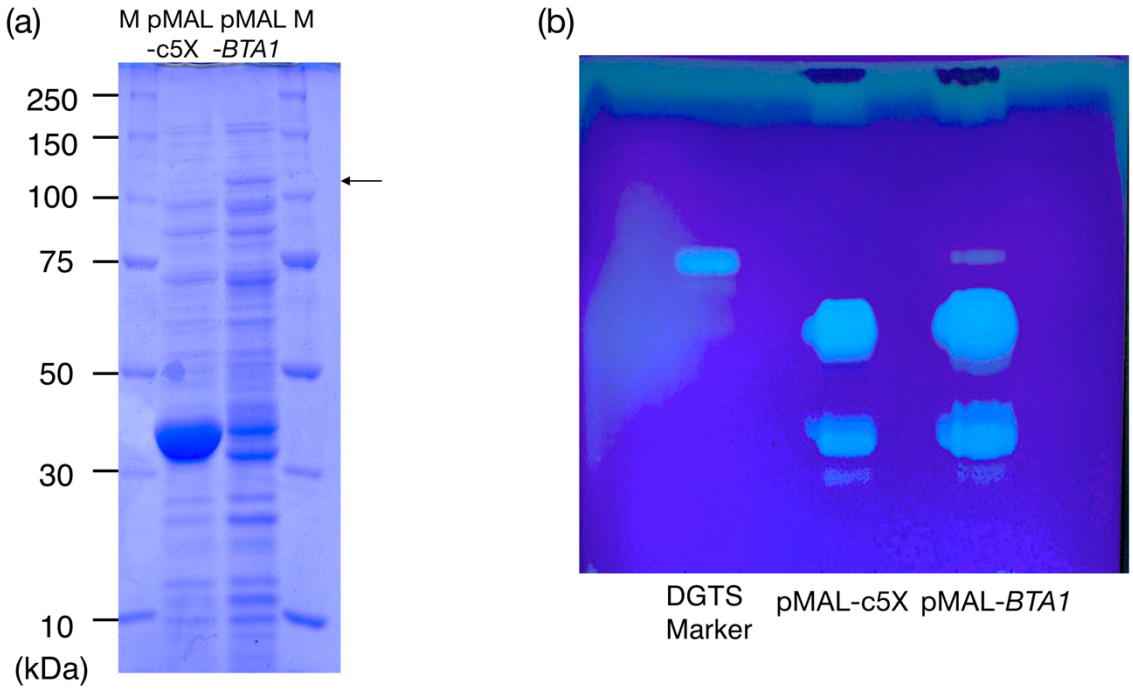
Supplementary Figure 1 Mass spectrometric identification of DGTS. (a) ESI mass spectra of DGTS expressed in *E. coli*. (b) Product ion spectrum of m/z 739 at (a). (c) Estimated fragmentation pattern for DGTS (16:0/18:1) from the product ion spectrum, in which the *sn* position of fatty acids is provisional.



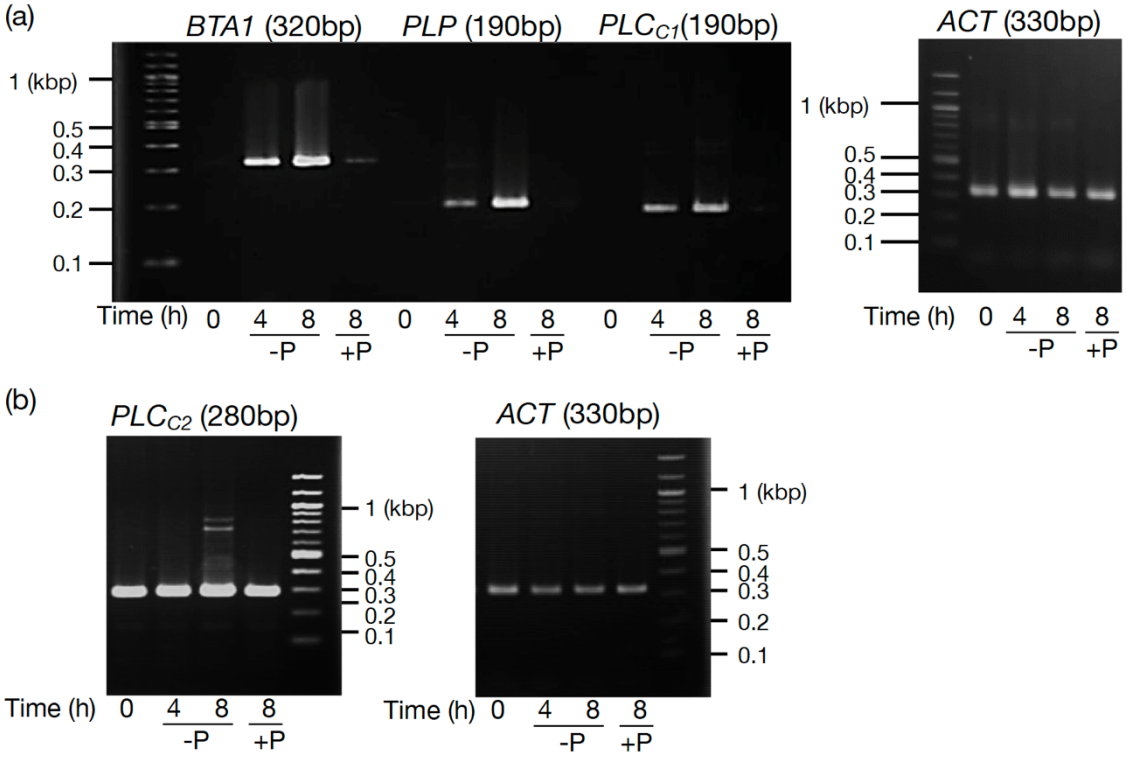
Supplementary Figure 2 Effects of -P on respective lipid contents in *C. kessleri*. Total lipids were extracted from cells before the shift to -P conditions (0 h) or at indicated times after the shift (24-72 h). (a) Total lipids were then separated into DGTS (Band 2) and PC (Bands 5) and also into mixed lipid classes (Bands 1, 3, and 4) through TLC with the solvent system of $CH_3Cl/CH_3OH/H_2O$ (65:25:4, by vol.). Mixed lipids extracted from silica gels of Bands 1, 3, and 4 were respectively subjected to TLC analysis with the solvent system of CH_3Cl/CH_3OH/conc. NH_3 solution (65:35:5, by vol.). Bands 1, 3, and 4 included MGDG (b), PE and DGDG (c), and PG and SQDG (d), respectively.



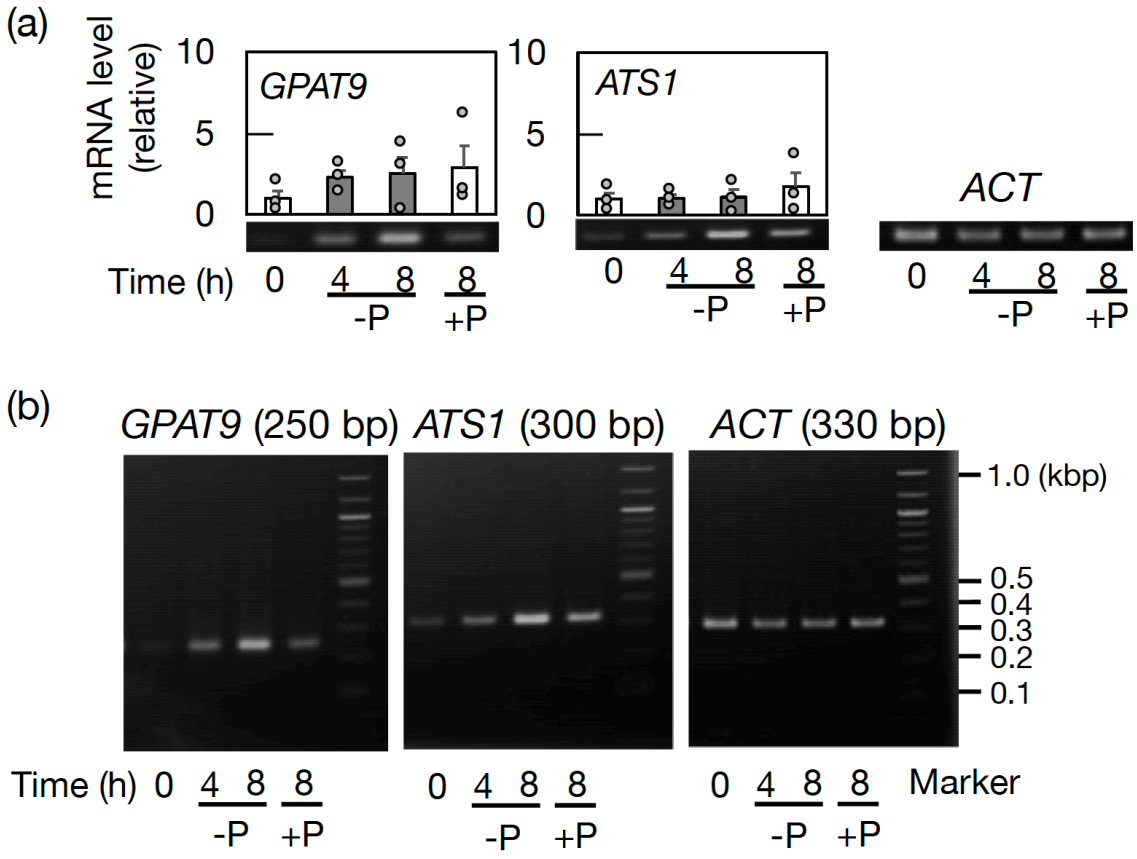
Supplementary Figure 3 TLC profile of polar lipids in *C. kessleri* cells at 24 h after the shift to -P conditions. The cells were cultured under normal conditions (Control), in the dark or low light conditions, or with application of DCMU, chroramphenicol (CAP), cycloheximide (CHI) or celurenin.



Supplementary Figure 4 Characterization of the *BTA1* homolog of *C. kessleri* in *E. coli*. (a) SDS-PAGE of total cellular proteins in *E. coli* cells having a pMAL-c5X empty vector or pMAL-*BTA1* vector. The former cells overexpressed maltose-binding protein (ca. 40 kDa) whereas the latter ones overexpressed the BTA1 homolog fused with the maltose-binding protein (see arrow). M indicates size markers. (b) TLC profile of polar lipids in transformed *E. coli* cells.



Supplementary Figure 5　Effects of -P on the expression of *BTA1*, *PLP*, and *PLC$_{C1}$* genes (a), and that of *PLC$_{C2}$* gene (b) in *C. kessleri*. Shown are images of agarose gel electrophoresis of DNA bands that correspond to mRNAs of the individual genes. The intensities of the DNA bands were used for determination of the values, relative to that of *ACT*, to obtain data of Figure 9.



Supplementary Figure 6　Effects of -P on the expression of *GPAT* and *ATS1* genes in *C. kessleri*. (a) The intensities of the DNA bands that correspond to mRNAs of the individual genes were used for determination of the values, relative to that of *ACT*. The values are expressed as averages ± SEM for three biological replicates. (b) Images of agarose gel electrophoresis of DNA bands to obtain data for (a).