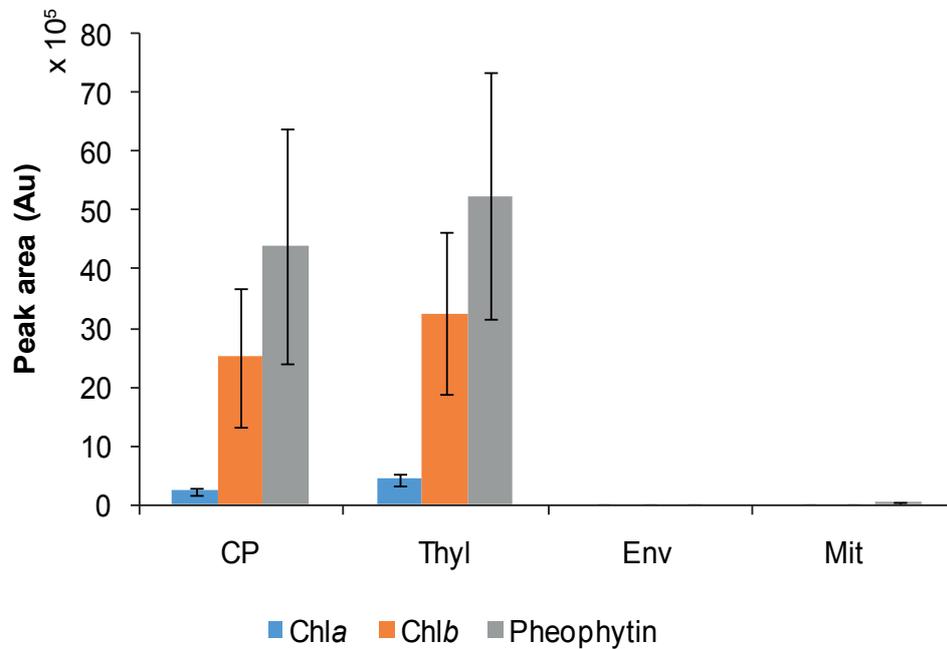


B

*** Summary of Monte Carlo test ***	
Test of significance of first canonical axis: eigenvalue = 0.628	
F-ratio = 10.113	
P-value = 0.0090	
Test of significance of all canonical axes : Trace = 0.778	
F-ratio = 10.497	
P-value = 0.0010	
(999 permutations under reduced model)	

Supplemental Figure 1. Correspondence analysis of obtained lipidomic records from different *E. gracilis* strains.

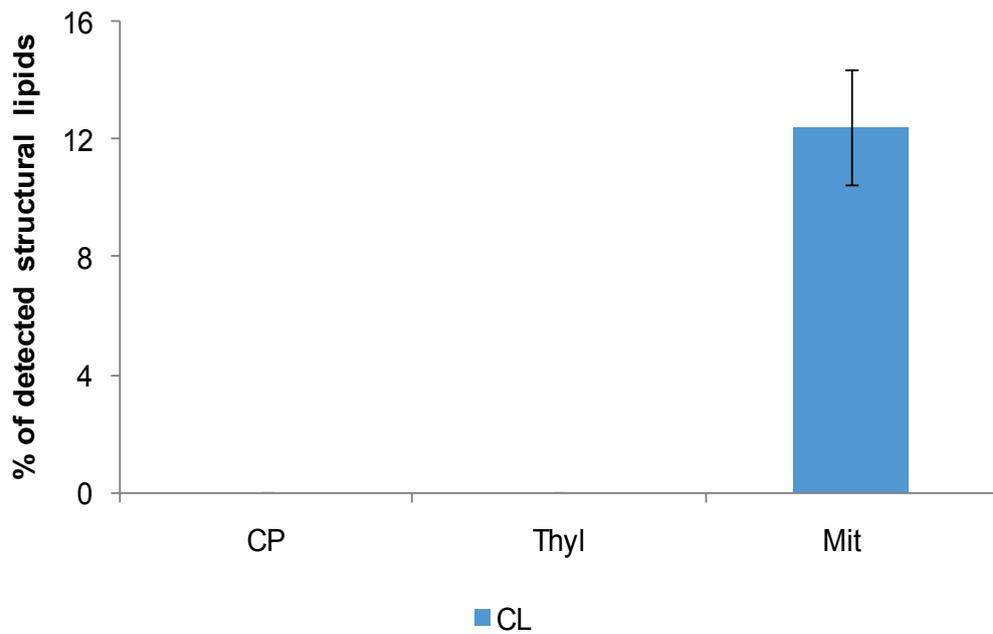
(A) A correspondence analysis, a PCA variant dealing with unimodal data of obtained lipidomic records (HPLC HR-MS/MS) from different *E. gracilis* strains. The PCA variant dealing with unimodal data, ordination biplot (1st and 2nd ordination axes) showing the similarity among the studied *E. gracilis* strains based on obtained lipidomic record (HPLC HR-MS/MS). The CCA and Monte-Carlo permutation test (unrestricted permutations, n=999) shows significant differences among obtained datasets p=0.001. Distribution of the data explains variability in the dataset by 84.7% in x-axis and 0.9% y-axis—that means that the differences among the samples are much more substantial in horizontal distances than in vertical distances. The particular samples are represented by colored spots (EgZ - green, W10 - grey, OFL - blue). The distances among the particular spots express the similarity—a smaller distance means more similar. When the spots are overlapping, the lipid profile is very similar or the same. Furthermore, the ordination biplot follows the lifestyles of *E. gracilis* strains. Two bleached strains are closer to each other than to photosynthetic EgZ strain. This means that the lipid profiles of bleached strains are more similar, while the lipid profile of EgZ strain is more divergent. (B) The CCA and Monte-Carlo permutation test (unrestricted permutations, n=999) revealed significant differences among obtained datasets p=0.001.



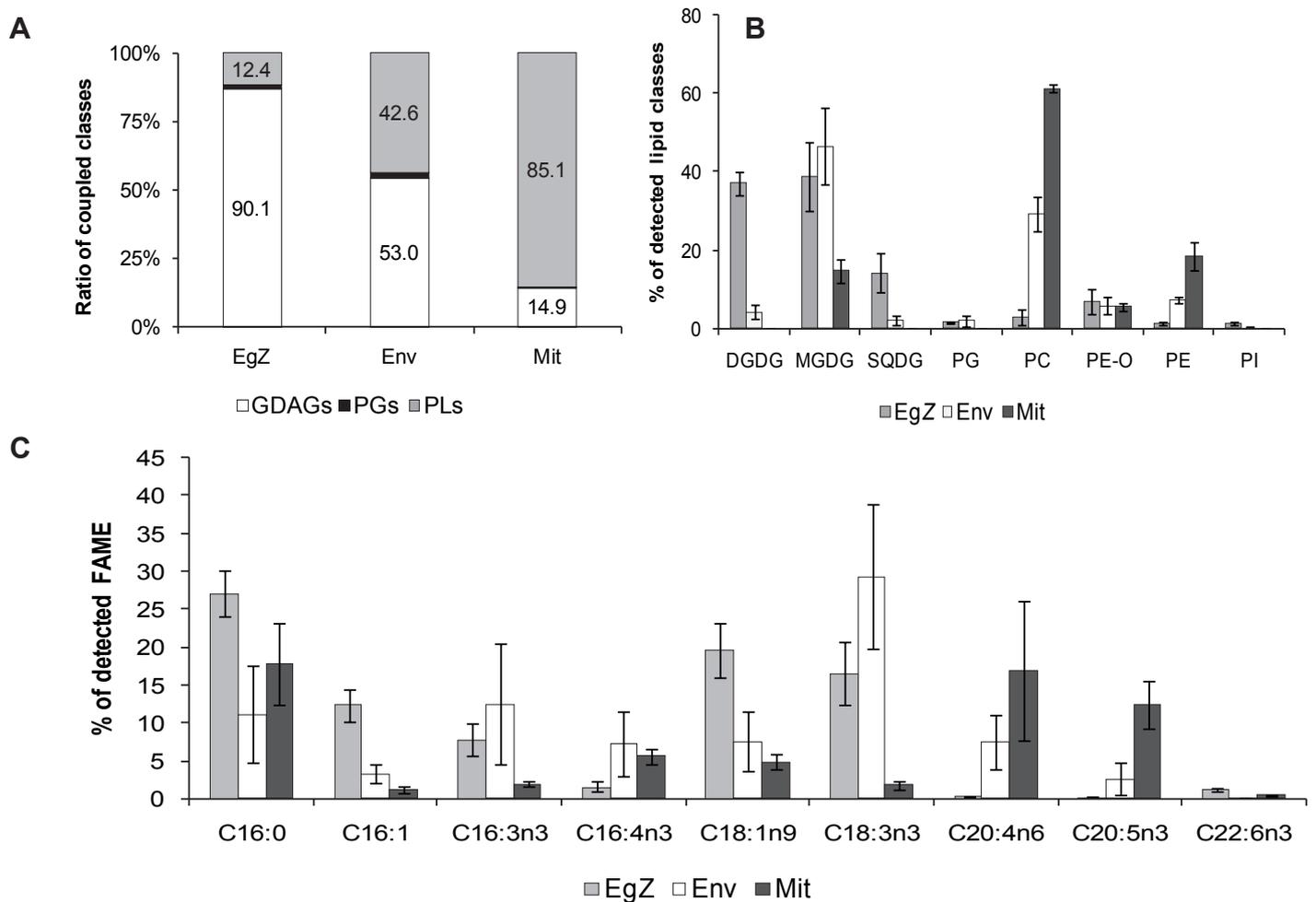
Supplemental Figure S2. Comparison of abundances of chlorophyll *a* and *b* and pheophytin, the chlorophyll precursor and also degradation product in *E. gracilis* strain Z cellular (sub)fractions.

Data were obtained by HPLC HR-MS/MS methodology same way as the structural lipids were assessed. Cells and their fractions were measured in triplicates and the standard deviations are expressed as error bars.

Chla – chlorophyll *a*, Chlb – chlorophyll *b*, CP- *E. gracilis* plastids, Thyl – thylakoids, Env – plastid envelopes, Mit – mitochondria



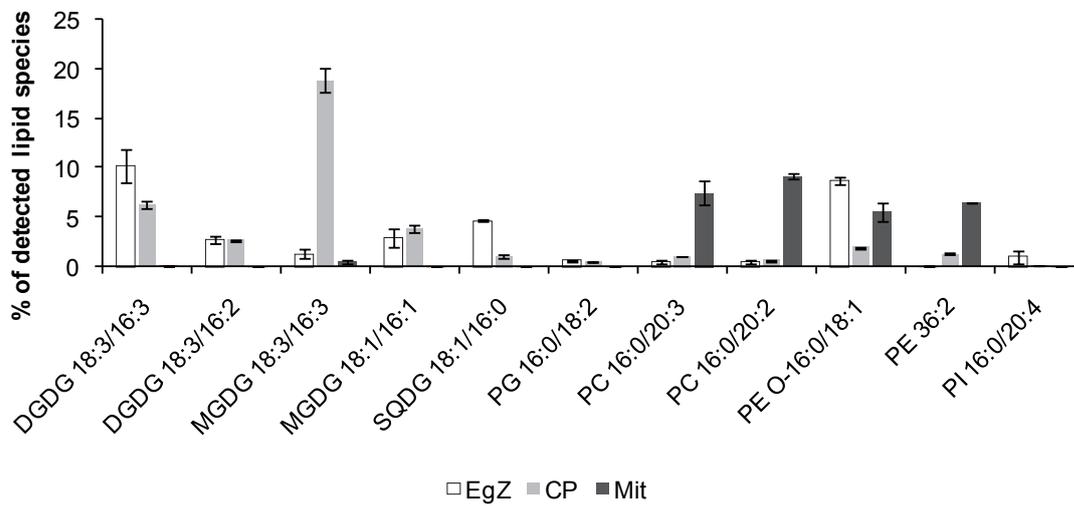
Supplemental Figure S3. Comparison of abundances of cardiolipin in *E. gracilis* plastid (CP), thylakoid (Thyl) and mitochondrial (Mit) fractions. Data were obtained by TLC methodology. Cell fractions were measured in triplicates and the standard deviations are expressed as error bars. CL - cardiolipin, CP - plastids, Thyl – thylakoids, Mit – mitochondria



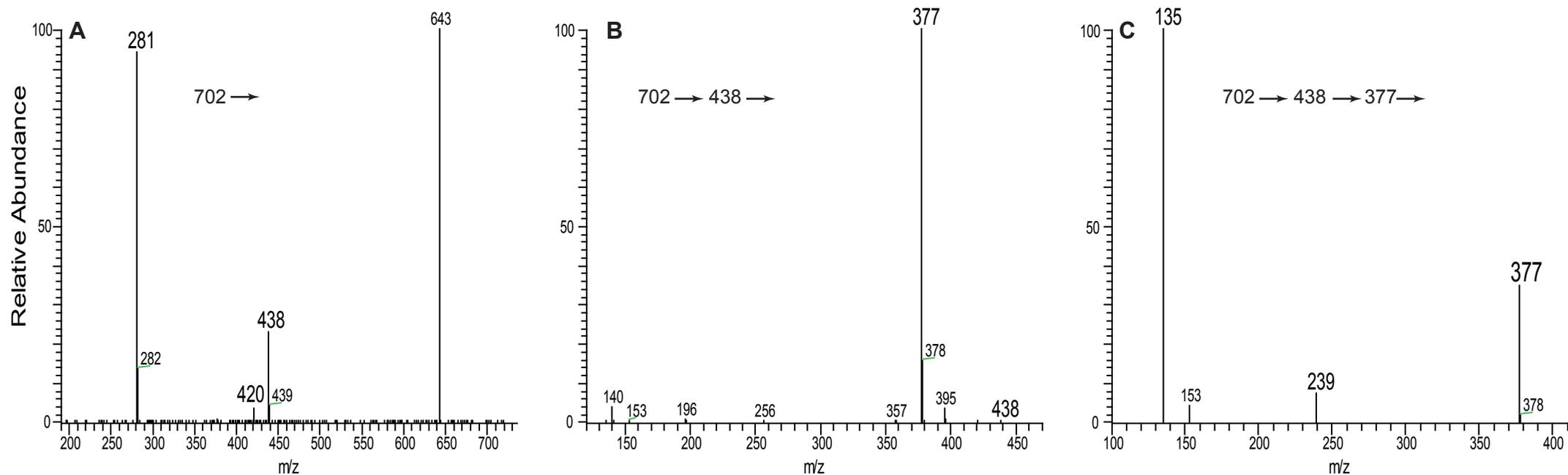
Supplemental Figure S4. Lipid and fatty acid composition of *E. gracilis* strain Z (EgZ), plastid envelopes (Env) and mitochondria (Mit).

Cells and their fractions were measured in triplicates and the standard deviations are expressed as error bars. (A) Ratio of coupled lipid classes detected by HPLC HR-MS/MS analysis. Data were obtained by coupled peak areas of intact lipid species. GDAGs cover DGDGs, MGDGs, and SQDG; PLs cover PCs, PE-Os, PEs, and PIs. (B) Ratio of lipid classes detected by HPLC HR-MS/MS analysis. Data were obtained by coupled peak areas of intact lipid species. (C) A graph of chosen methyl esters of fatty acids detected by GC-FID analyses. Depicted fatty acids represent approximately 80% of all detected FAMEs in whole cell and envelope fraction, and 60% in mitochondrial fraction.

GDAGs – glycosyldiacylglycerols, PLs – phosphoglycerolipids, DGDG – digalactosyldiacylglycerol, MGDG – monogalactosyldiacylglycerol, SQDG – sulfoquinovosyldiacylglycerol, PG – phosphatidylglycerol, PC – phosphatidylcholine, PE-O- plasmanyl phosphatidylethanolamine, PE – phosphatidylethanolamine, PI – phosphatidylinositol.



Supplemental Figure S5. A graph of representative intact lipid species in *E. gracilis* cells (EgZ), plastids (CP) and mitochondria (Mit). The data were obtained by HPLC HR-MS/MS. Cells and their fractions were measured in triplicates and the standard deviations are expressed as error bars. Depicted lipid species represent approximately 33%, 39%, and 30% of all detected lipids in EgZ, CP, and Mit respectively. DGDG – digalactosyldiacylglycerol, MGDG – monogalactosyldiacylglycerol, SQDG – sulfoquinovosyldiacylglycerol, PG – phosphatidylglycerol, PC – phosphatidylcholine, PE-O - plasmalogen phosphatidylethanolamine, PE – phosphatidylethanolamine, PI – phosphatidylinositol.



Supplemental Figure S6. Fragmentation pattern of compound $m/z = 702$ obtained from lipidic extract of *E. gracilis* - MS², MS³ and MS⁴ experiments. The spectral peaks labelled by larger font correspond to analytical parental and daughter ions. The parental ion for a particular MS experiment is depicted as a number before the last arrow. The direction of the arrows symbolizes the fragmentation pattern. (A) MS² spectrum of [M-H]⁻ ion at m/z 702 contains a dominating 18:1-carboxylate anion at m/z 281. The ions 438 and 420 correspond to losses of the 18:1-fatty acid substituent at the sn-2 position as a keten and as an acid respectively. (B) MS³ spectrum of ion at m/z 438 derived from [M-H]⁻ ion at m/z 702 (702→438); the most intense is anion at m/z 377 arising from loss of the ethanolamine residue. The spectrum also shows phosphoethanolamine anion at m/z 140 together with the ion at m/z 196, arising from loss of 1-O-hexadecenyl residue as an alcohol. (C) MS⁴ spectrum of ion at m/z 377 is dominated by the ion at m/z 135 arising from further loss of 1-O-alkyl ether as an alcohol. The identity of particular ions and their ratio are described according Hsu and Truk (2007).