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Phosphatidylglycerol is important in the assembly and function of PSII reaction center

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Phosphatidylglycerol (PG) is a ubiquitous anionic phospholipid in almost all organisms. The structural and functional roles of anionic lipids in photosynthesis have raised scientific interest for a long time. The role of PG in photosynthetic organisms has previously been studied using either biochemical or molecular genetic approaches. The recent identification of genes encoding enzymes required for the biosynthesis of PG in cyanobacteria and eukaryotic plants, and the subsequent generation of mutants defective in the biosynthesis of PG, has provided powerful molecular tools to understand the function of PG in photosynthetic organisms. The role of PG has been extensively studied in two PG-less mutant strain of *Synechocystis sp.* PCC6803: Δ*pgsA* (Hagio 2000) and Δ*cdsA* (Sato 2000). Previously it was demonstrated that PG is required for the formation and function of thylakoid membranes in cyanobacteria and plants (Wada and Murata 2007; Domonkos 2008).

In the present investigation we constructed and characterized a new PG deficient mutant of *Synechocystis sp.* PCC6803. We inactivated the *cdsA* gene in phycobiliproteinless mutant, PAL, which compensates the missing light harvesting complex by high cellular content of PSII (Ajlani 1998). The PAL/Δ*cdsA* mutant provided a unique experimental system for a more detailed study of the role of PG in PSII function/assembly. We analyzed the influence of PG depletion on the fluorescence induction, thermoluminescence, biosynthesis and assembly of PSII protein subunits. The mutant cells grew only in a medium supplemented with PG. Depletion of PG in the cells resulted (i) in an inhibition of cell growth/division, (ii) in a small change in pigment composition, (iii) in the inactivation of oxygen evolution, (iv) in a modification of the fluorescence induction curve that pointed to some damage of Q_B, but not the donor side, (v) in a modification of the TL glow curve to give only shifted Q-band which is an indicator for suppression of electron transfer between Q_A and Q_B, and it does not affect the redox levels of Q_A and S_2. Two-dimensional PAGE showed that in the absence of PG (a) PSII dimer was monomerised, and (b) the CP43 protein was detached from a major part of the PSII core complex. [35S]-methionine labeling confirmed that PG depletion did not block de novo synthesis of PSII proteins. We conclude that PG is required for the binding of CP43 within the PSII core complex (Laczko-Dobos 2008). This is in good agreement with the presence of a PG molecule localized between D1 and CP43 subunits by X-ray crystallographic structure of *Thermosynecococcus elongatus* (Guskov 2009).

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Characterization of catalase genes in *Rhizopus oryzae*

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Zygomycosis is a diverse group of mycotic diseases caused by members of the class Zygomycetes. The main risk factors are diabetic ketoacidosis; cancer and its therapy; solid organ or bone marrow transplantations; prolonged steroid use; neutropaenia; deferoxamine treatment to manage iron overload and burn injuries (Papp et al. 2008). Thermophilic members of the genus *Rhizopus*, especially *R. oryzae*, are considered as the main causative agents of zygomycoses. During the past decades, such infections have emerged in an increasing number due to the widespread use of immunosuppressive therapy, intensive cancer chemotherapeutic regimens and broad-spectrum antimicrobial agents. High mortality rates, difficulties in the diagnosis and resistance to the most widely used antifungal drugs are characteristic features of zygomycoses underlying the importance of this fungal group (Ribes et al. 2000). All these aspects indicate that development of new strategies to prevent and treat these infections is urgently needed.

The aim of our study is identification and analysis of the genetic background of the virulence of opportunistic pathogen Zygomycetes.