#### S13-3

# Physiological significance of chlorophyll biosynthesis under micro-oxic conditions for diazotrophic growth of the non-heterocystous cyanobacterium *Leptolyngbya boryana*

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## ヘテロシストを形成しない窒素固定ラン藻 Leptolyngbya boryana の窒素固定的生育には低酸素環境 下でのクロロフィル生合成が必要である

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#### Key word : cyanobacteria, nitrogen fixation, chlorophyll biosynthesis, transcriptional regulator, ChIR

Leptolyngbya boryana is a non-heterocystous cyanobacterium that is able to grow by nitrogen fixation under micro-oxic conditions. Recently we found a 50-kb gene cluster containing 13 nif genes and nif-related genes encoding a cytochrome oxidase, transcriptional regulators, a Mo-transporter and some enzymes for anaerobic metabolism. To reveal physiological role of one of the transcriptional regulators, we isolated a mutant in which the gene, ORF136, encoding a MarR-type transcriptional regulator is inactivated. The mutant  $\Delta$  ORF136 lost diazotrophic growth ability. Even in the presence of nitrate,  $\Delta$  ORF136 did not grow under micro-oxic conditions accompanied with a remarkable decrease in chlorophyll content. This phenotype is quite similar to that of the *chlR*-lacking mutant of the model cyanobacterium Synechocystis sp. PCC 6803. In Synechocystis 6803, ChlR plays a role as a transcriptional activator of the *chlA*<sub>u</sub>-ho2-hemN operon in response to hypoxia to compensate or bypass oxygen-dependent steps in chlorophyll biosynthesis. In  $\Delta$  ORF136 in the *nif* gene s of L boryana were not induced under micro-oxic conditions. Thus, we concluded that ORF136 in the *nif* gene cluster is the *chlR* ortholog in L. boryana. The results imply efficient chlorophyll biosynthesis under micro-oxic conditions is required for nitrogen-fixing growth in L. boryana.

#### **S13-4**

#### The supramolecular organization of photosystem II in Chlamydomonas reinhardtii

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### 緑藻クラミドモナスにおける光化学系Ⅱの超分子構造

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Photosystem II (PSII) is a multiprotein complex that splits water and initiates electron transfer in photosynthesis. The central part of PSII, the PSII core, is surrounded by light-harvesting complex II proteins (LHCIIs). In higher plants, two or three LHCII trimers are seen on each side of the PSII core whereas only one is seen in the corresponding positions in *Chlamydomonas reinhardtii*, probably due to the absence of CP24, a minor monomeric LHCII. Here, we re-examined the supramolecular organization of the *C. reinhardtii* PSII-LHCII supercomplex by determining the effect of different solubilizing detergents. When we solubilized the thylakoid membranes with *n*-dodecyl- $\beta$ -d-maltoside ( $\beta$ -DM) or n-dodecyl- $\alpha$ -d-maltoside ( $\alpha$ -DM) and subjected them to gel-filtration, we observed a clear difference in molecular mass. The  $\alpha$ -DM-solubilized PSII-LHCII supercomplex bound twice more LHCII than the  $\beta$ -DM-solubilized supercomplex and retained higher oxygen-evolving activity. Single-particle image analysis from electron micrographs of the  $\alpha$ -DM-solubilized and negatively stained supercomplex revealed that the PSII-LHCII supercomplex had a novel supramolecular organization, with three LHCII trimers attached to each side of the core.