



中央研究院生物多樣性研究中心

Biodiversity Research Center, Academia Sinica

biodiv@gate.sinica.edu.tw

02-2789-9621

Microbial Diversity and Bioinformatics

Symbiotic Interactions with Bacteria and Plants: Their Biogeochemical Functions and Evolutionary Processes



Prof. Kiwamu Minamisawa

**Graduate School of Life Sciences
Tohoku University**

Time: 2019. 11. 07 Thu. 15:30

Venue: Auditorium A134,

Agricultural Technology Building

農業科技大樓1樓A134演講廳

Host: Dr. Sen-Lin Tang 湯森林研究員

Dr. Chih-Horng Kuo 郭志鴻副研究員



Abstract

Biogeochemical processes and microbial functions in rice paddies have been the focus of a large number of studies. Methane-nitrogen cycle interaction is a key unresolved issue in research on rice paddies. A rice symbiotic gene likely accommodates diazotrophic methanotrophs under low-N fertilizer management, which may permit rice plants to acquire N via N_2 fixation. CH_4 oxidation by methanotrophs is a driving force in shaping bacterial communities in rice roots grown in CH_4 -rich environments (Minamisawa *et al.* 2016, Shinoda *et al.* 2019).

Soybean rhizosphere provides active transformation of nitrogen including nitrous oxide (N_2O), a greenhouse gas. N_2O -producing processes occur via bacterial nitrification and fungal denitrification. N_2O is further reduced to N_2 by N_2O reductase (N_2OR), encoded by a *nosZ* gene in *Bradyrhizobium diazoefficiens*. N_2O emission from soybean ecosystems can be mitigated by the inoculation of *nosZ*⁺⁺ strains of *B. diazoefficiens* at field scale (Itakura *et al.* 2013). Comparative genomics showed that mutation of *nasS* gene of the two-component NasST regulatory system resulted in *Nos*⁺⁺ phenotype. We revealed how NasST regulatory system enhances N_2OR activity (Sanchez *et al.* 2014, 2017). The knowledge would improve our understanding of N-cycle biology and mitigation options of global N_2O emission from soils.

Rj2-soybeans and *B. diazoefficiens* USDA122 express symbiotic incompatibility by NopP protein (Sugawara *et al.* 2019) via Type III secretion system (T3SS) (Tsukui *et al.* 2013). Large deletions were found including *nif* and *rhc* genes on symbiosis island between identical insertion sequences (ISs). I will discuss the drastic lifestyles of soybean bradyrhizobia.