

Dr. Mitsuhiro Matsuo  
(Department of Applied Biological Science)

**E-mail** mitsuhiro.matsuo@setsunan.ac.jp

**Keywords** Bioinformatics, Endosymbiosis, Evolution, Giant virus  
Genome editing, Environmental genomics

## Research topics

### Purpose

- Elucidation of the the evolutionary dynamics of photosynthetic organisms genomes.
- Creating market value crops with genome editing technology
- Assessment of the agricultural environment with genomics approach

### Main achievements

- Elucidation of the genome of a photosynthetic amoeba, which is a key organism to unveil the evolutionary process for the birth of eukaryote.
- Presenting new hypothesis for the role of large DNA virus on the plant endosymbiotic evolution.
- Elucidation of the role of a transcription factor RRTF1 on the oxidative stress response in plant.

## Prospects for collaboration

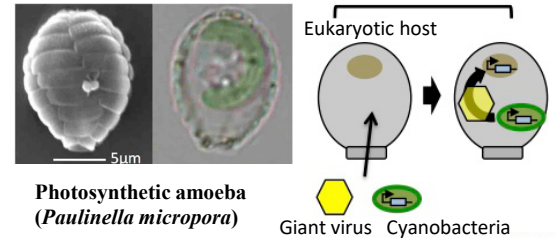
### 【Agriculture】

Development of the oxidative stress resistant plant with molecular genetics approach and genome editing.

### 【Environmental business】

Assessment of agricultural environment with virome analysis for eukaryotic large DNA virus.

### Begging of Primary endosymbiosis



### New endosymbiosis evolution model

At the beginning of the endosymbiosis evolution, viruses might mediate the massive gene transfer from endosymbiotic prokaryote to host eukaryotic cell.

### Wild type RRTF1 knockout RRTF1 overexpressor



### Oxidative stress response caused by RRTF1

Plant oxidative stress response is regulated by a master transcription factor RRTF1. Aberrant expression of RRTF1 induces the generation of reactive oxygen species, making the leaves pale green.



Assessment of the agricultural soil by analysis of microbiome and virome.



### Research feature

- Genome and transcriptome analysis of microorganisms and viruses.
- Studying the contributions of microorganisms and virus on plant evolution.
- Analysis of plant oxidative stress responses.