Title : Pangenomic Analysis of *Methylomonas* Reveals Its Potential as a Bioresource for Agricultural Methane Mitigation

Author(s) : Ms. Chanakan khamchet **Student ID :** 640510214

Major : Microbiology

Advisor(s) : Lecturer Dr. Nuttapol Noirungsee

Type of presentation :
- ☐ Oral Presentation
- ☑ Poster
- ☐ Cooperative Education

ABSTRACT

Methylomonas species are methanotrophic bacteria that utilize methane as their primary carbon and energy source, playing a crucial role in methane mitigation. Despite their significance in reducing greenhouse gas emissions, their ecological role in agricultural systems remains underexplored. By analyzing the pangenome of *Methylomonas* strains isolated from aquatic and terrestrial habitats, we identified key genes associated with bacterial colonization of plant roots. These include genes involved in chemotaxis toward root exudates, motility over root surfaces, primary and secondary attachment, and plant growth promotion. These findings suggest that *Methylomonas* is a promising microbial resource for agricultural applications, particularly in methane-rich environments such as rice paddies. Given its ability to associate with plant roots while contributing to methane oxidation, *Methylomonas* holds potential as a biological tool for sustainable agriculture and greenhouse gas mitigation.