Predominant but previously-unseen prokaryotic drivers of reductive nitrogen transformation in paddy soils, unveiled by metatranscriptomics.

*Yoko Masuda¹, Hideomi Itoh², Yutaka Shiratori³, Kazuo Isobe¹, Shigeto Otsuka¹, Keishi Senoo¹

1. Graduate School of Agricultural and Life Sciences, The University of Tokyo, 2. National Institute of Advanced Industrial Science and Technology, Hokkaido center, 3. Niigata Agricultural Research Institute

Waterlogged paddy soils possess anoxic zones in which microbes actively induce reductive nitrogen transformation (RNT). In the present study, a shotgun RNA sequencing analysis (metatranscriptomics) of paddy soil samples revealed that most RNT gene transcripts in paddy soils were derived from Deltaproteobacteria; in particular, the genera Geobacter and Anaeromyxobacter. Despite the frequent detection of their rRNA in paddy soils, their RNT-associated genes have been rarely detected by previous PCR-based studies. Therefore, the present metatranscriptomics has provided novel insights into the diversity of RNT microbes present in paddy soils as well as the ecological function of Deltaproteobacteria predominating in such soils.

Keywords: Reductive nitrogen transformation, Deltaproteobacteria, Metatranscriptome, Soil ecosystem, iron-reducing bacteria