



Theme 1

Status and trends
of global soil
nutrient budget



Factors in the formation of paddy soil bacterial communities

Hajime Igarashi², Kana Katashima², Rasit Asiloglu¹, Naoki Harada³, Kazuki Suzuki⁴

1 Faculty of Agriculture, Niigata University, 2 Graduate School of Science and Technology, Niigata University,

3 Institute of Science and Technology, Niigata University, 4 Institute for Research Promotion, Niigata University

Introduction, scope and main objectives

- Soil bacteria are one of the components that play the following important role:
 - ✓ Decomposition of organic matter
 - ✓ Nutrient storage as microbial biomass
 - ✓ Nutrient supply for crop growth
 - ✓ Formation of the soil aggregates
 - ✓ Transformation and cycling of nitrogen
- In paddy soils, an anaerobic bacterial community structure is formed after flooding, and then stabilized.
- This process is influenced by soil physicochemical properties and agricultural management: e.g. pH, organic matter content, nutrients, fertilization, etc.
- But it has not been determined which of them is critical.

The objectives of this study are:

- Effect of the soil type and field management on bacterial communities in paddy soils.
- To clarify the relationship between bacterial community composition and soil type.
- The effects of active Al and humic acid on soil microbial community composition.

The detailed procedure for the amplicon sequencing analysis

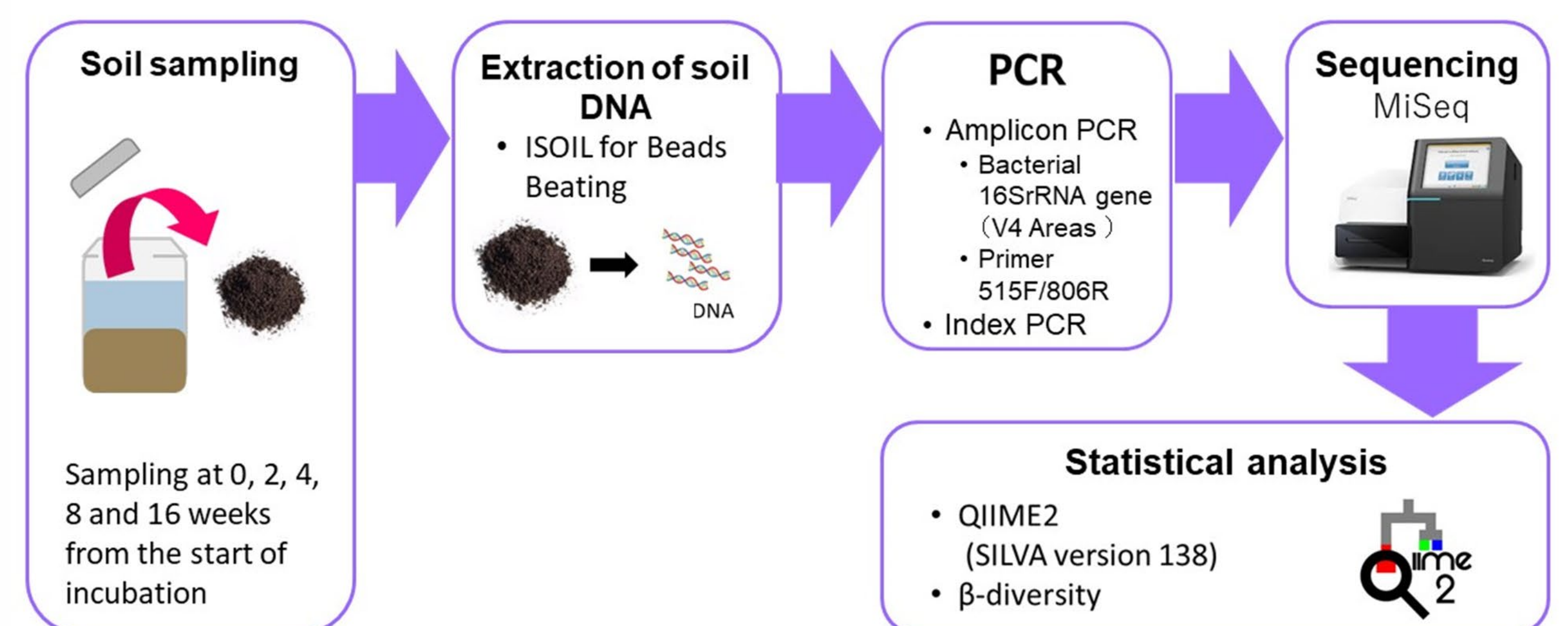


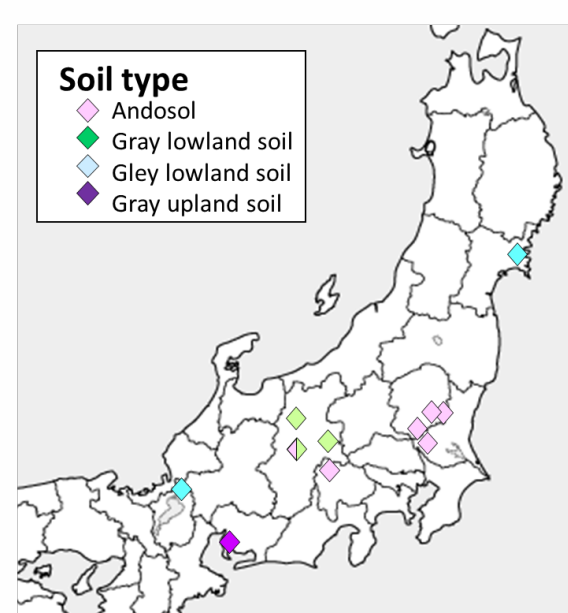
Fig.1 Flowchart of Amplicon sequencing analysis of soil DNA for bacterial 16S rRNA genes

I. Effect of the soil type and field management

How are soil bacterial communities characterized in the paddy fields?

Methodology

- Paddy soil DNA was extracted from 57 fields in Japan
- Bacterial community compositions were compared based on
 - Agricultural practice
 - Soil type



Soil type	Management	Number of fields
Andosol	Organic	9
Gray lowland soil	Natural-farming	10
Gray lowland soil	Conventional	6
Gray lowland soil	Organic	2
Gley lowland soil	Natural-farming	6
Gley lowland soil	Conventional	4
Gley lowland soil	Organic	9
Gley lowland soil	Natural-farming	0
Gray upland soil	Organic	1
Gray upland soil	Natural-farming	4
Gray upland soil	Conventional	0
Gray upland soil	Conventional	2

Fig.2 Sample soil information

Results

- Soil type had greater impact on soil bacterial community formation than agricultural practice

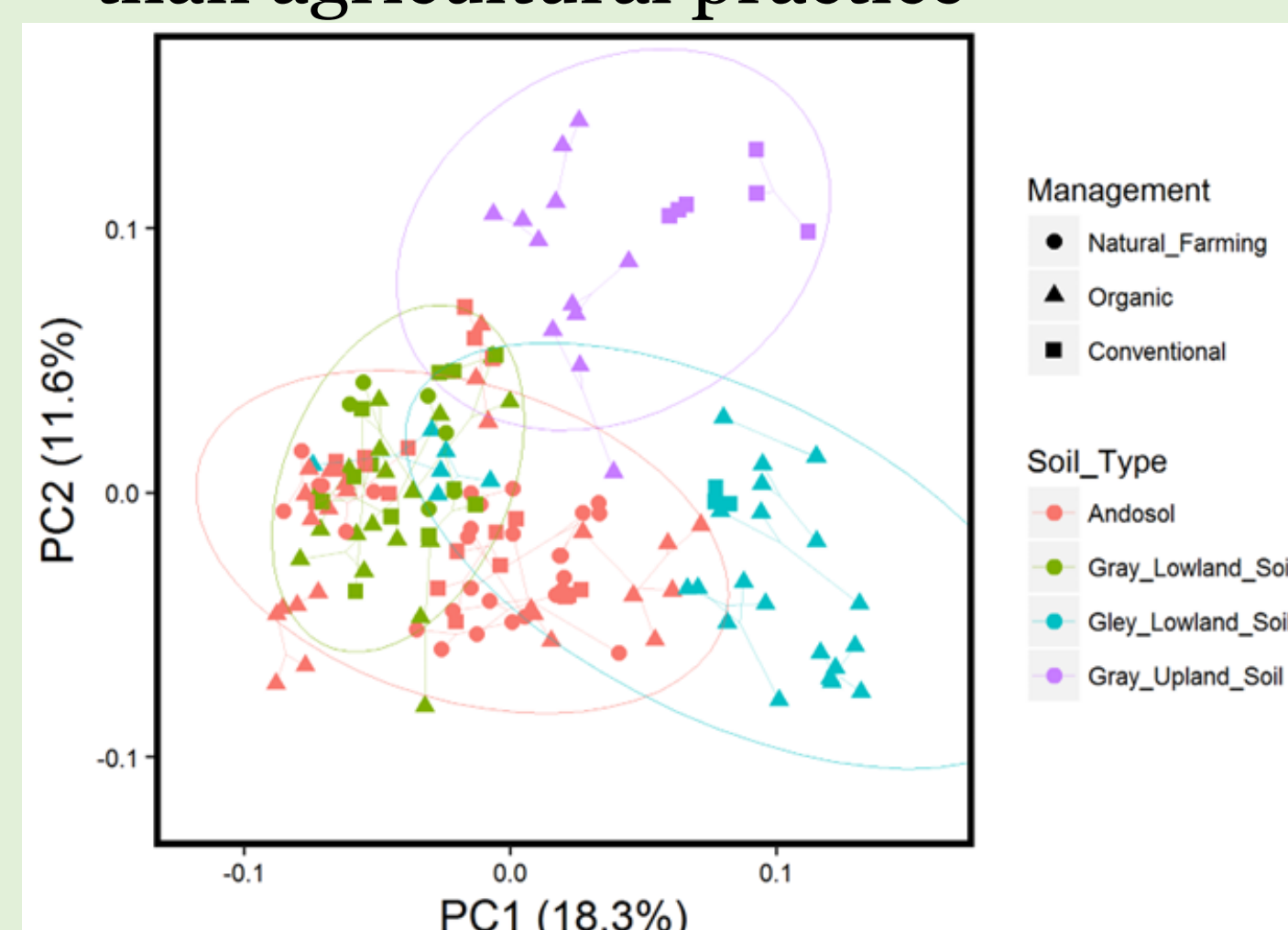


Fig.3 Principal Coordinate Analysis (PCoA) based on weighted UniFrac distance

II. Bacterial flora exchange experiments

How do differences in soil type affect bacterial community?

Methodology

- Bacterial communities were extracted from soil, and inoculated into different soil types after sterilization
- Incubated under submerged conditions at 30 °C

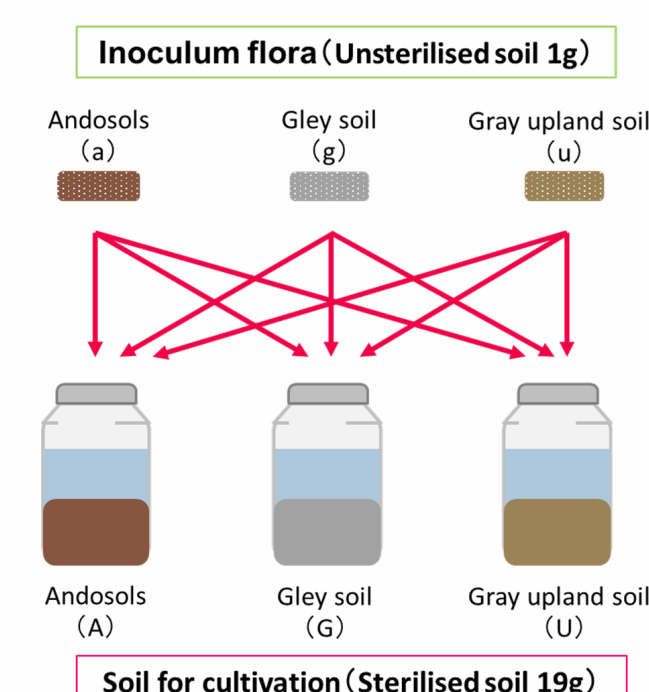


Fig.4 Experimental system

Results

- Beta-diversity of the bacterial community was more influenced by the soil type of the culturing soil than the source of inoculum

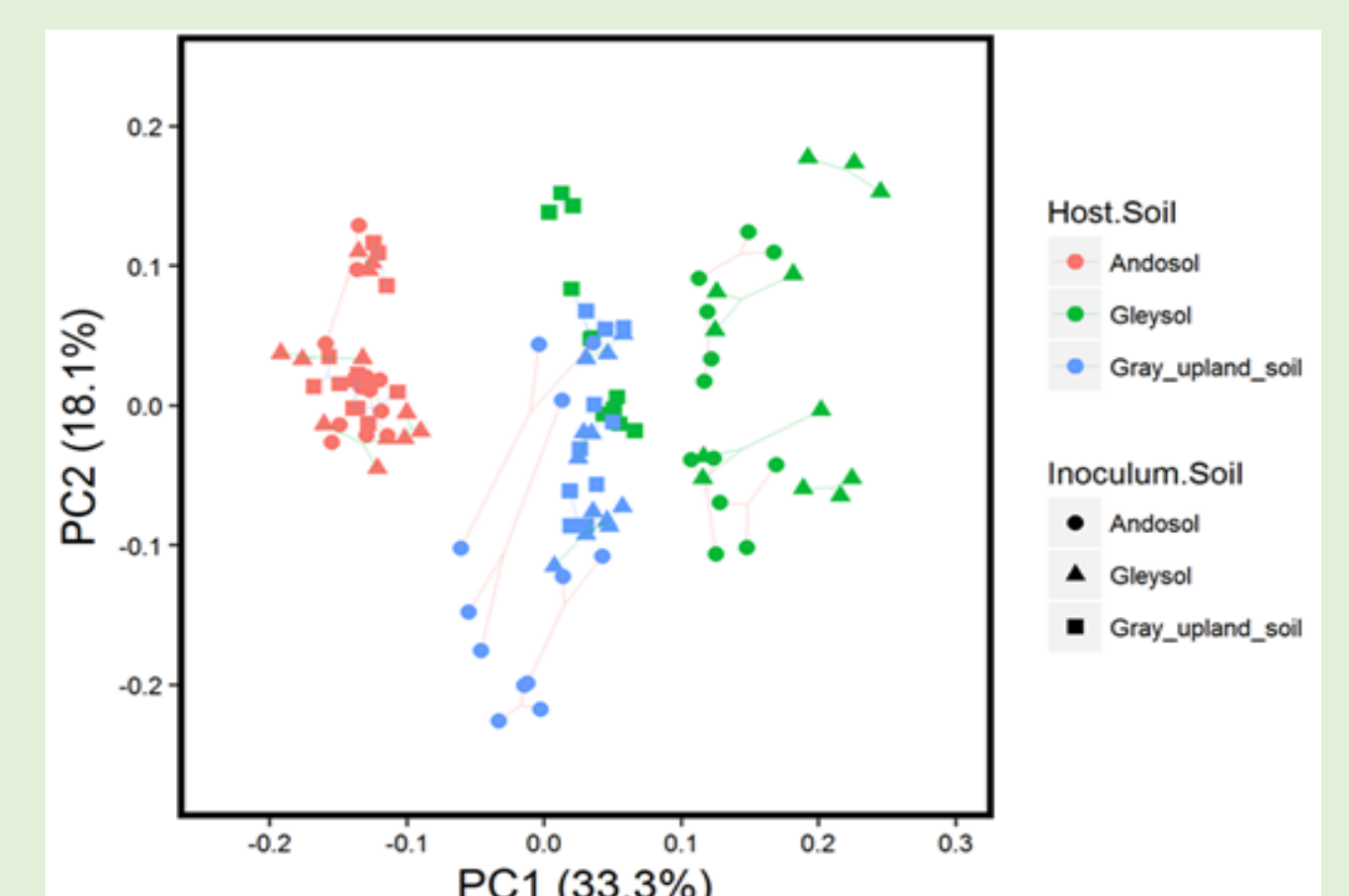


Fig.5 Principal Coordinate Analysis (PCoA) based on weighted UniFrac distance

III. The effects of active Al and humic acid on soil microbial community composition

Do the two soil physicochemical properties affect on bacterial communities?

Methodology

- Al source: alophene and aluminum hydroxide gel
Humic acid: extracts from andosol and a commercial product
- Incubated under submerged conditions at 30 °C

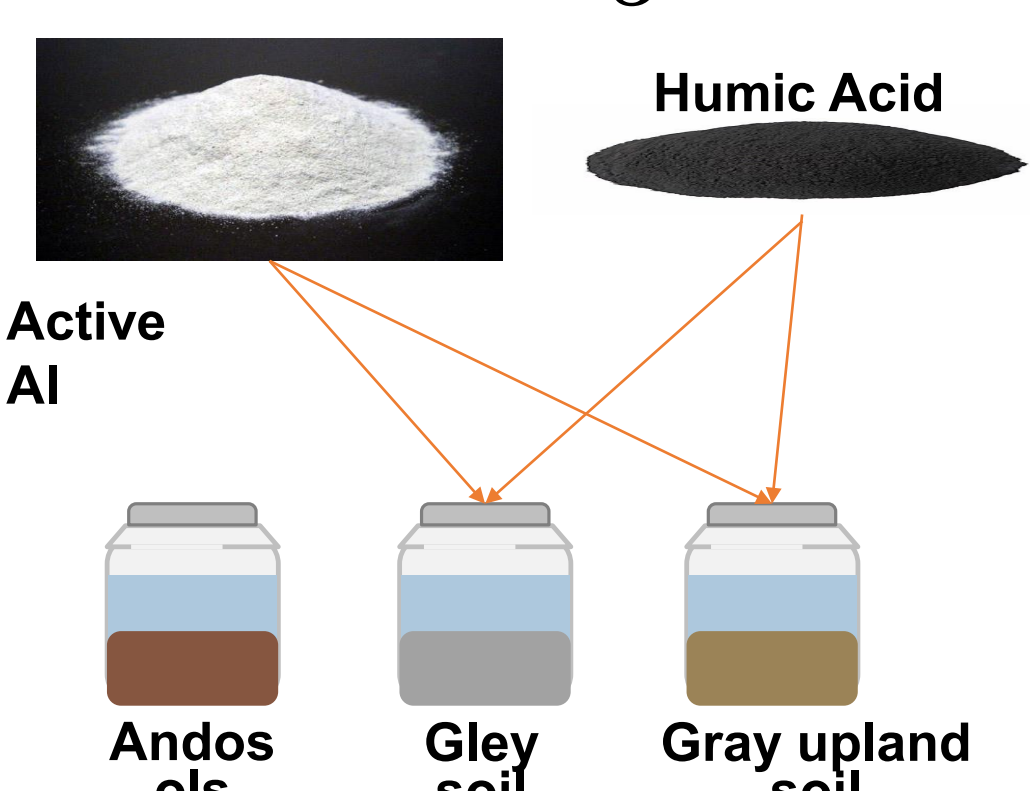


Fig.6 Experimental system

Results

- Amplicon sequencing analysis on soil DNA did not show significant impacts of active Al and humic acid on the bacterial community composition

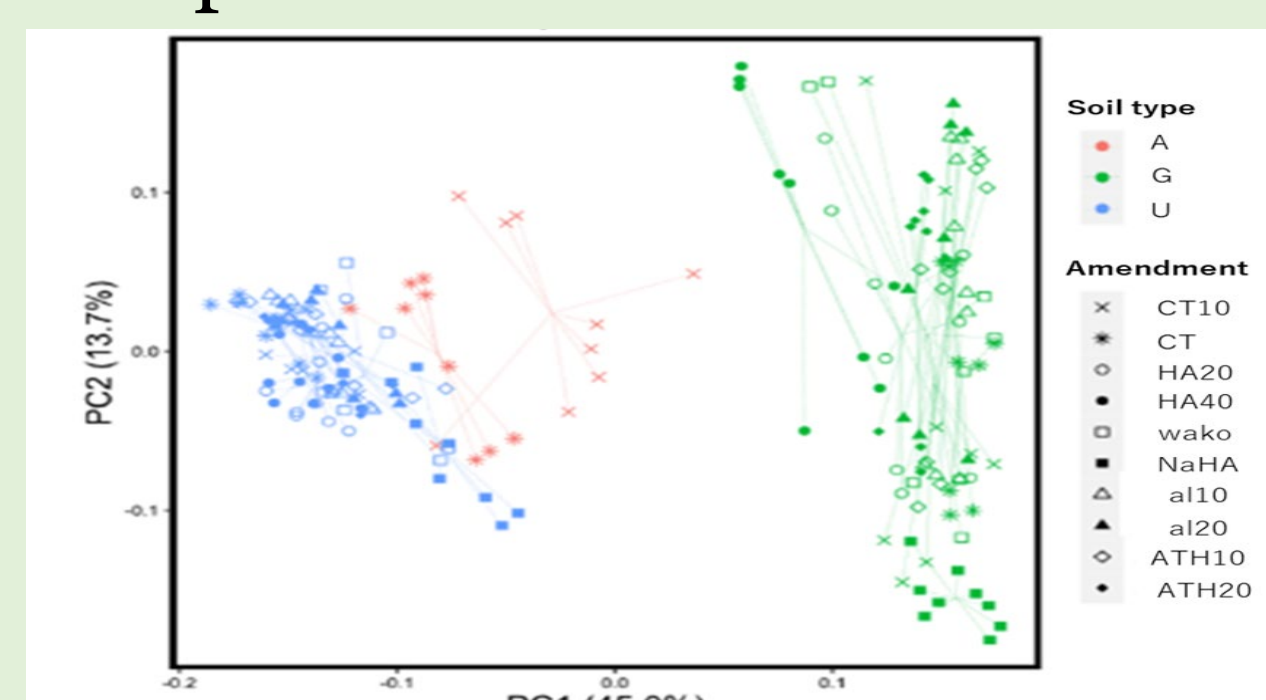
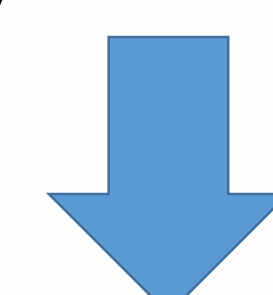


Fig.7 Principal Coordinate Analysis (PCoA) based on weighted UniFrac distance

Conclusions

- Fertilizer management and geographical distance are unlikely to be significant factors in determining bacterial community structure
- The present experiments showed that some factors of soil type may affect the bacterial community



- Based on the above findings, it is necessary to examine the effects of the other soil physicochemical properties to clarify the mechanism of bacterial community formation under flooded conditions

Acknowledgements

This work was partially supported by JSPS KAKENHI Grant Number JP21K14952