Changes of Forest Microbiome Driven by Soil Properties after Clear-cut Logging in South Korea

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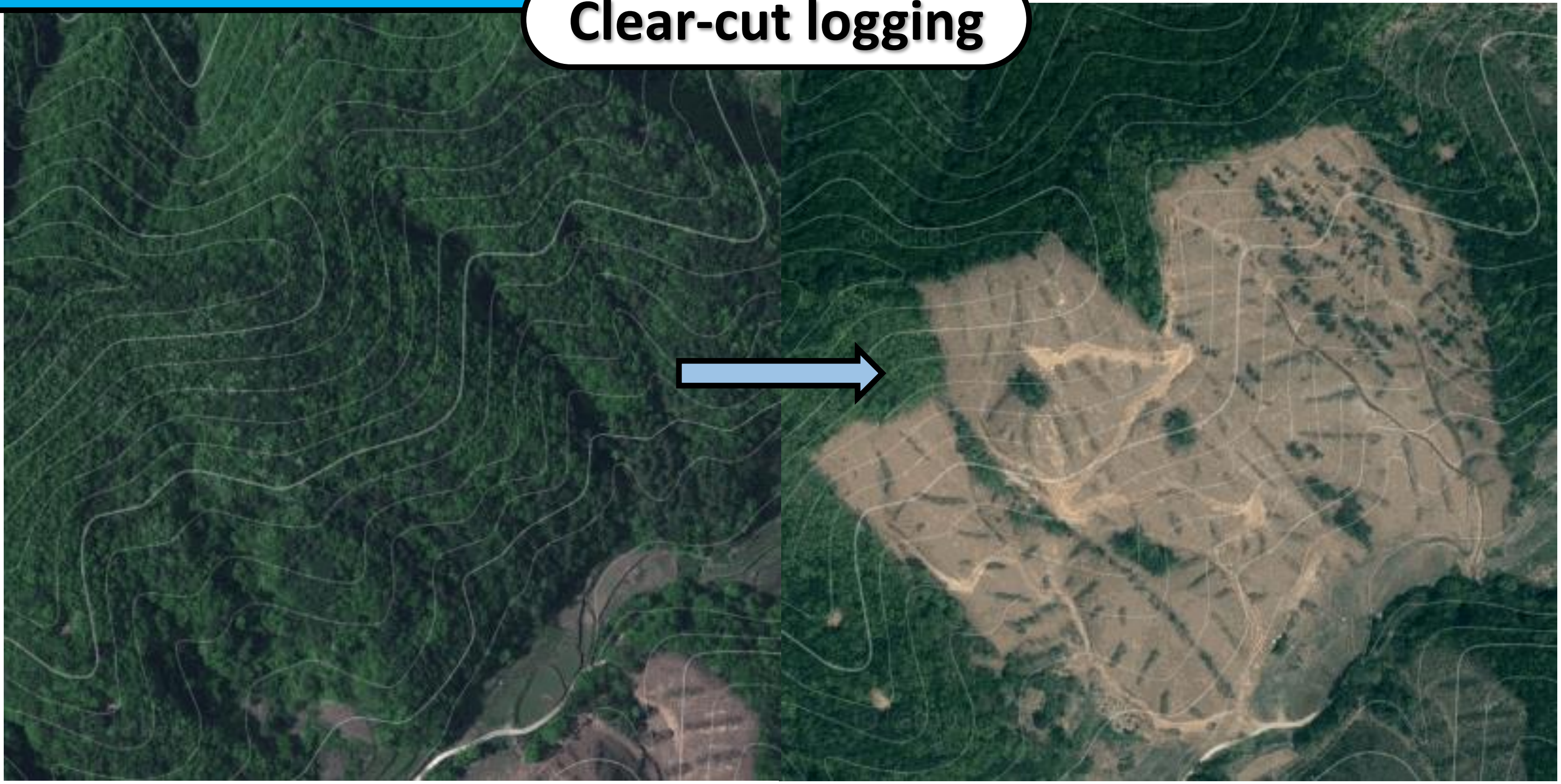
Introduction

Habitat Disturbance

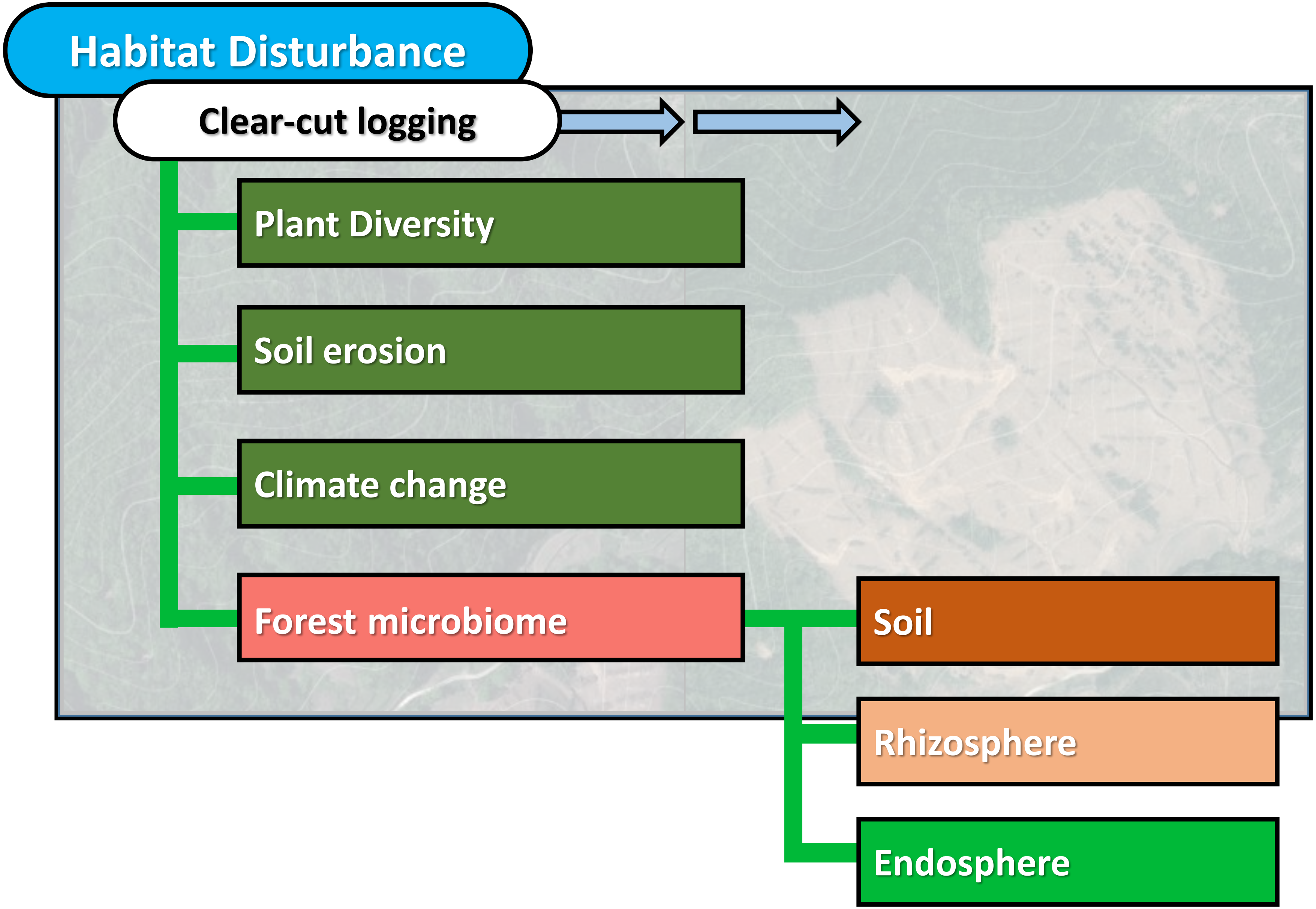
Clear-cut logging



Before

After

Introduction



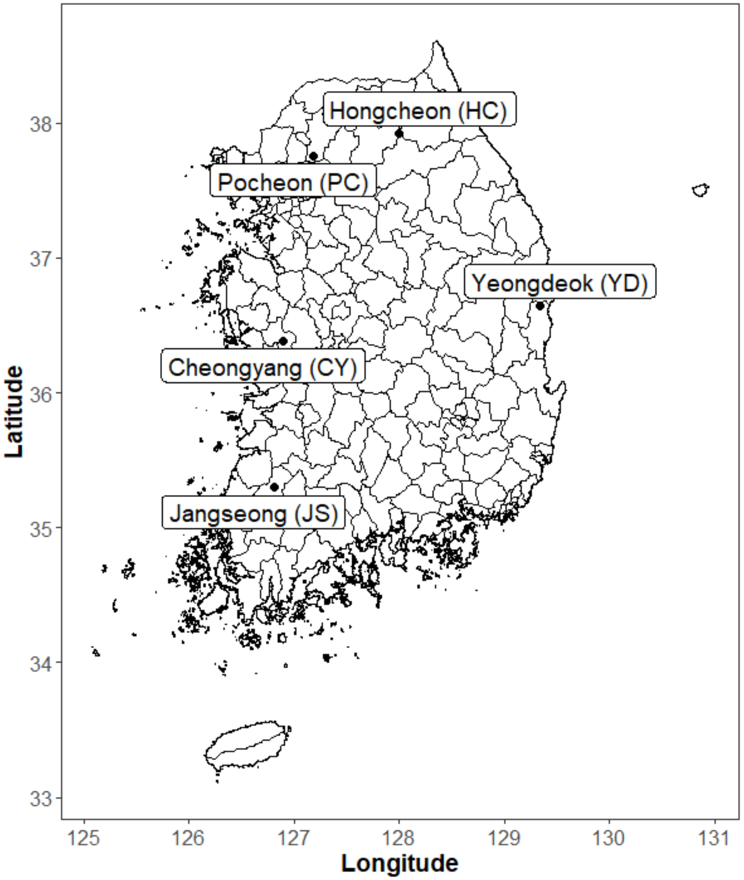
Habitat Disturbance

- **Clear-cut logging**
  - Plant Diversity
  - Soil erosion
  - Climate change
  - Forest microbiome
    - Soil
    - Rhizosphere
    - Endosphere

Materials and Methods

1. Experimental Design

1) Experimental sites (2020 ~ 2022)



2) Treatment (Clear-cut logging)

Logged (Log) **Control (Con)**

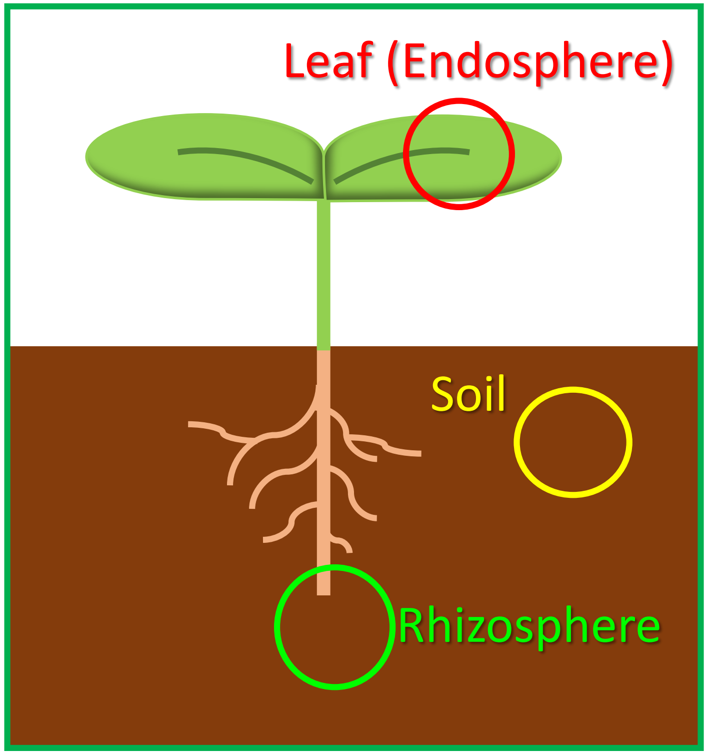
3) Target species

Quercus mongolica

Quercus serrata

Lindera obtusiloba

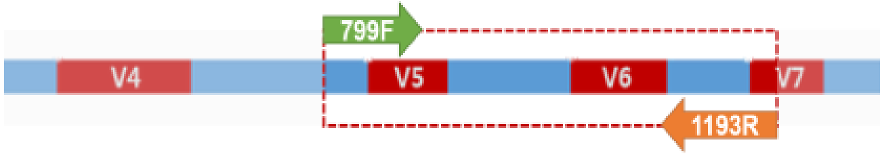
Materials and Methods



2. Soil chemical properties analysis

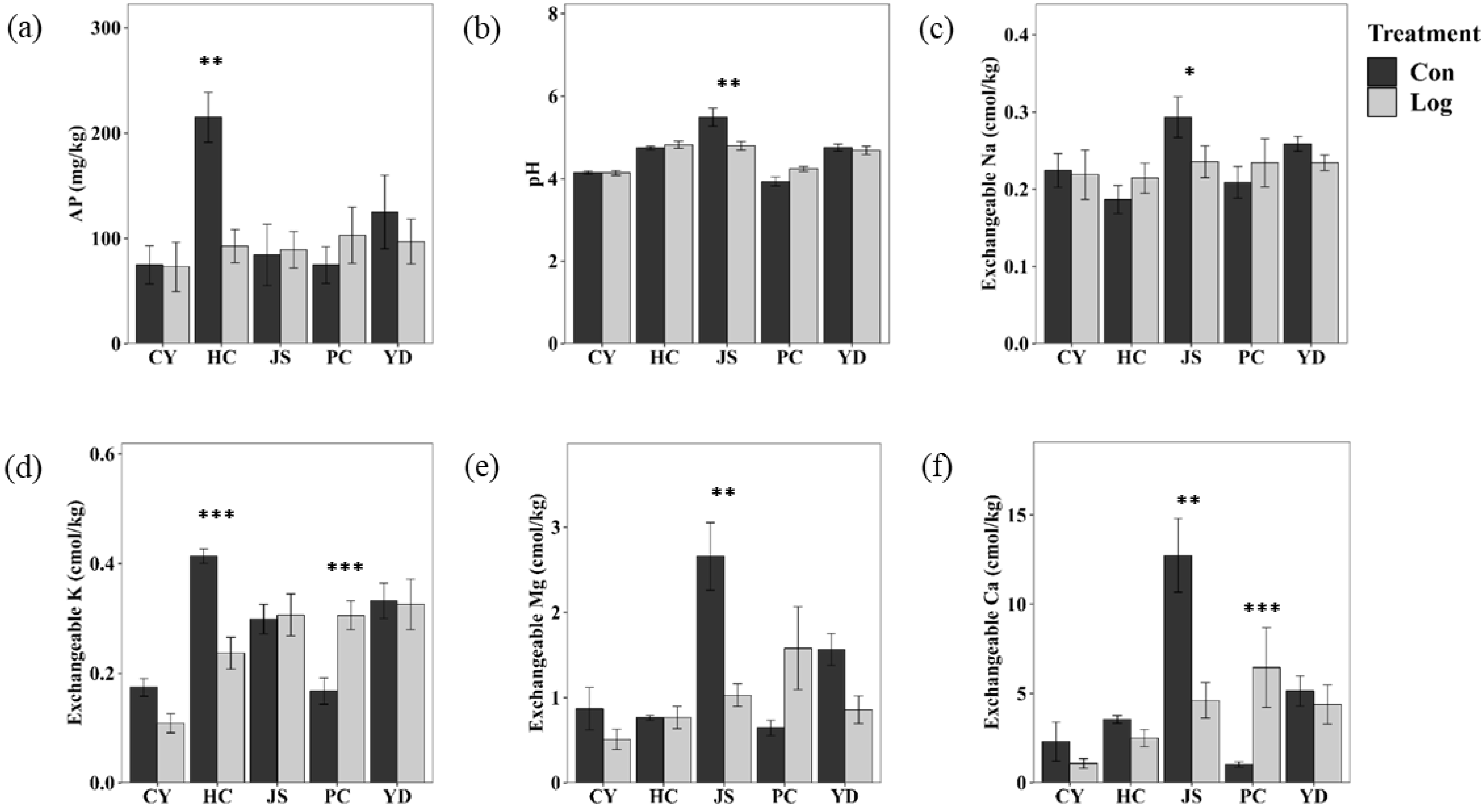
- Total nitrogen (TN)
- Available Phosphorus (AP)
- Organic matter (OM)
- pH
- Exchangeable cation (K^+, Na^+, Mg^{2+}, Ca^{2+})

3. Bacterial community analysis (16s rRNA)



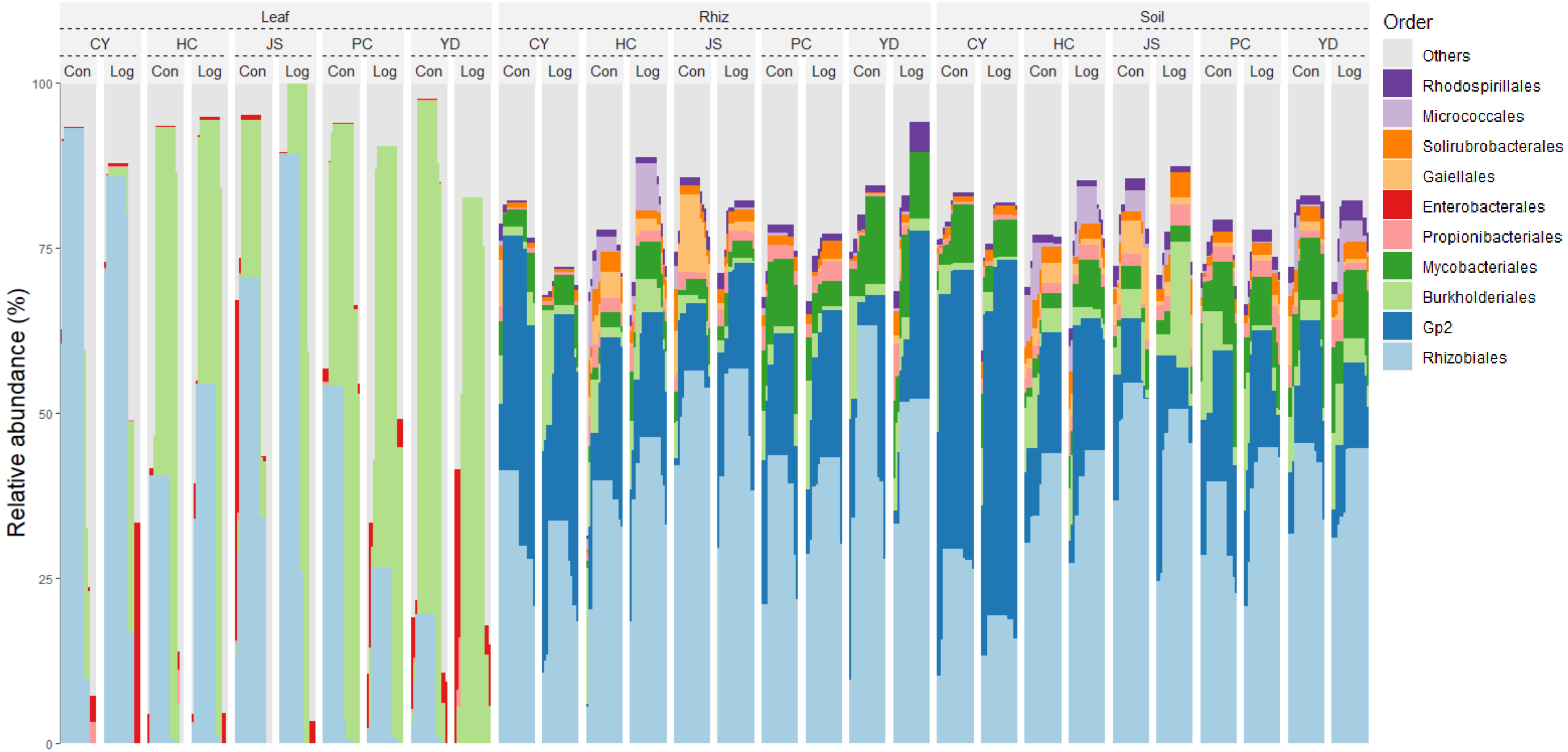
- PCR : 799F-1193R (V5-V7)
- Illumina amplicon sequencing
- DADA2, Amplicon Sequence Variants (ASVs)

Changes of soil chemical properties after clear-cut logging



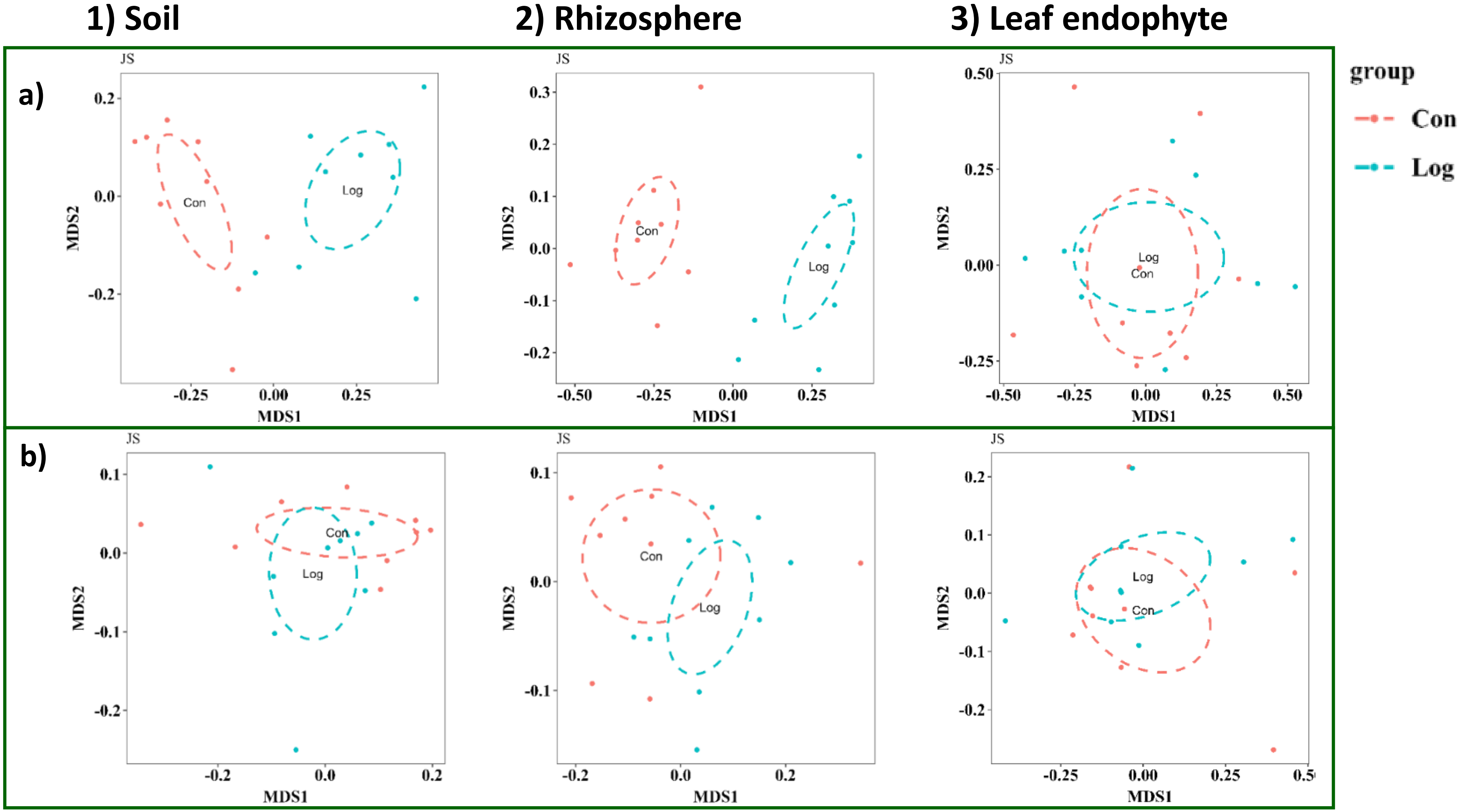
- Soil chemical properties were changed after clear-cut logging in HC, JS and PC.
- The properties that showed differences were higher in control area in HC and JS and higher in logged area in PC.

Bacterial community composition at Order level



- Soil and rhizosphere showed a similar bacterial community compositions, whereas leaf endophyte had a different composition from the two.
- In soil and rhizosphere, Rhizobiales (30.30%), Gp2 (19.80%), Mycobacteriales (7.02%) and Burkholderiales (6.69%) were dominant Orders.

Changes of bacterial community composition after clear-cut logging

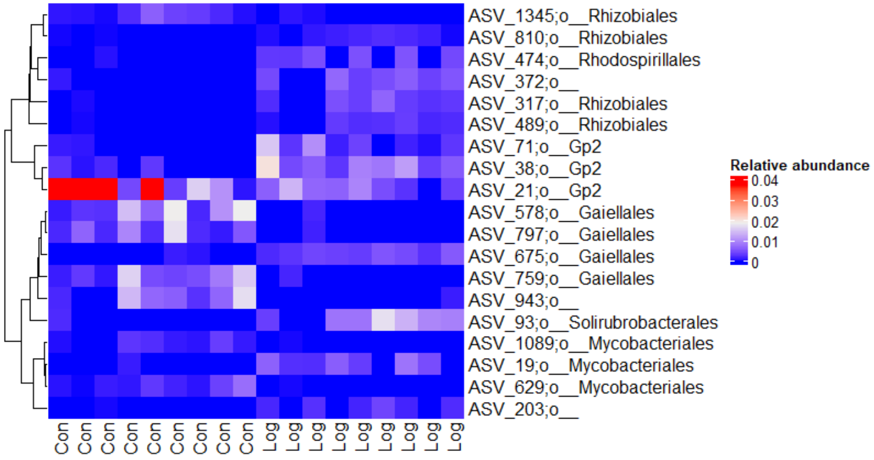


1) Soil 2) Rhizosphere 3) Leaf endophyte

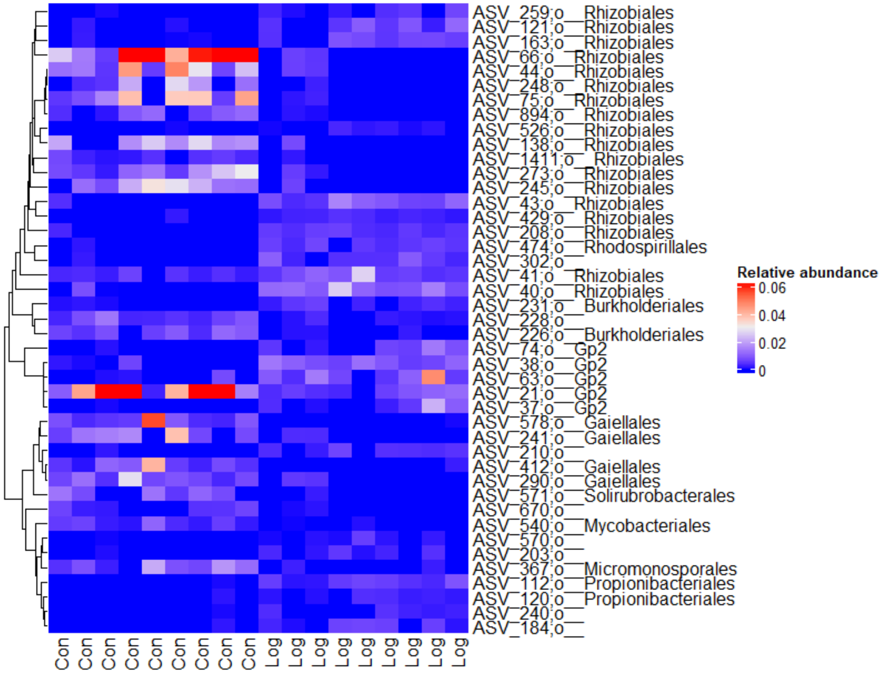
- There were significant differences between control and logged areas in bacterial communities of soil and rhizosphere.
- Differences was made by differences in relative abundance, not members.

Differential abundant taxa between control and logging area

1) JS - Soil



2) JS - Rhizosphere



- Among the results of all sites, Rhizobiales, Gp2, Mycobacteriales, and Burkholderiales were commonly and mainly identified.
- Genetically close bacteria (ASVs) showed similar relative abundances in same treatment.

Relationship between soil bacterial communities and soil properties

Mantel test with Spearman’s correlation

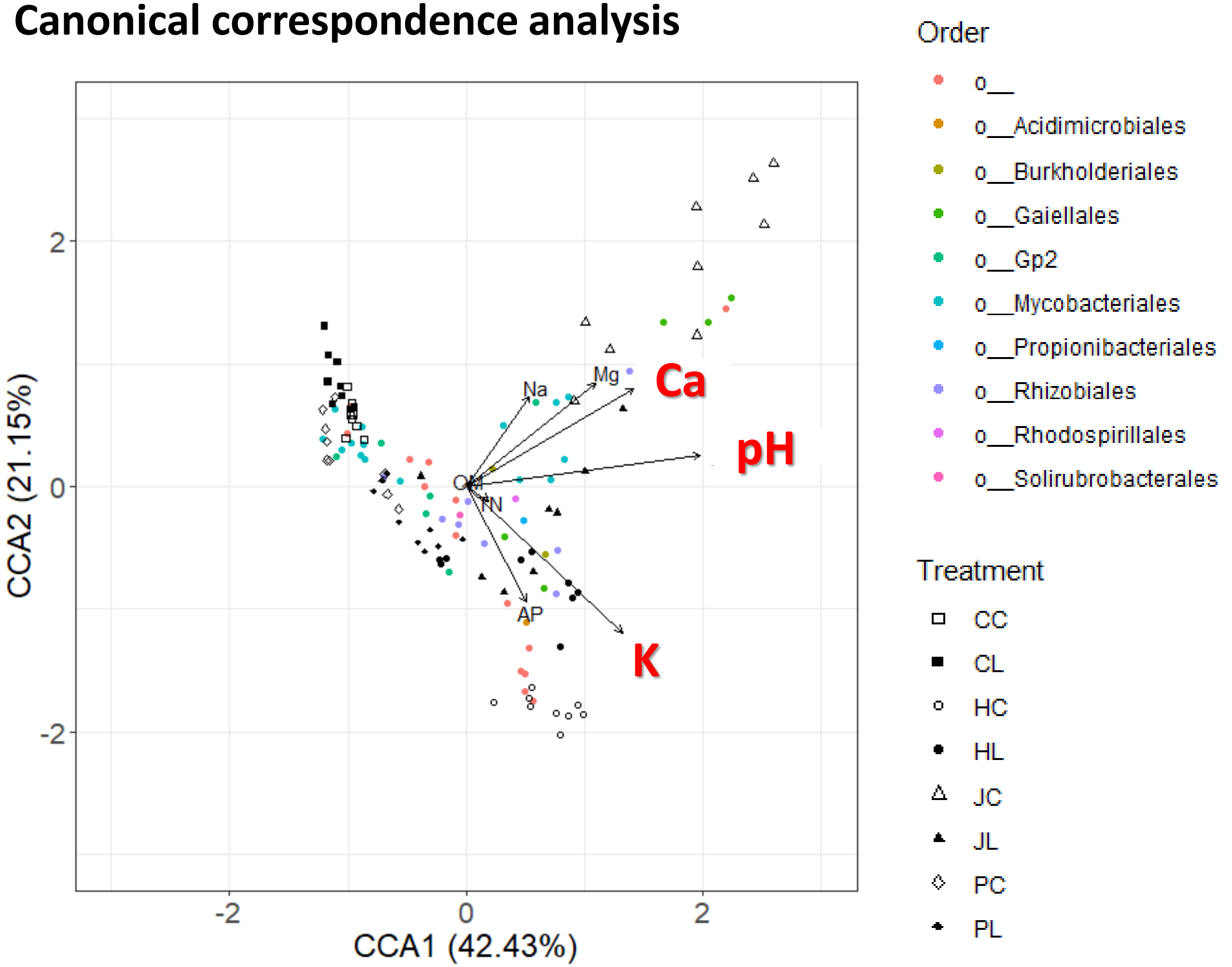
1) Control area

2) Logged area

- Most of the soil chemical properties affected the composition of soil bacterial communities in the control area.
- The exchangeable K, Ca and pH affected the community composition of the logged area .

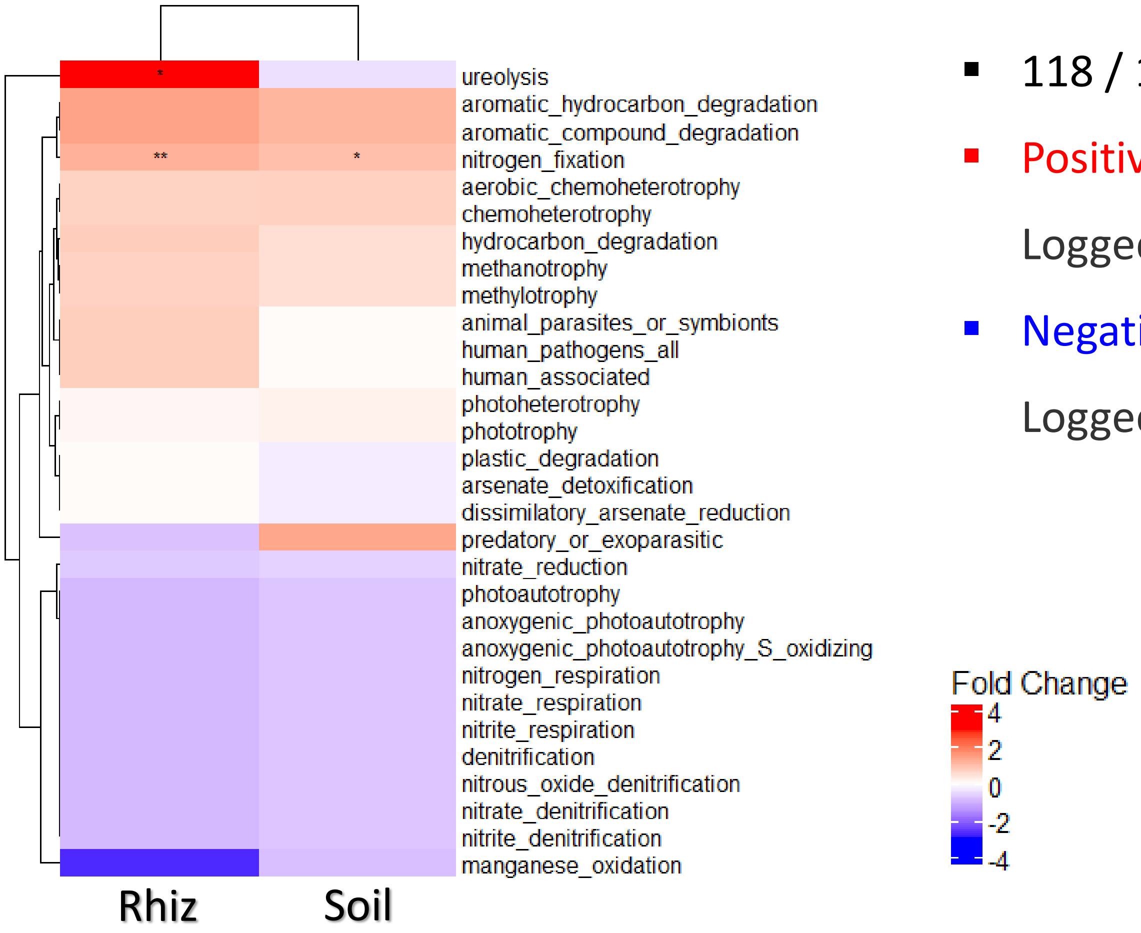
Relationship between soil bacterial communities and soil properties

Canonical correspondence analysis



- Differences in the bacterial communities among sites were related to pH.
- Differences in the bacterial communities by clear-cut logging were related with exchangeable K and Ca.

Shifts in functions of bacteria in soil and rhizosphere after clear-cut logging



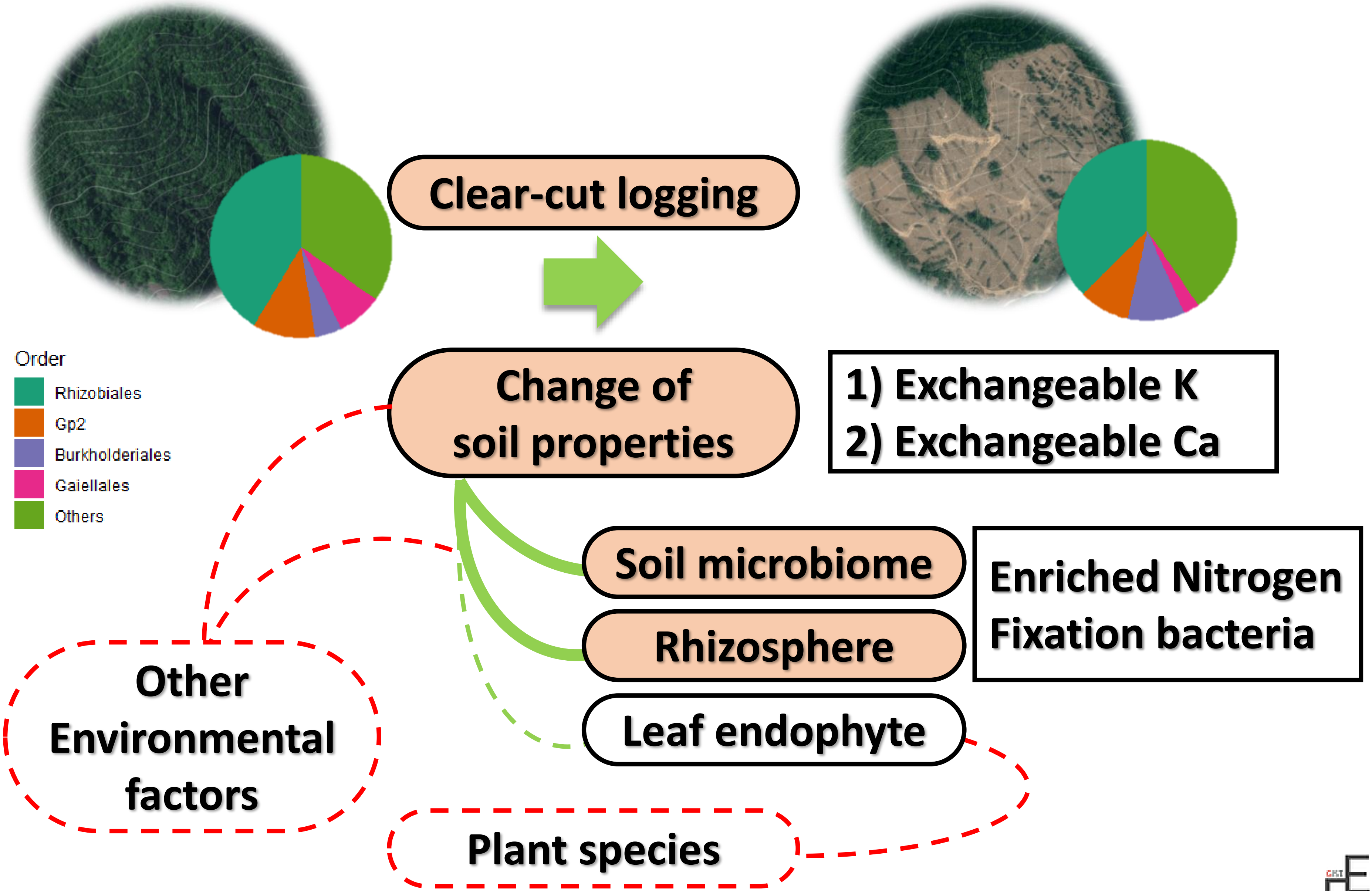
- 118 / 1,182 (9.98%)
- Positive fold change value (Red)

  Logged >> Control
- Negative fold change value (Blue)

  Logged << Control

- Dominant functions were chemoheterotrophy (32.3–34.9%), aerobic chemoheterotrophy (32.1–34.7%) and nitrogen fixation (11.3-19.0%) in both soil and rhizosphere.
- Bacteria having nitrogen fixation function was significantly enriched in both soil and rhizosphere of logged area.

Conclusion



Clear-cut logging

Change of soil properties

1) Exchangeable K
2) Exchangeable Ca

Soil microbiome

Rhizosphere

Leaf endophyte

Enriched Nitrogen Fixation bacteria

Other Environmental factors

Plant species

Thank You For Listening

Q&A