

Soil temperature increase effects on maritime Antarctic soil microbial community and humic acid degradation

Dockyu Kim^a, Ha Ju Park^a, Hyoungseok Lee^b, and Soon Gyu Hong^a

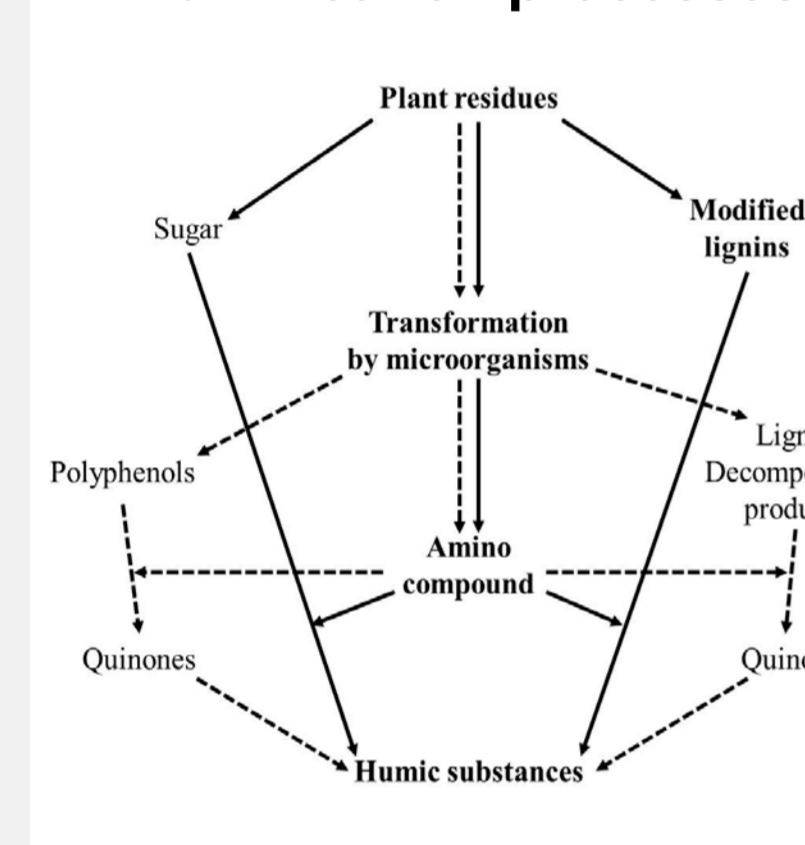
^a Division of Polar Life Sciences, ^b Unit of Polar Genomics, Korea Polar Research Institute, Incheon 21990, South Korea

ABSTRACT

Soil humic substance (HS) is the largest constituent of soil organic matter. A major extractable component, humic acid (HA), of HS is dark brown to black high molecular weight organic polymer. To assess the effects of warming both on HA degradation and microbial community, microcosm beakers with HA-rich soils from King George Island in the maritime Antarctic were incubated at elevated temperature of 5°C and 8°C, compared to the Antarctic soil temperature (below 2.0°C) during thawing period. Under the microcosm systems, HA content steadily decreased to approximately 63% and 55% until 90 days-incubation at 5°C and 8°C, respectively, compared to untreated control (100%, 287.0±2.8 mg/g dried soil), presumably by microbial degradation process. Culture-independent community analysis of 16S rRNA genes showed that, during the microcosm experiments, the relative abundances of bacterial phyla *Proteobacteria* (copiotrophic) and *Actinobacteria* (polymer-degrading) slightly increased and decreased, respectively, in parallel with the incubation temperature rising to 5°C and 8°C. In contrast, archaeal community, dominated by phylum *Thaumarchaeota*, hardly responded to the soil temperature increase, indicating that bacterial community was much more affected than archaea by warming, although fungal response was not consistent. Culture-dependent community analyses were subsequently performed for the indigenous bacteria at 5°C and 8°C which were enriched in an artificial mineral medium containing HA. Consequentially, addition of HA resulted in a rapid increase of *Proteobacteria* dominance at both 5°C and 8°C, with the relative abundance of class *Alphaproteobacteria*-related bacteria highly increasing to over 72.7% among *Proteobacteria* (100%) under HA-degradation process. The overall results of this study indicate that HA degradation is in progress by bacteria in maritime Antarctic soil, and soil temperature rise by global climate change can change the bacterial community structure and HA degradation rate. This work was supported by grant to KOPRI (PE18090).

INTRODUCTION

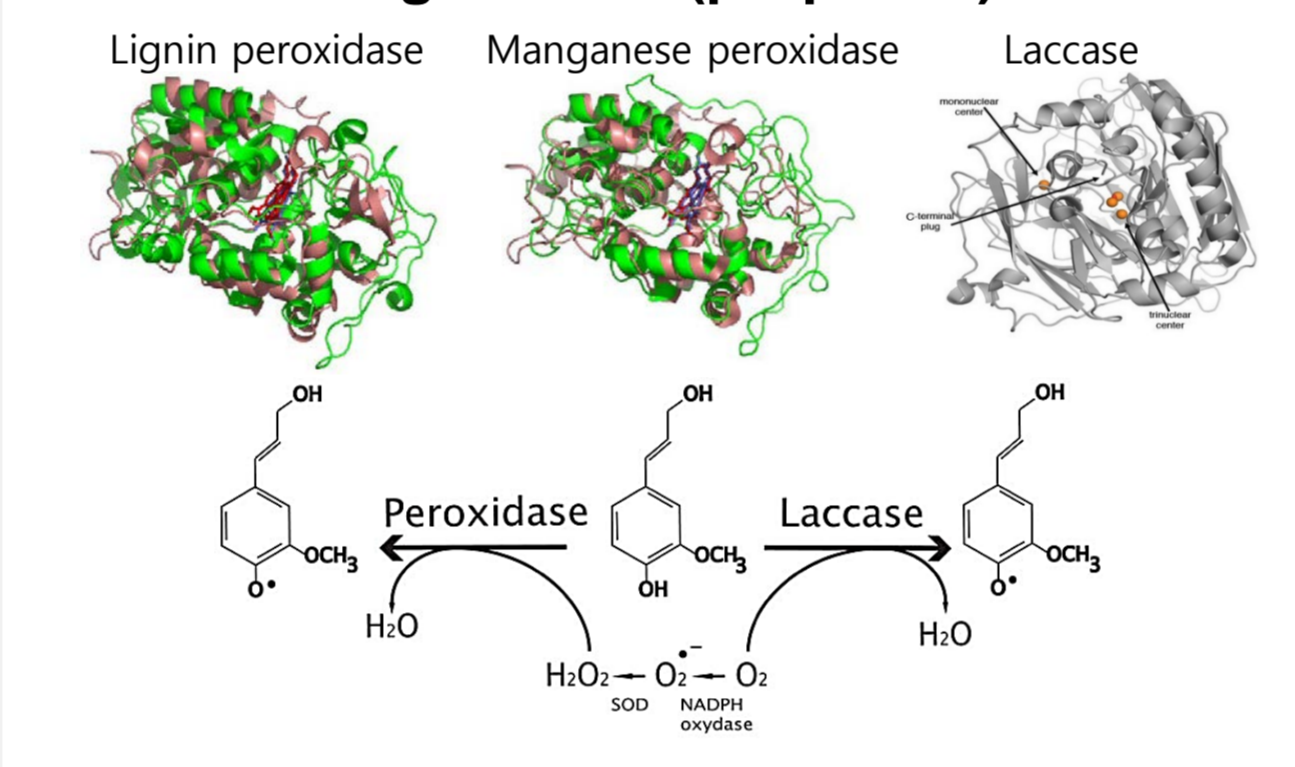
Humification processes



Main fractions of HS

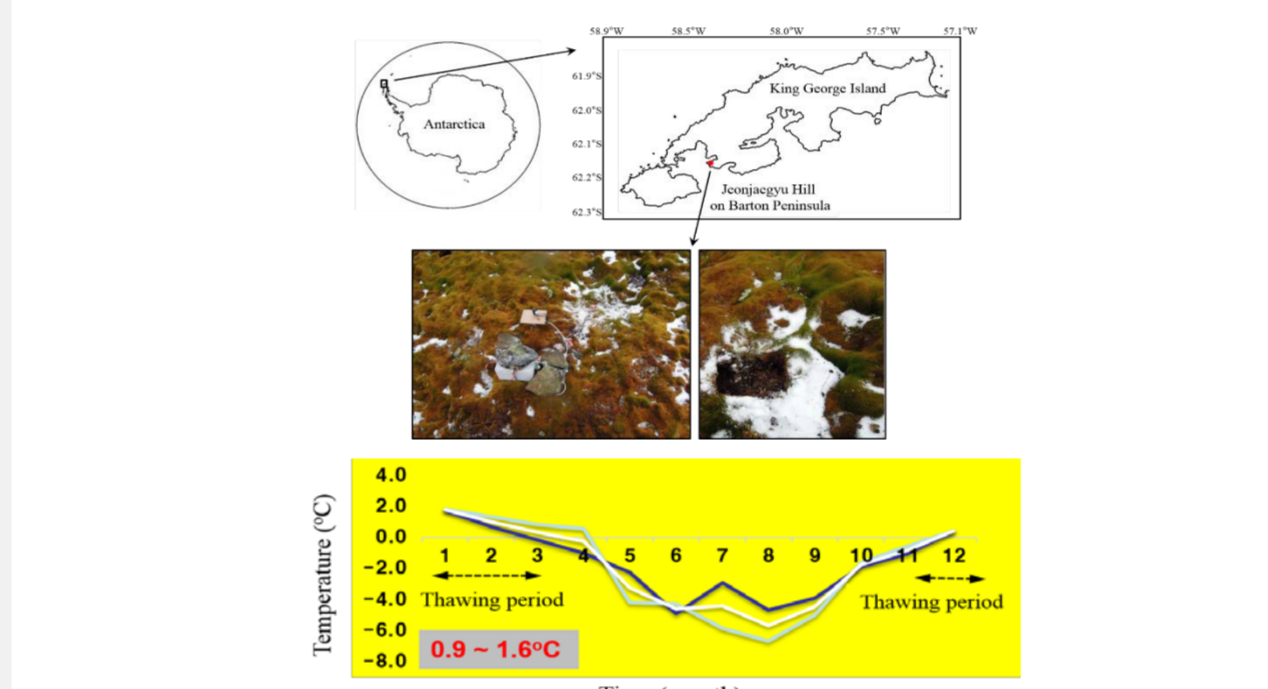
HS fraction	In acids	In alkalis	Component proportion ratio (%)
Humic acid (HA)	Insoluble	Soluble	50 - 65% C
Fulvic acid (FA)	Soluble	Soluble	40 - 50% C
Humins	Insoluble	Insoluble	-

Nonspecific oxidizing enzymes for initial HS degradation (proposed)



METHODS

Site for HA-rich soil (KS 2-1) sampling and temperature measuring in King George Island



HA extraction and content measuring

- HA extraction and content measuring
- Spectrophotometric structural analysis of HA
- Microbial community analysis (16S rRNA gene pyrosequencing)

RESULTS

Fig. 1. Average metabolic response calculated from well color development over time in EcoPlates inoculated with KS 2-1 soil suspension and incubated at 5°C and 8°C.

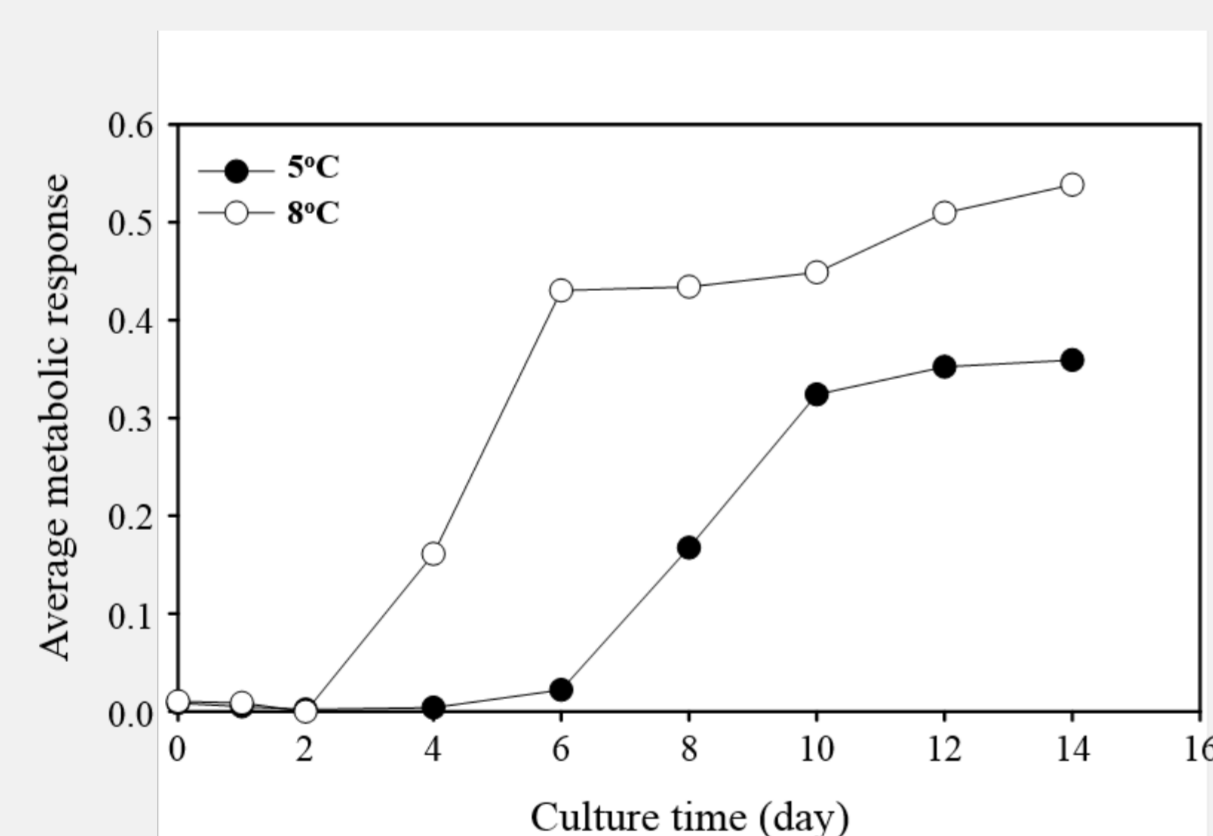


Fig. 2. Time-course changes in HA content and structure, determined by direct weighing (A), gel permeation chromatography (B), and fourier transform infrared spectroscopy (C), during microcosm experiments at 5°C and 8°C for 90 days.

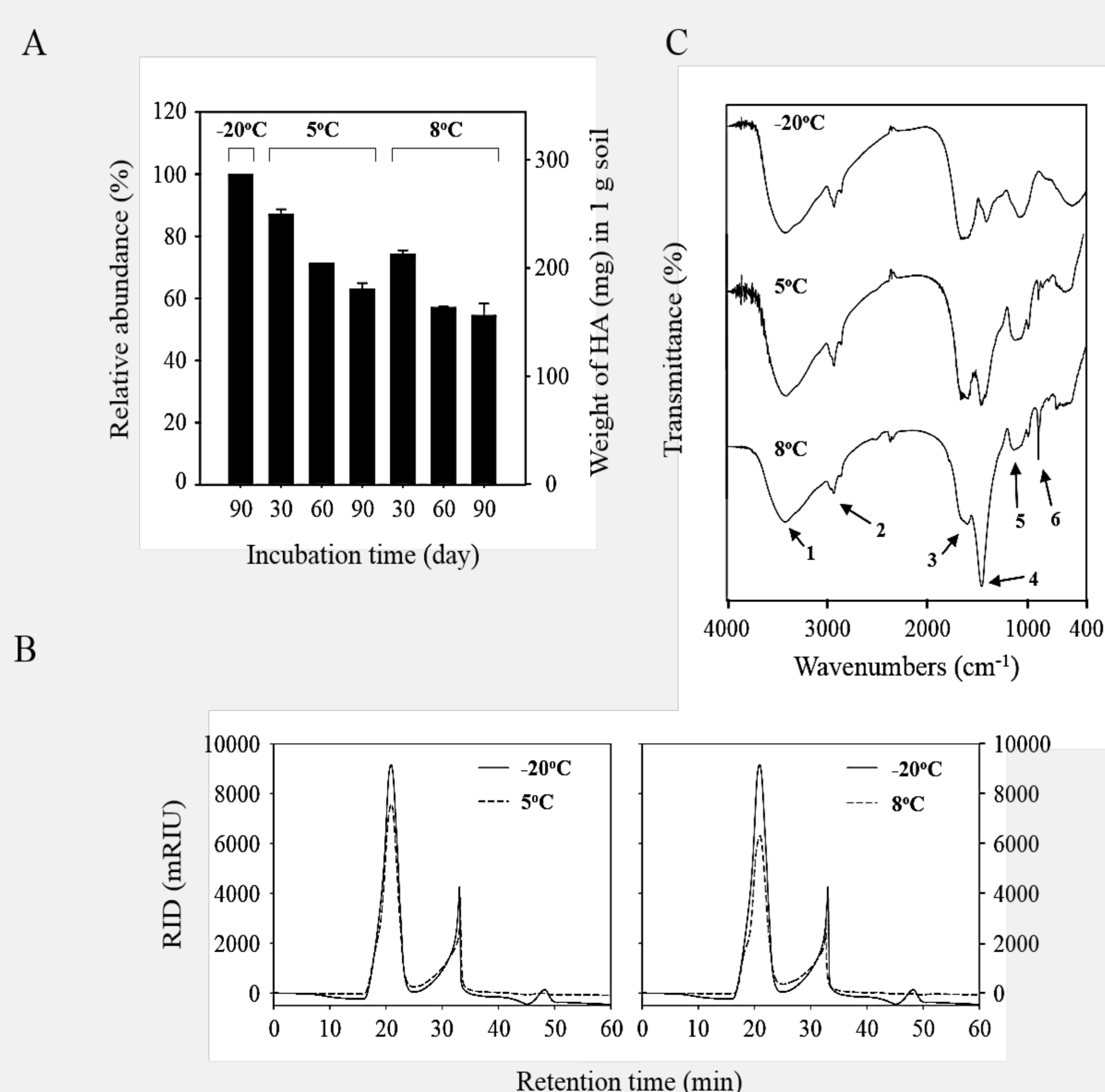


Fig. 3. Changes (culture-independent) in the relative abundances of bacterial (A), archaeal (B), and fungal (C) phyla during the microcosm experiments with KS 2-1 soil at 5°C and 8°C for 90 days. (D) Changes (culture-dependent) in the relative abundances of bacterial phyla during enrichment of KS 2-1 soil suspension at 5°C and 8°C for 90 days.

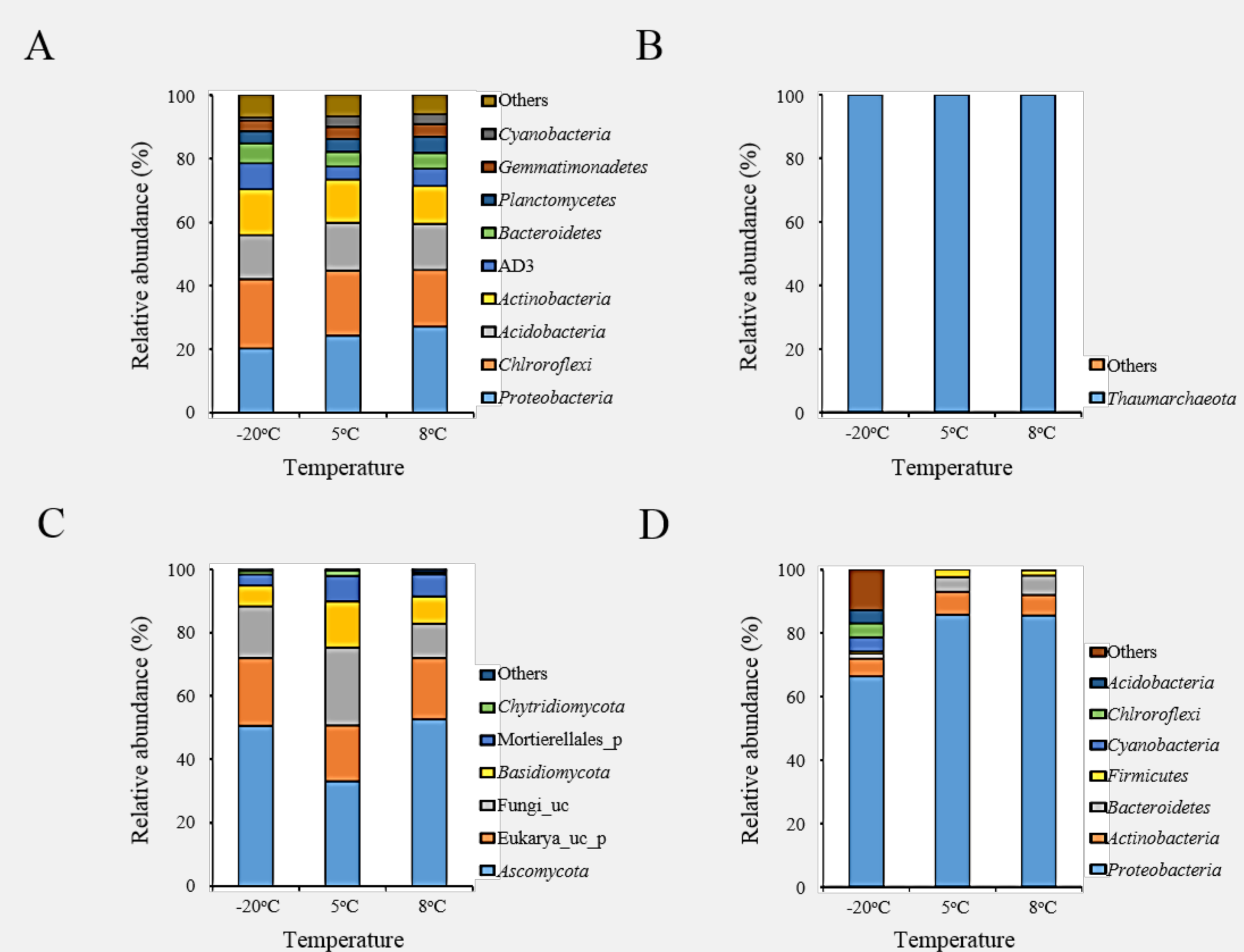


Table 1. Summary of pyrosequencing results and statistical analysis of microbial communities during microcosm experiments with KS 2-1 soil

Microorganism	Sample	Normalized reads	OTU richness			OTU diversity (Shannon)
			Incubation temperature and time	Observed	Chao1	
Bacteria	-20°C, 90 d	1947	709	1418	2039	5.924
	5°C, 90 d	1947	729	1827	3082	5.894
	8°C, 90 d	1947	711	1621	2782	5.875
Archaea	-20°C, 90 d	2750	21	39	47	1.151
	5°C, 90 d	2750	6	6	6	0.562
Fungi	8°C, 90 d	2750	9	9	9	0.425
	-20°C, 90 d	6137	234	387	425	3.149
Fungi	5°C, 90 d	6137	402	586	566	4.568
	8°C, 90 d	6137	403	493	498	4.559