



한국미생물학회

The Microbiological Society of Korea

## International Meeting of the Microbiological Society of Korea

# MSK2018

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- The Microbiological Society of Korea

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B001

### Artificial Warming Effect on Microbial Community and Humic Substance Degradation in Maritime Antarctic Soil in King George Island

Ha Ju Park<sup>1</sup>, Jung Ho Kim<sup>2</sup>, Ui Joung Youn<sup>1</sup>, Angélica Casanova-Ka<sup>3</sup>, Soon Gyu Hong<sup>1</sup>, and Dockyu Kim<sup>1\*</sup>

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B002

### Endophytic Bacteria from Turmeric Plant as Plant Growth Promoter and Antifungal Agents

Min-Ok Jun<sup>1,2</sup>, Cheol-Hee Kim<sup>2</sup>, Suk Weon Kim<sup>1\*</sup>, and Jiyoung Lee<sup>1\*</sup>

<sup>1</sup>Korea Research Institute of Bioscience & Biotechnology (KRIBB), <sup>2</sup>Department of Biology, Chungnam National University

B004

### Comparison of Microbiome and Virome in Chicken Farm under Diverse Environmental Factors

Jongbin Park<sup>1</sup>, Gwi-Deuk Jin<sup>1</sup>, Inhwan You<sup>1</sup>, Soo Jin Kim<sup>1</sup>, Sukjung Choi<sup>1</sup>, and Eun Bae Kim<sup>1,2,3\*</sup>

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B005

### Microbial Communities Responsible for Glucose and Acetate in Organic-enriched Sediment of the Fin-fish Farm in the South Coast of Korea

Ayeon Choi<sup>1</sup>, Hyeyoun Cho<sup>1</sup>, Hyun-Ji Lee<sup>1</sup>, Hyun-Soo Beak<sup>1</sup>, Ju-Wook Baek<sup>1</sup>, Ui-jung Jung<sup>1</sup>, SungUk An<sup>1</sup>, Hyung Chul Kim<sup>2</sup>, Won-Chan Lee<sup>2</sup>, and Jung-Ho Hyun<sup>1\*</sup>

<sup>1</sup>Department of Marine Science and Convergent Technology, Hanyang University, <sup>2</sup>Marine Environment Research Division, National Institute of Fisheries Science (NIFS)

B006

### Metagenomic Study of the Upper Airway Microbiome Associated with Childhood Asthma

Min-Jung Lee, Doo-heon Son, and Bong-Soo Kim\*

Department of Life Sciences, Multidisciplinary Genome Institute, Hallym University

B007

### Synergistic Effect of Antimicrobial Substances from Some Bacteria against Human Skin Pathogens

Da-Sol Lee and Hong-Gyu Song\*

Department of Biological Sciences, Kangwon National University

B008

### Aflatoxin B<sub>1</sub> Biodegradation and Inhibition against Aflatoxigenic Fungi by *Streptomyces* spp.

Ji-Seon Hwang and Hong-Gyu Song\*

Department of Biological Sciences, Kangwon National University

B009

### Bacterial Degradation of Ochratoxin A and Growth Inhibition of Ochratoxigenic *Aspergillus* spp.

Ho-Yeong Choi and Hong-Gyu Song\*

Department of Biological Sciences, Kangwon National University

B010

### Insight the Genome of *Lacinutrix venerupis* Strain DOK2-8 Isolated from Dokdo, Republic of Korea

Se Ra Lim<sup>1,2</sup> and Ji Hyung Kim<sup>1\*</sup>

<sup>1</sup>Infectious Disease Research Center, Korea Research Institute of Bioscience and Biotechnology, <sup>2</sup>Bio-Analytical Science Division, University of Science and Technology

B011

### An *in vitro* Study to Assess the Impact of Tetracycline on the Human Intestinal Microbiome

Ji Young Jung

Applied Bioresources Research Division, Freshwater Bioresources Utilization Bureau, Nakdonggang National Institute of Biological Resources (NNIBR)

B012

### Characterization of Root-associated Microbiome Inhabiting in Different Compartments of Tomato Plants

Shin Ae Lee<sup>1</sup>, Yiseul Kim<sup>1</sup>, Jae-Ho Joa<sup>2</sup>, Bora Chu<sup>1</sup>, Mee Kyung Sang<sup>1</sup>, Jaekyeong Song<sup>1</sup>, and Hang-Yeon Weon<sup>1\*</sup>

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Ha Ju Park<sup>a</sup>, Jung Ho Kim<sup>b</sup>, Ui Joung Youn<sup>a</sup>, Angélica Casanova-Katny<sup>c</sup>, Soon Gyu Hong<sup>a</sup>, and Dockyu Kim<sup>a,\*</sup>

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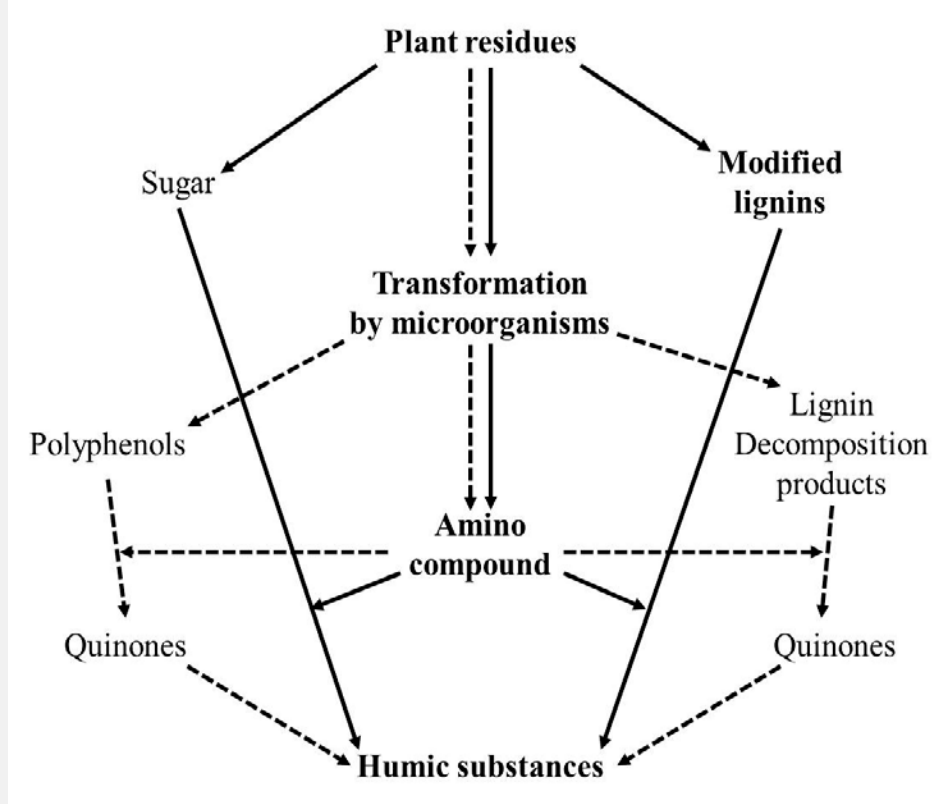
<sup>c</sup> School of Environmental Science, Catholic University of Temuco, Rudecindo Ortega 02950, Temuco, Chile

## ABSTRACT

Although the maritime Antarctic has undergone rapid warming, the effects on indigenous soil-inhabiting microorganisms are not well known. Artificial warming experiments using open-top chamber (OTC) have been performed on the Fildes Peninsula in the maritime Antarctic since 2008. When the soil temperature was measured at a depth of 2–5 cm during the 2013–2015 summer seasons, the mean temperature inside OTC (OTC-In) increased by approximately 0.8°C compared with outside OTC (OTC-Out), while soil chemical and physical characteristics were not changed. Soils from OTC-In and OTC-Out were subjected to analysis for change in microbial community and degradation rate of humic substances (HS, the largest pool of recalcitrant organic carbon). Archaeal and bacterial communities in OTC-In were minimally affected by warming compared with those in OTC-Out, with archaeal methanogenic *Thermoplasmata* slightly increased in abundance. The abundance of heterotrophic fungi *Ascomycota* was significantly altered in OTC-In. Total bacterial and fungal biomass in OTC-In increased by 20% compared to OTC-Out, indicating that this may be due to increased microbial degradation activity for soil organic matter (SOM) including HS, which would result in the release of more low-molecular-weight growth substrates from SOM. Despite the effects of warming on the microbial community over the 8-years-experiments warming did not induce any detectable change in content or structure of polymeric HS. This work was supported by grant to KOPRI (PE18090)

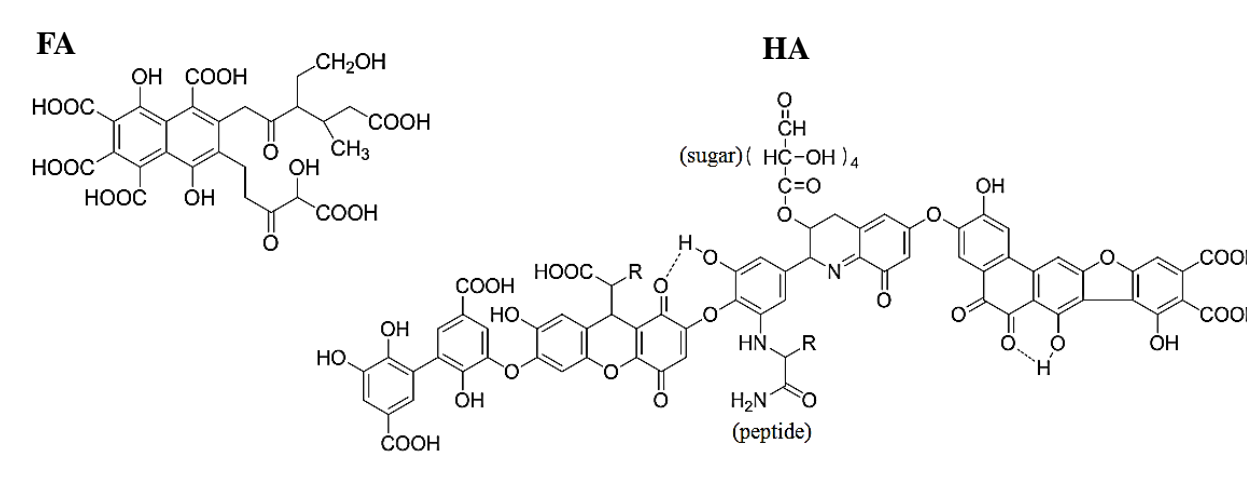
## INTRODUCTION

### Humification processes

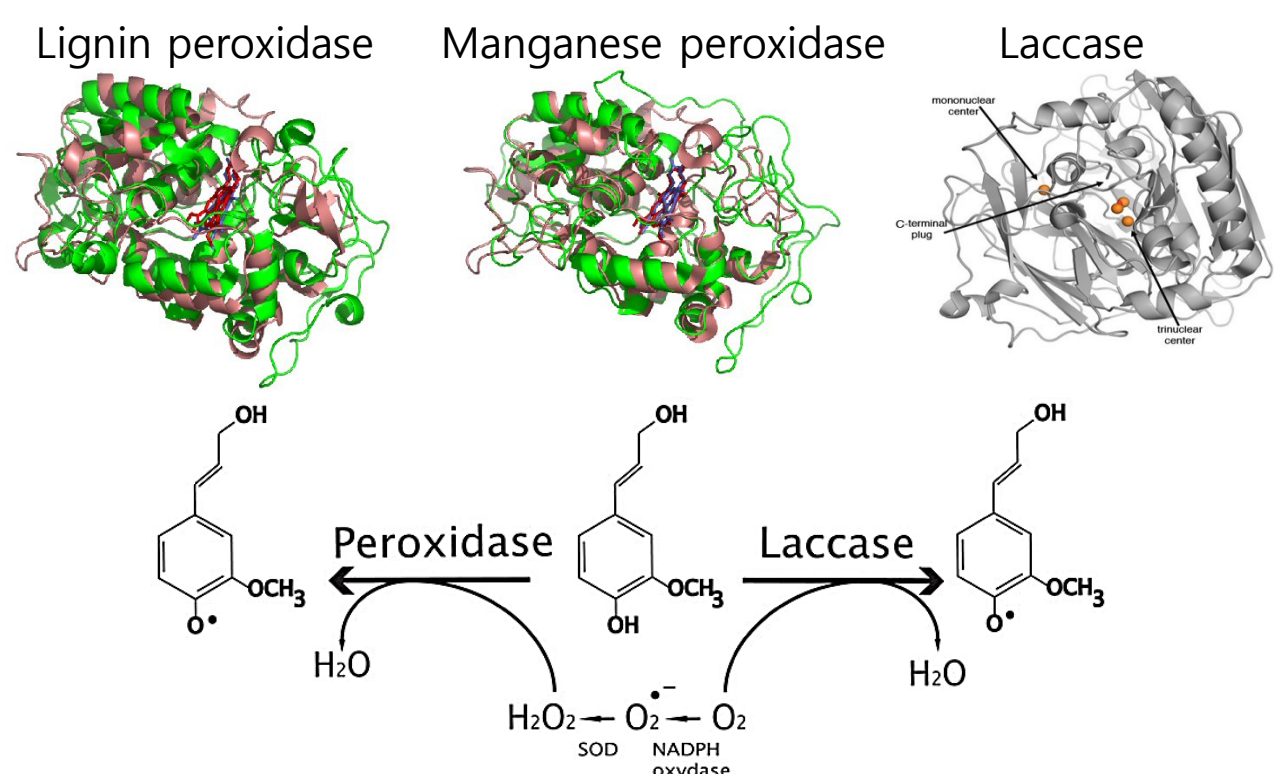


### Main fractions of HS

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
Humin	Insoluble	Insoluble	-

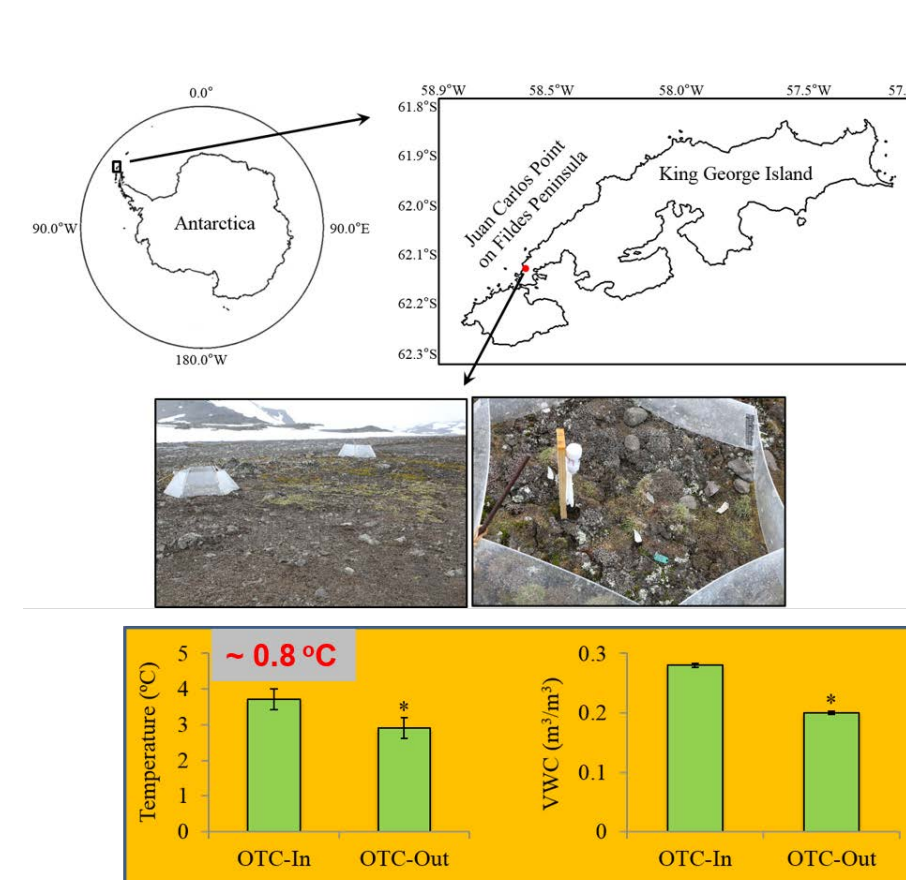


### Nonspecific oxidizing enzymes for initial HS degradation (proposed)

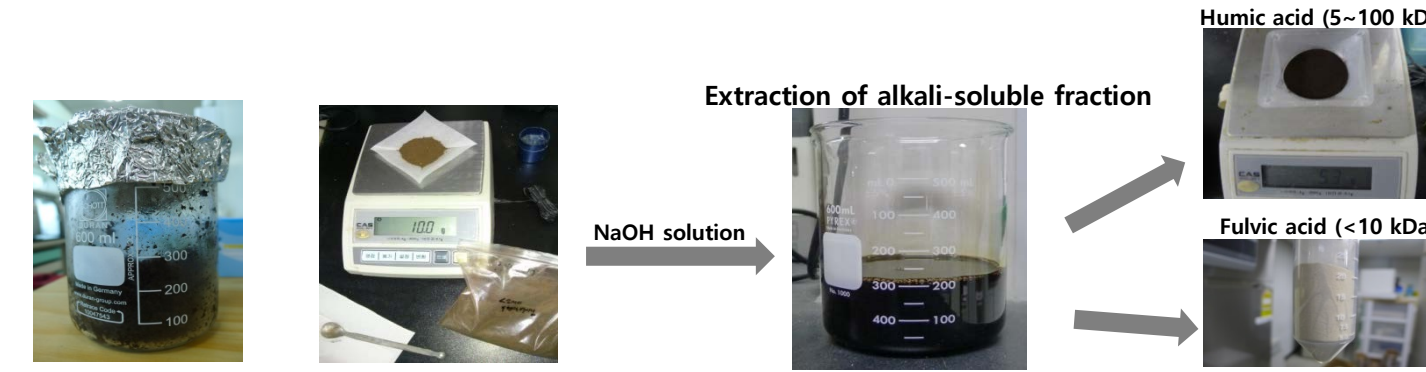


## METHODS

### - Sampling site and open top chamber (OTC) installation



### - HA and FA extraction and content measuring



### - NMR-based structural analysis of HA and FA

### - Microbial community analysis (16S rRNA gene pyrosequencing & PLFA)

## RESULTS

Table 1. Soil chemical and physical characteristics inside the OTCs (OTC-In) and in control plots (OTC-Out)

Sample	Chemical and physical characteristics of soil							
	EC (μs/m)	pH	% N	% C	C/N	% sand	% lime	% clay
OTC-Out	59.6 (±16.8)	6.5 (±0.2)	0.094 (±0.021)	0.968 (±0.218)	10.3 (±0.4)	71.7 (±2.6)	23.7 (±2.1)	4.5 (±0.5)
OTC-In	64.4 (±23.7)	6.6 (±0.3)	0.092 (±0.018)	0.994 (±0.171)	10.8 (±0.7)	69.6 (±3.1)	25.2 (±2.6)	5.2 (±0.5)

The statistical data are the mean values of three independent analyses for each OTC-Out and OTC-In soil.

Table 2. Summary of pyrosequencing results and statistical analyses of microbial communities in soil samples from open-top chamber (OTC) passive warming experimental sites

Target microorganism		Number of reads	OTU richness			OTU diversity (Shannon)
			Observed	Chao1	ACE	
Bacteria	OTC-Out	8064±1030	1783±276	3016±422	4007±494	6.49±0.08
	OTC-In	6888±364	1917±399	3301±1022	4425±1632	6.74±0.24
Archaea	OTC-Out	5919±3883	34±10	39±11	44±14	1.48±0.48
	OTC-In	6167±4824	28±13	31±13	31±13	1.42±0.68
Fungi	OTC-Out	8826±2049	463±74	576±69	581±69	4.39±0.70
	OTC-In	9987±1006	401±25	524±49	505±40	3.98±0.05

The statistical data are the mean values of three independent analyses for each OTC-Out and OTC-In soil.

Table 3. Quantity of fungal and bacterial phospholipid-derived fatty acids (PLFAs) in soil samples from open-top chamber (OTC) passive warming experimental sites

	Amount of phospholipid fatty acids (mg/kg soil)	
	OTC-Out	OTC-In
Fungi	6.8	8.0
Bacteria	5.8	7.5
Gram+	3.2	4.4
Gram-	1.8	2.0
Actinomycete	0.8	1.1
Total	12.6	15.5
Ratio of fungal/bacterial biomass	1.17	1.07

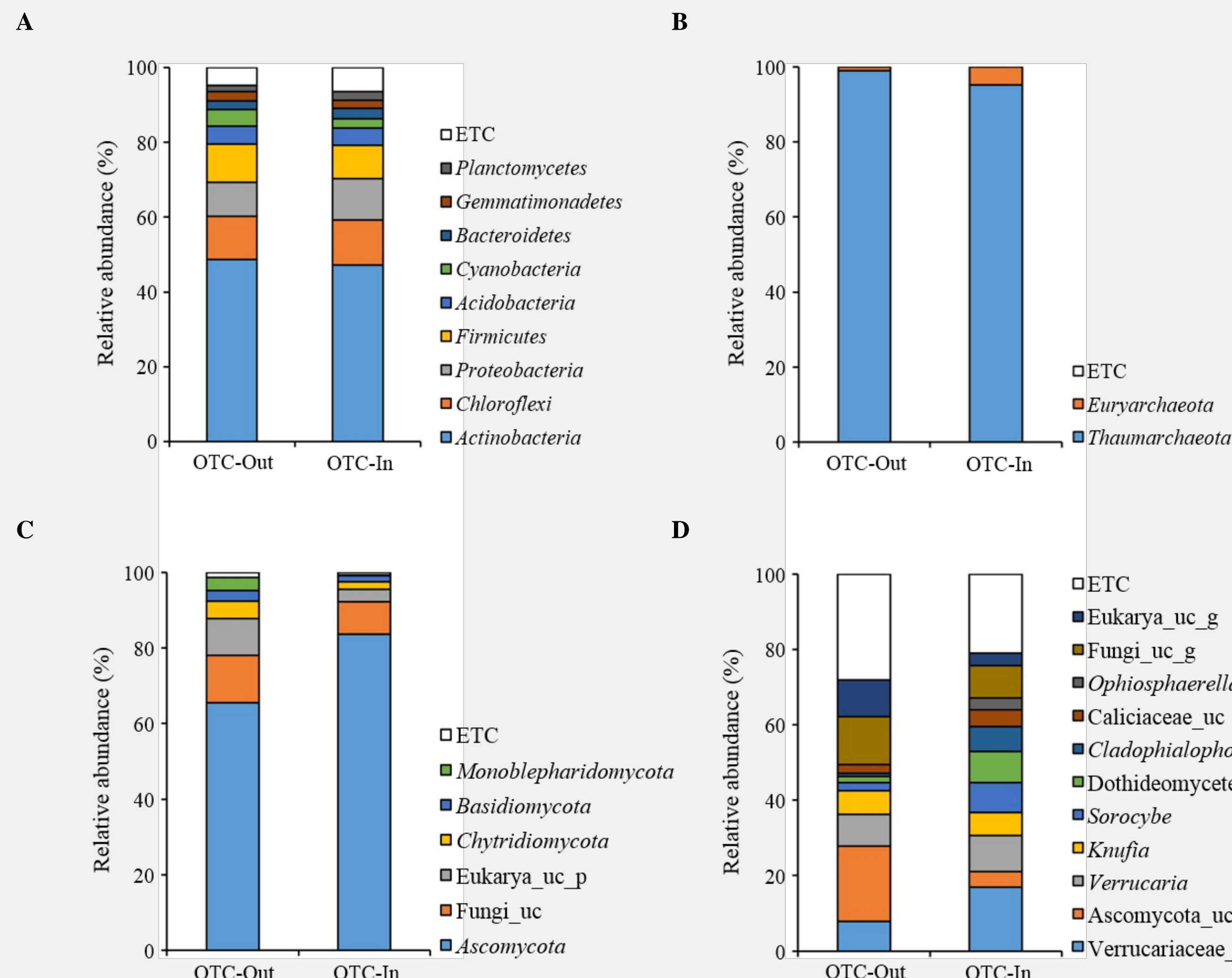


Fig. 1. Changes in abundance and taxonomic composition of soil microbes induced by the OTC warming experiment. Relative abundances of (a) bacterial phyla, (b) archaeal phyla, (c) fungal phyla, and (d) different genera within the fungal phylum *Ascomycota* are shown. ETC denotes the sum of minor taxa (< 1.0% in relative abundance). Relative abundances are the mean values of three independent analyses for each OTC-Out and OTC-In soil.

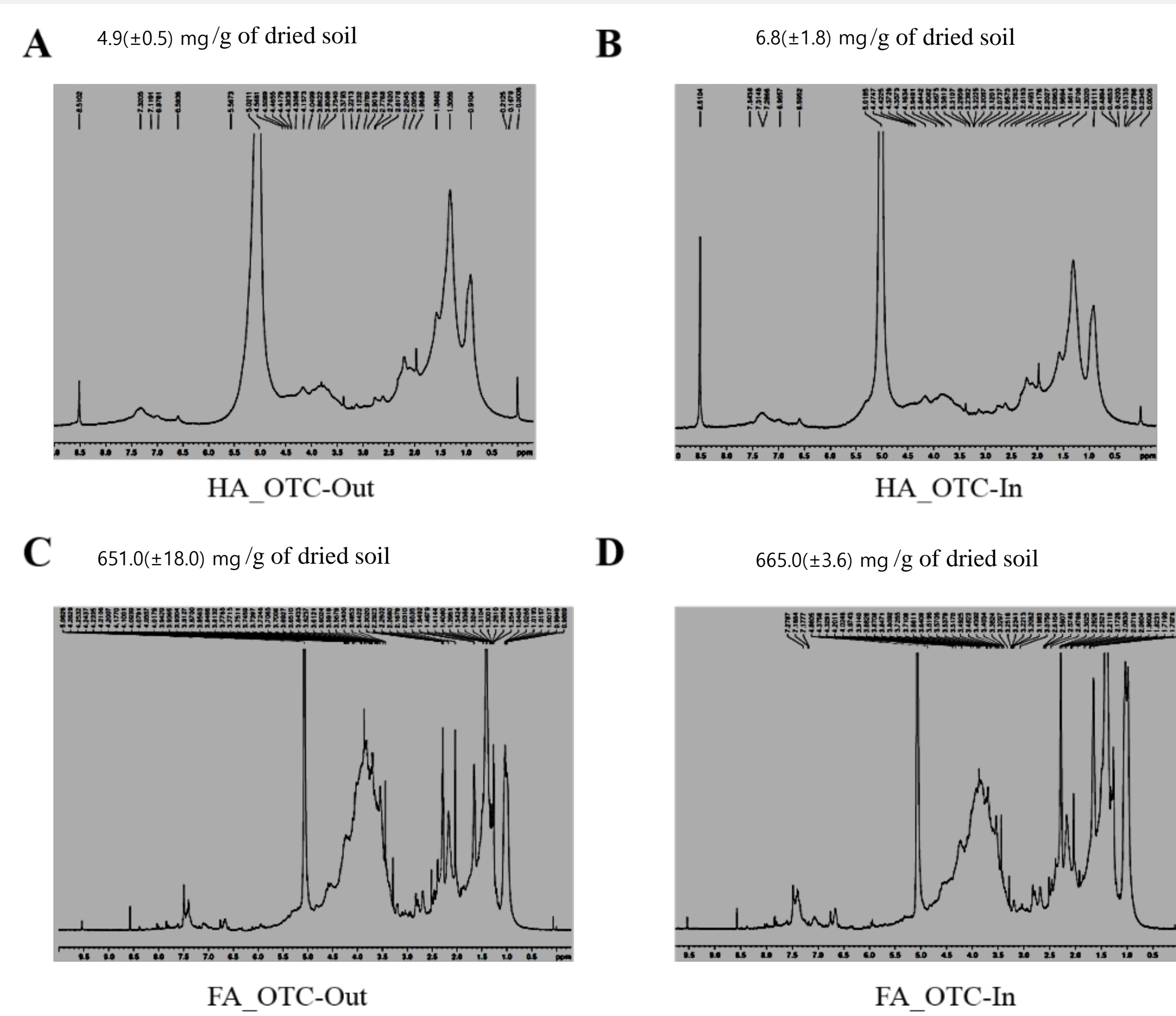


Fig. 2. <sup>1</sup>H-NMR spectral analysis of humic acid (HA) and fulvic acid (FA) in OTC warming experimental soils. (a) HA in OTC-Out; (b) HA in OTC-In; (c) FA in OTC-Out; (d) FA in OTC-In.