Changes of soil microbes related with carbon and nitrogen cycling after long-term CO_2 enrichment in a typical Chinese maize field

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8th GLOBAL NITROGEN CONFERENCE
30 MAY – 3 JUNE 2021 | ONLINE

Introduction

- Rising atmospheric CO_2 concentration may lead to an increased input of available C from plants to the soil through rhizodeposition and may affect soil microbes with implications for the interaction between the C- and N-cycling.

- Changes of soil functional microbes associated with C- and N-cycling under long-term elevated CO_2 level (eCO_2) suggest concomitant alterations of microbial biomass, N availability and gaseous N emissions.

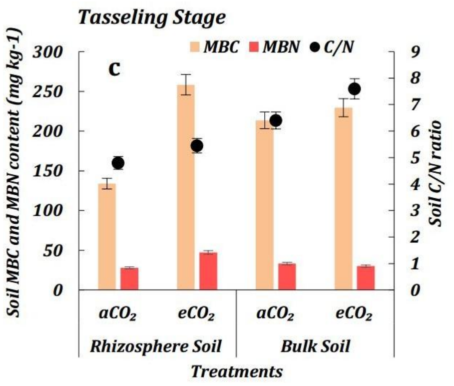


Fig.1 Effects of eCO_2 on MBC and MBN

Objectives

- To investigate the impacts of 10-year eCO_2 onthe microbial abundance and composition in both rhizospheric and bulk soils, based on functional marker genes for ammonia oxidation (bacterial *amoA*) and denitrification (*nirK*, *nirS*, *nosZ*), as well as fungi (ITS) and bacteria (16S rRNA).

- To examine the responses of soil microbial biomass (microbial biomass-C and -N) and soil N availability (mineral N) in both rhizospheric and bulk soils to long-term eCO_2.

Table 1. The copy number of 16s rDNA and ITS in rhizospheric and bulk soil of maize at tasseling stage under elevated CO_2 concentration. Data are the mean ± S.E., n = 3. Different letters indicate significants differences among CO_2 concentration, rhizophere and bulk soil at $p < 0.05$.

Treatment	16s rDNA (*10^9)	ITS (*10^7)	16s rDNA/ITS
aCO_2-R	2.36 ± 0.28 a	1.58 ± 0.05 b	149.38 b
eCO_2-R	1.77 ± 0.10 b	2.01 ± 0.16 a	88.67 c
aCO_2-B	1.37 ± 0.30 c	0.16 ± 0.02 d	547.90 a
eCO_2-B	1.95 ± 0.26 b	1.21 ± 0.09 c	137.35 b

Table 2. The copy number of AOB, nirS, nirK and nosZ in rhizospheric and bulk soil of maize at tasseling stage under elevated CO_2 concentration. Data are the mean ± S.E., n = 3. Different letters indicate significants differences among CO_2 concentration, rhizophere and bulk soil at $p < 0.05$.

Treatment	AOB (10^7)	nirS (*10^6)	nirK (*10^9)	nosZ (*10^8)	nosZ/ (nirS + nirK)
aCO_2-R	6.38 ± 0.10 b	2.77 ± 0.17 d	4.64 ± 0.30 b	4.75 ± 0.48 c	0.16 b
eCO_2-R	6.56 ± 0.39 b	6.31 ± 0.37 b	7.63 ± 0.13 a	25.41 ± 5.53 b	0.59 a
aCO_2-B	6.58 ± 0.99 b	3.54 ± 0.39 c	5.29 ± 0.82 ab	8.56 ± 0.84 c	0.10 b
eCO_2-B	7.54 ± 0.23 a	9.29 ± 0.54 a	6.39 ± 0.55 ab	52.3 ± 2.51 a	0.33 ab

Materials & Methods

1. FACE experiment

- Ambient CO_2 (aCO_2, 400 ppm)
- Elevated CO_2 (eCO_2, 550 ppm)

2. Studied soil

- Rhizospheric soil and bulk soil at 0-20 cm depth at tasseling stage of maize growth period

3. Measurements

- Ammonium and nitrate concentrations
- Microbial biomass-C and -N (MBC and MBN)
- Quantity of microbial groups based on qPCR
- Composition of microbial communities based on DNA sequencing.

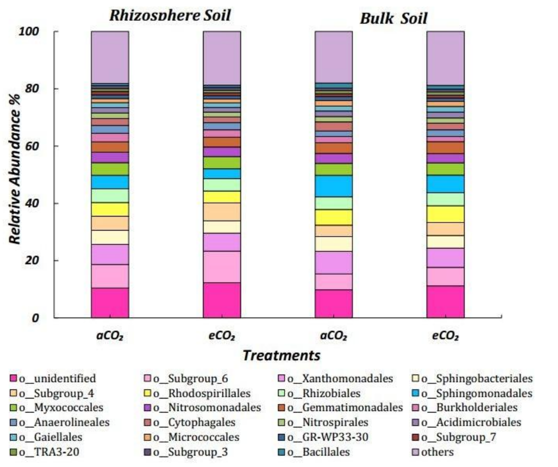


Fig.2 The composition of 16S rRNA at order level

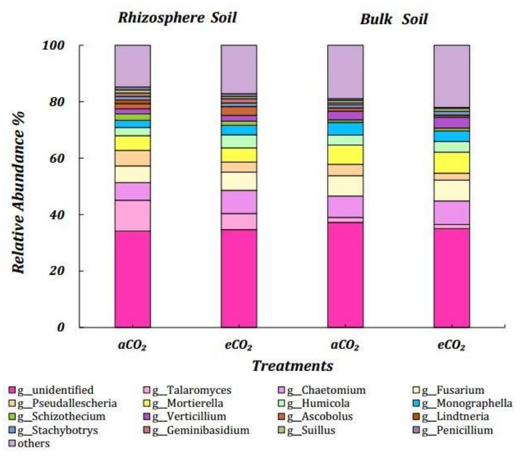


Fig.3 The composition of ITS at genus level

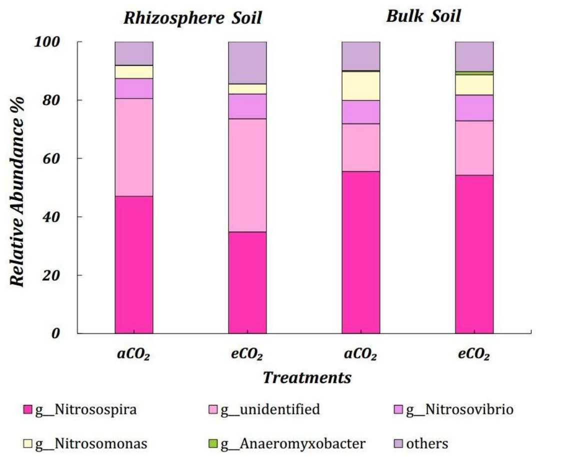
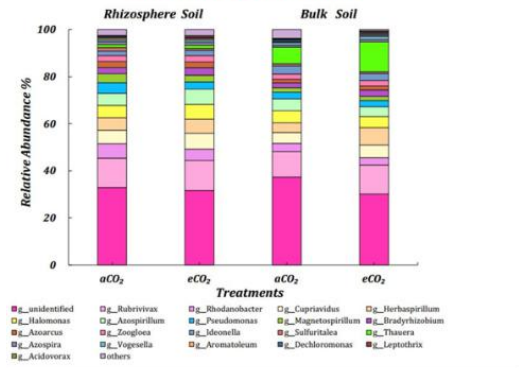
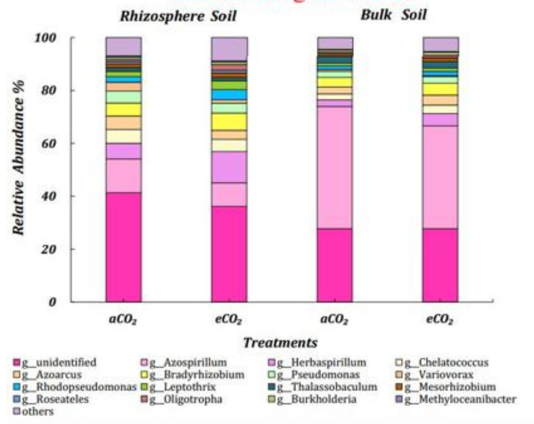


Fig.4 The composition of AOB at genus level

nirS at the genus level



nosZ at the genus level



nirK at the genus level

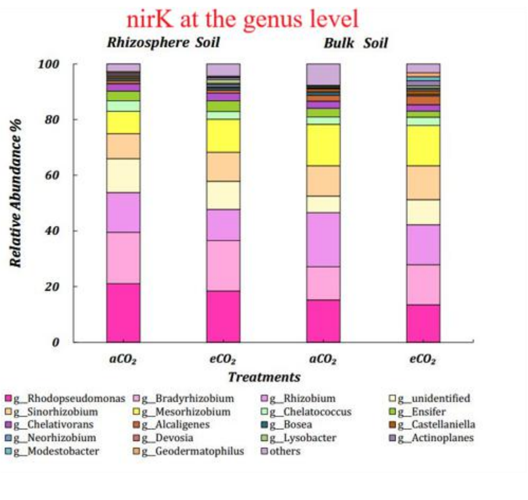


Fig.5 The composition of nirS, nirK and nosZ

Results & Discussion

1. MBC and MBN in rhizospheric soil were significantly increased under eCO_2. This may due to the increased roots exudates and root exfoliations induced by eCO_2.

2. In rhizospheric soil, increased quantity of fungi under eCO_2 and reduced bacterial quantity were observed, illustrating that the effect of eCO_2 mainly reflected in the increase of fungi.

3. For bacterial community, *Sphingomonadales* that can produce catalase, was declined in relative abundance under eCO_2, suggesting that oxygen content may be altered under eCO_2. For fungal communities, Chaetomium and Humicola that can synthesize cellulase, hemicellulase and amylase, were increased in relative abundance under eCO_2, possibly due to the increase in dead root litter.

4. The quantity of AOB and denitrifiers were promoted under eCO_2, particularly in rhizospheric soil.

5. The changes of microbial cummunity compositions associated with N-cycling were reflected on the decrease in Nitrosospira for AOB, increase in Mesorhizobium for *nirK*, increase in Herbaspirillum and Bradyrhizobium for *nosZ*.

Conclusion

Ten years of CO_2 enrichment did not significantly change the cummunity compositions of functional microbes associated with C- and N-cycling, possibly due to the differences in the form and quantity of soil C and N under eCO_2, especially in rhizospheric soil.

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