Differential response of soil CO_2, CH_4, and N_2O emissions to edaphic properties and microbial attributes following afforestation in central China

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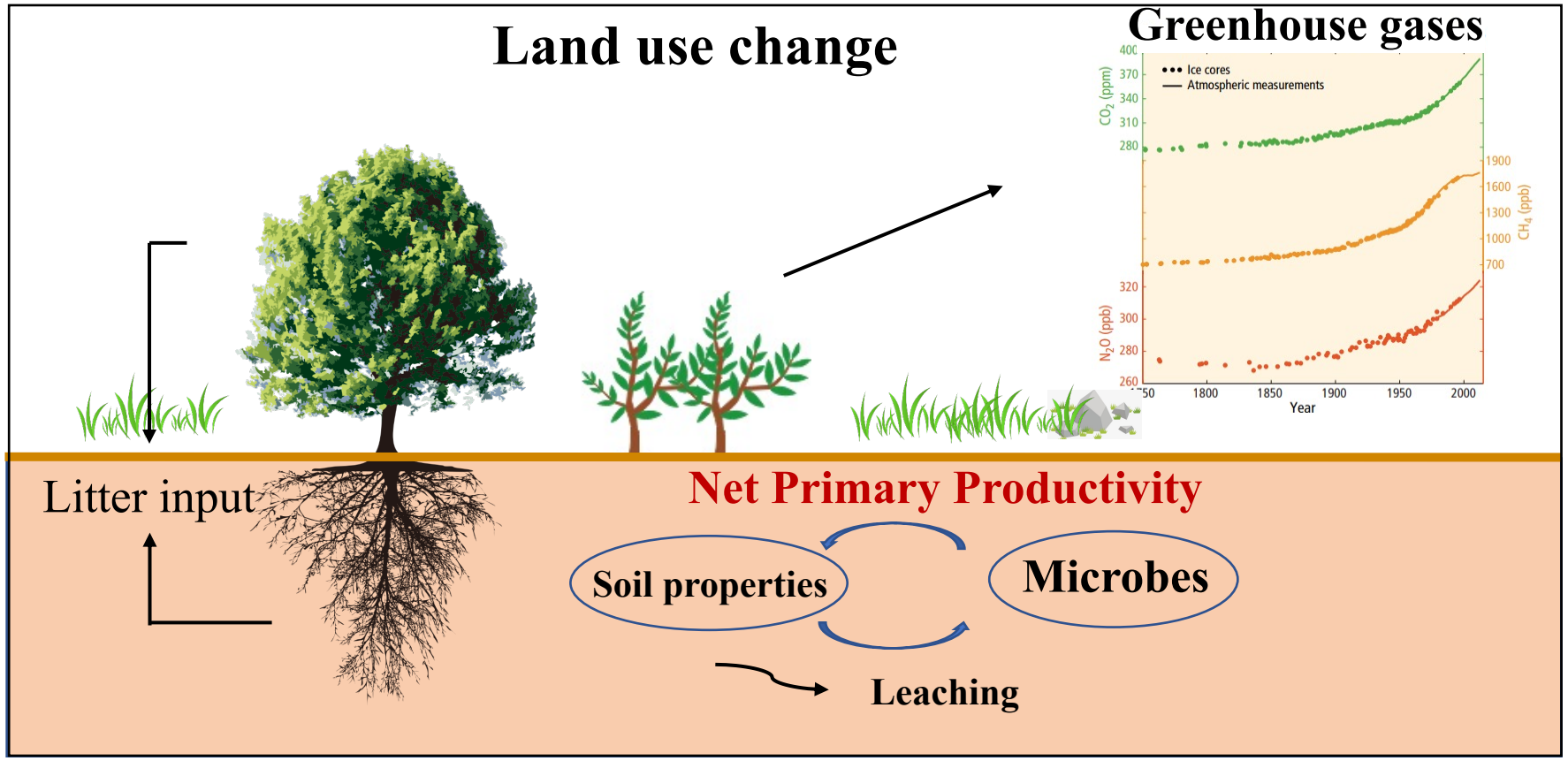
BACKGROUND



CO_2

CH_4

N_2O

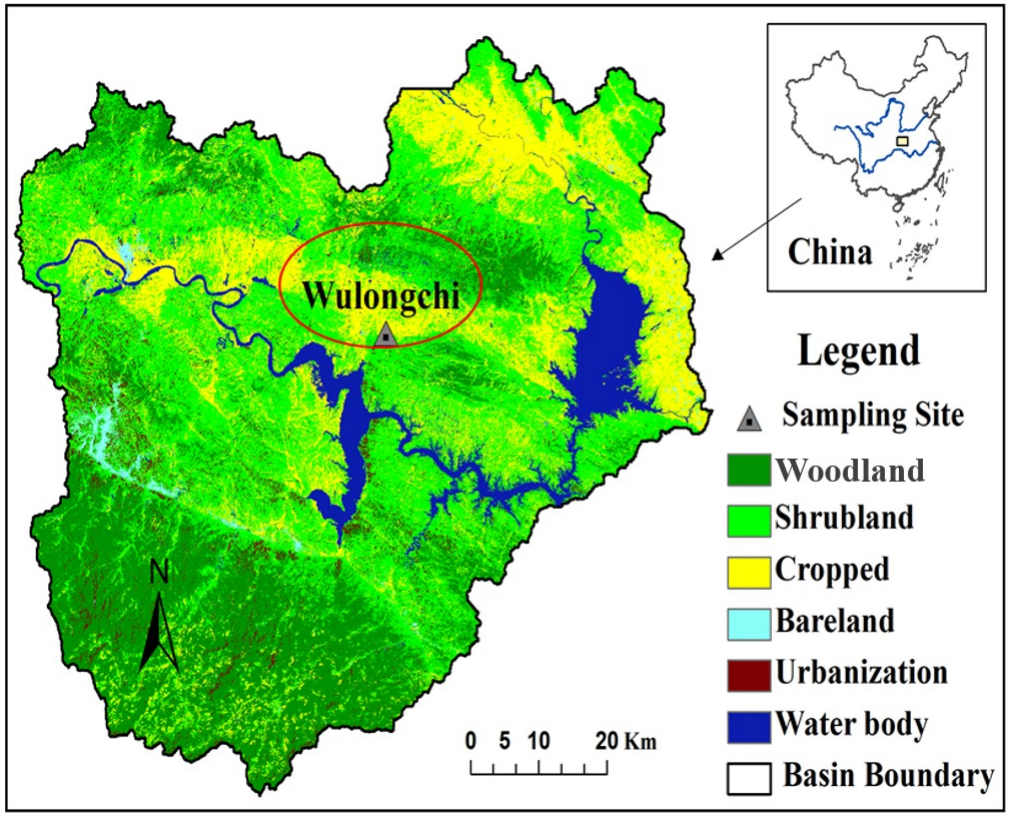
- Land use change has been identified as the large anthropogenic source and sink of greenhouse gas emission
- Microorganisms participate in the greenhouse gas emission

Elser et al., EL, 2007; Nazaries et al., ISME, 2011; Han et al., GCB, 2020; Tian et al., 2019, GCB

OBJECTIVE

- To examine the influences of the afforestation on **soil greenhouse gases emissions**, and to explore the **underlying mechanisms** on how variations in the soil environmental/microbial properties control soil greenhouse gases emissions.

STUDY SITE

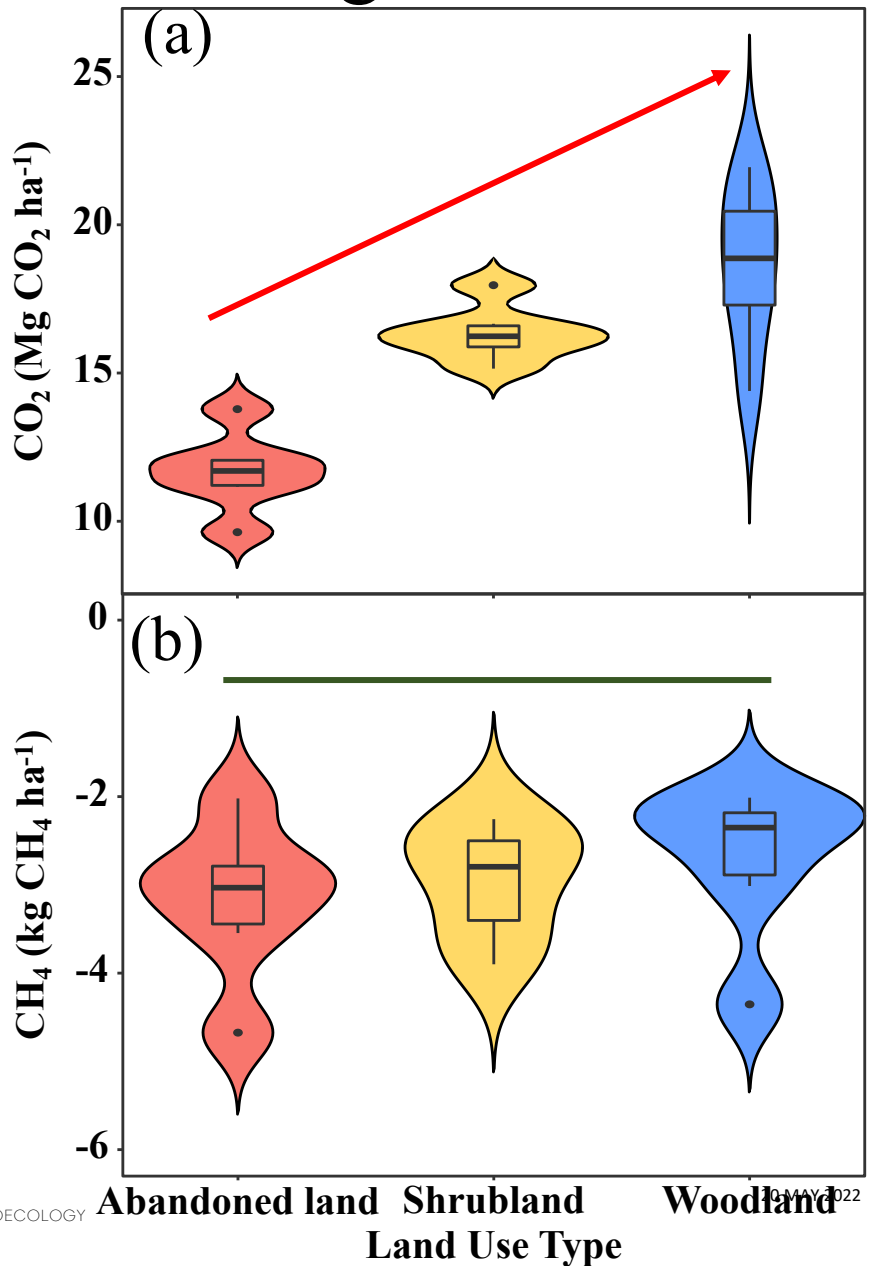


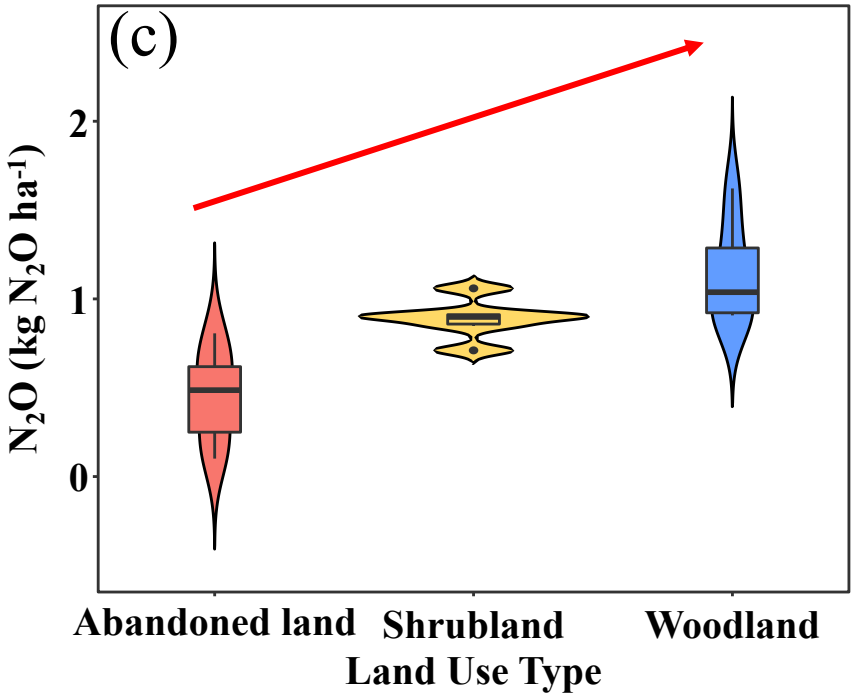
Static chambers

Greenhouse gases	Typical microbes	Class
CO_2	Total PLFAs	
CH_4	18:1ω7c	Methanotroph
N_2O	AOA, AOB	Nitrifying genes
	nirS, *nirK*, *nosZ*	Denitrifying genes

Tian et al., 2019, Global Change Biology

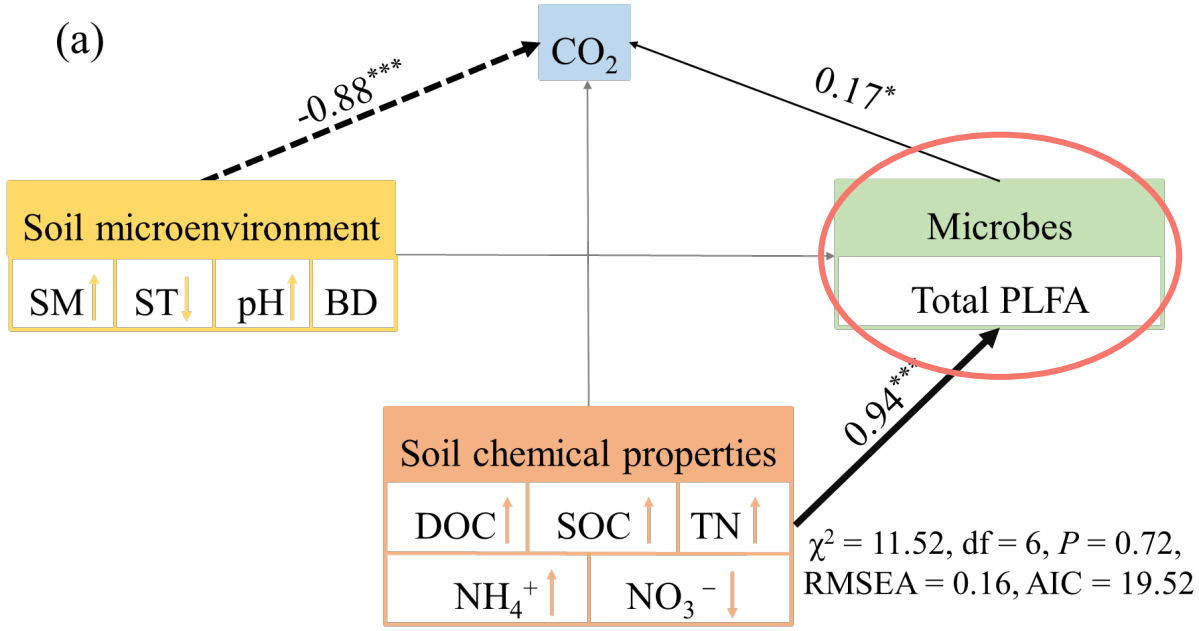
RESULTS: Soil greenhouse emissions

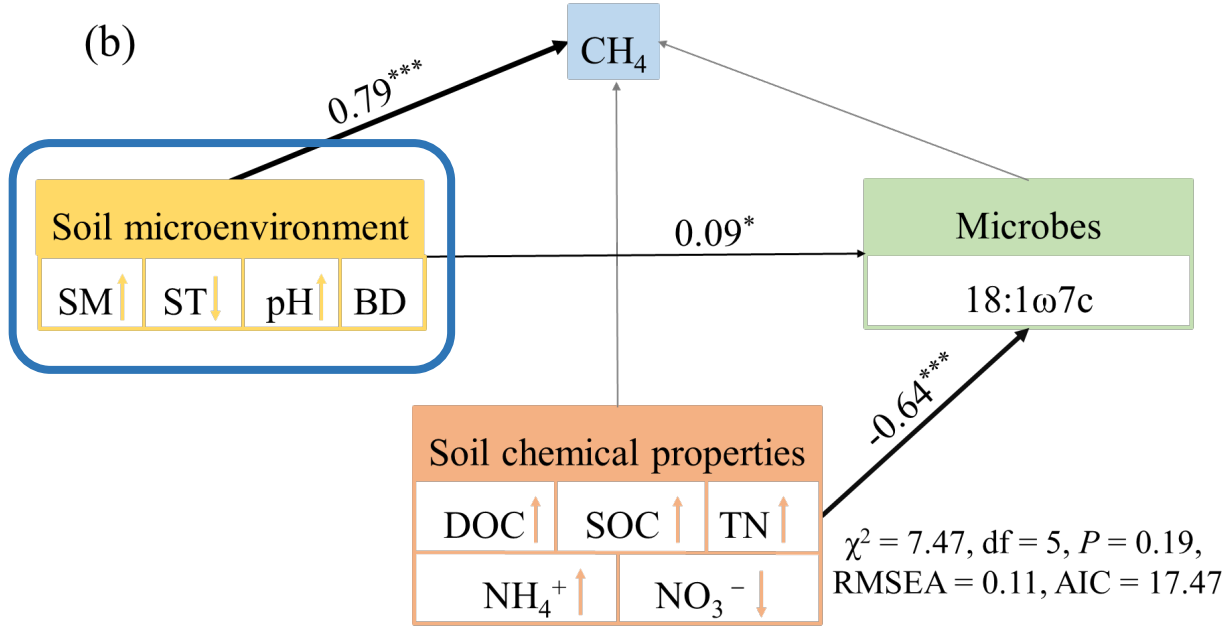




- CO_2/N_2O: Woodland > Shrubland > Abandoned land
- CH_4: No Significance

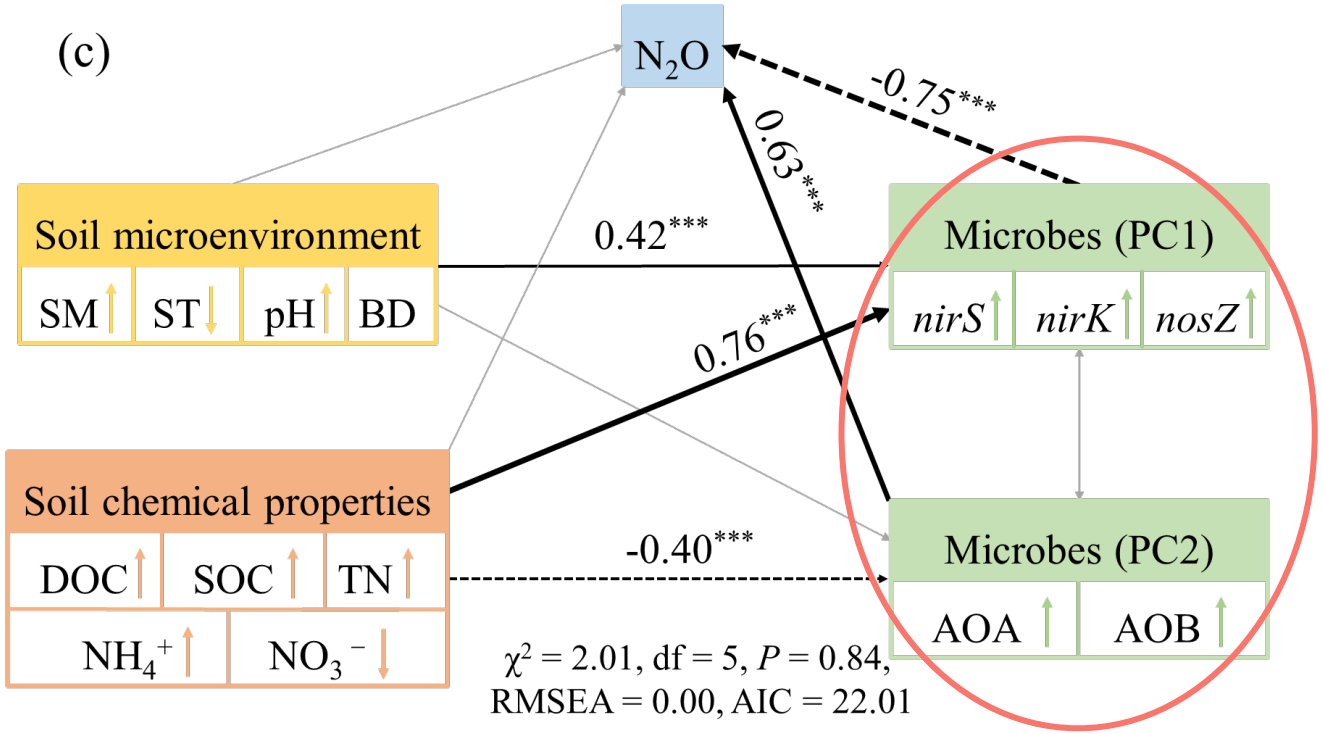
RESULTS: Drivers over greenhouse emissions

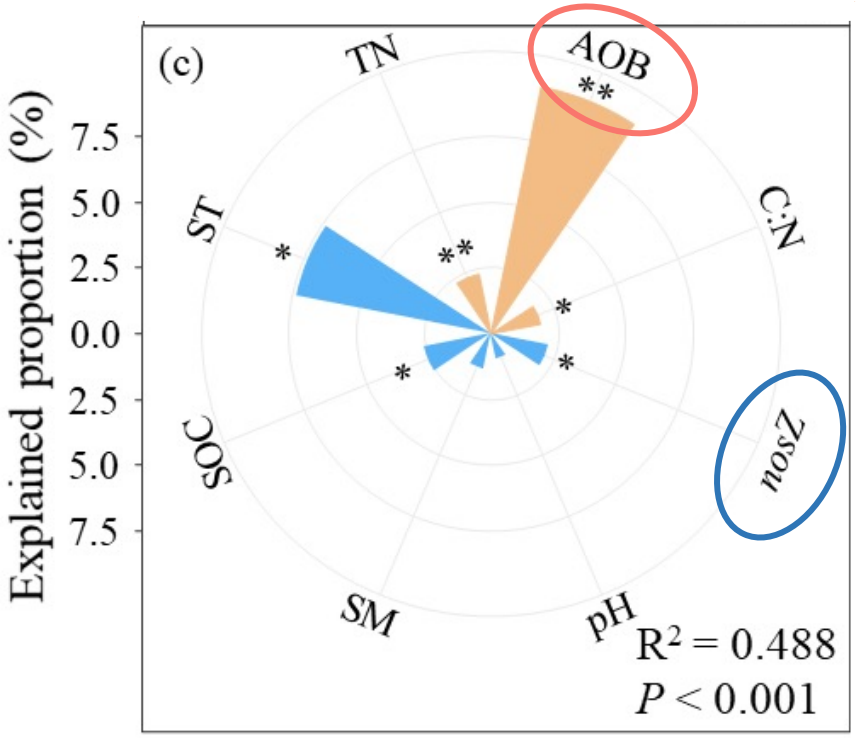




- CO_2: microbes (PLFAs)
  - plant residue & root exudation
- CH_4: soil microenvironment
  - methane oxidation & methane reduction

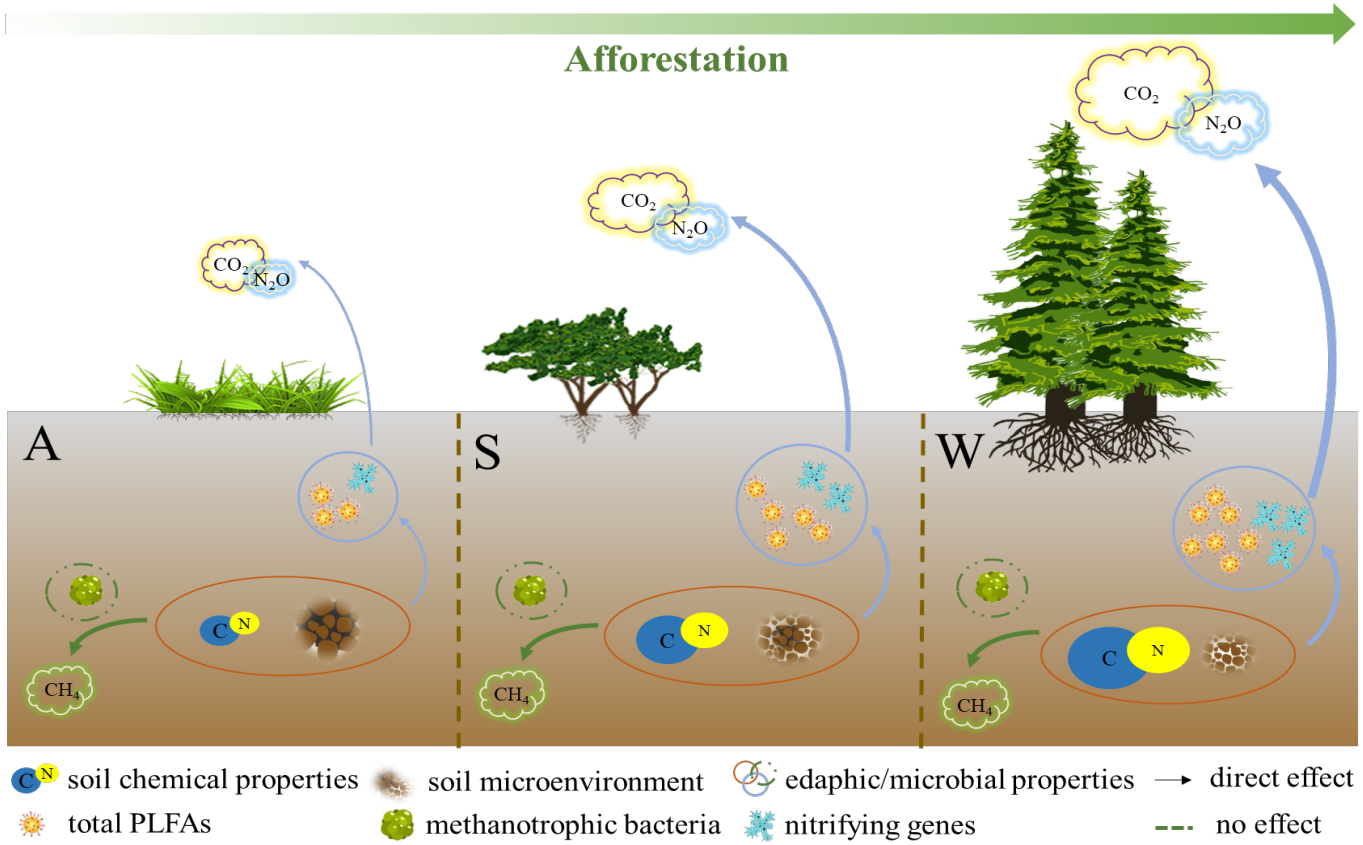
RESULTS: Drivers over greenhouse emissions





- N_2O: microbes AOB (+) *nosZ* (−)
- niche differentiation of AOA/AOB $N_2O - N_2$

CONCLUSIONS



- Soil CO_2 and N_2O emissions were higher under afforestation, which were directly dependent on microbial attributes across land use types
- Soil CH_4 uptake did not differ among all land use types, which was directly related to edaphic properties