

Linkage of N₂O emission to functional gene abundance in an intensively managed calcareous flu-aquic soil



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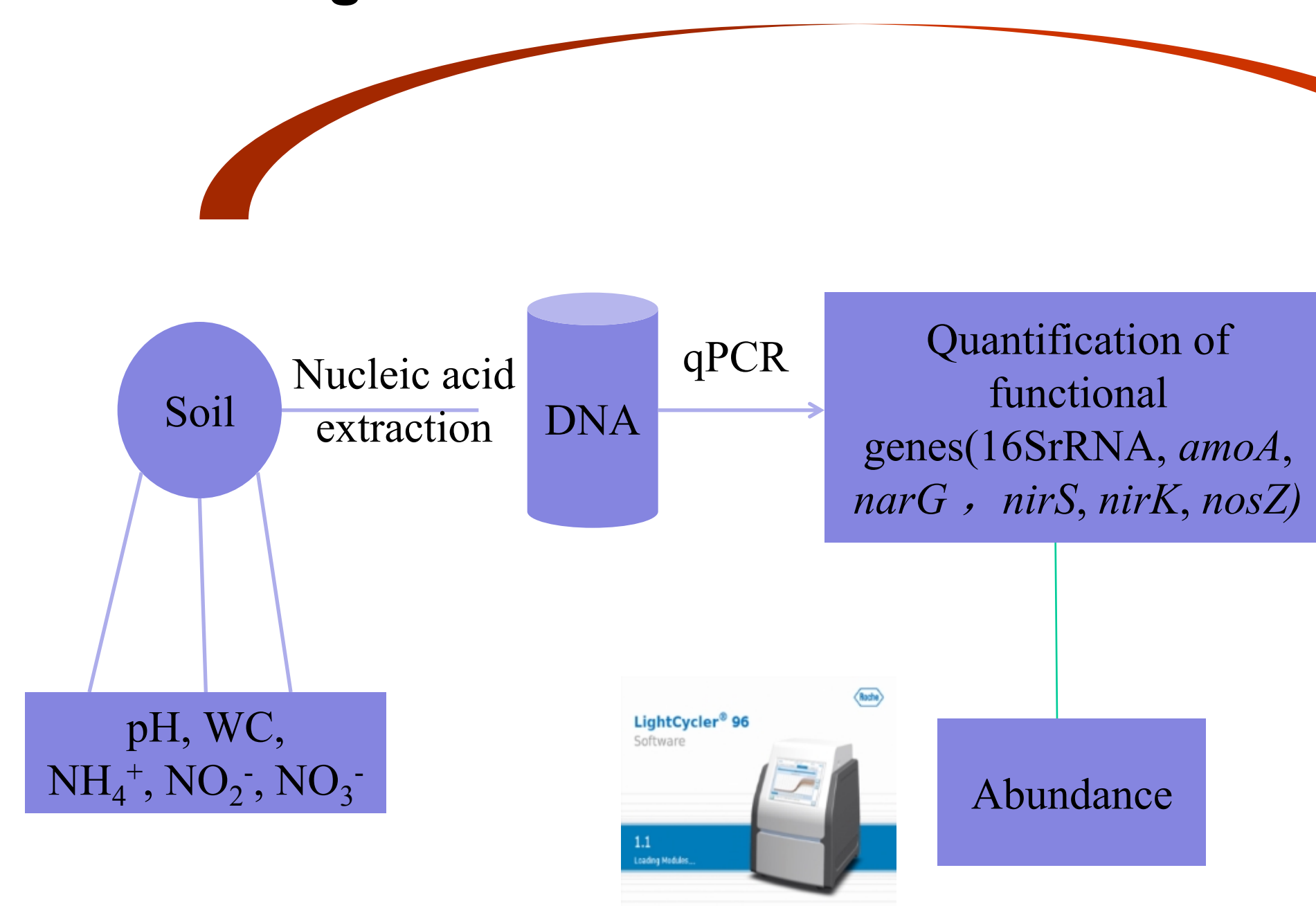
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Introduction: N₂O is a powerful long-lived greenhouse gas and has **300-times** stronger warming effect than carbon dioxide in the troposphere on a 100-yr time horizon¹; It comes from **both natural and anthropogenic sources** and **agricultural soils with nitrogen fertilizers or/and manure** are mainly anthropogenic sources which contributed **up to 66%** of current anthropogenic N₂O emissions at global scale²; Large amounts of N fertilizer and irrigation lead to substantial total N₂O emissions in North China Plain, which has become a **'hotspot' of national N₂O emissions** with global significance³. A better understanding of the processes, mechanisms and factors controlling N₂O production and emission is a prerequisite for managing agricultural N₂O emissions.

Scientific Questions: How does the **abundance** of *amoA* gene of bacteria response to short-term fertilization? What's the **linkage between annual N₂O emission and abundance of functional genes** including *amoA* of bacteria, *narG*, *nirS*, *nirK*, *nosZ* and 16S rRNA gene? How does long-term nitrogen and carbon management **affect this linkage**?

Methods



Treatment code	Nitrogen and straw management
N ₀	Zero N application, wheat and maize straw removal
N _{opt}	Improved N _{min} test, wheat and maize straw removal
CN _{opt}	Improved N _{min} test, wheat straw mulching and maize straw return
CM	Cattle manure with chemical fertilizer N based on N balance calculation, wheat straw mulching and maize straw return

Results

Table 1. Spearman's rank correlation matrix of annual N₂O emission, some soil properties, abundances of functional genes and 16S rRNA gene

N ₂ O ^a	1	1.00												
TN ^b	2	0.76**	1.00											
TOC ^c	3	0.66*	0.84**	1.00										
PNR ^d	4	0.53	0.52	0.60*	1.00									
PDR ^e	5	0.83**	0.76*	0.81**	0.75**	1.00								
<i>amoA</i>	6	0.71*	0.34	0.53	0.73**	0.72**	1.00							
<i>narG</i>	7	0.74**	0.79**	0.78**	0.69*	0.90**	0.61*	1.00						
<i>nirS</i>	8	0.70**	0.82**	0.75**	0.71*	0.83**	0.59*	0.92**	1.00					
<i>nirK</i>	9	0.71**	0.69*	0.84**	0.75**	0.93**	0.77**	0.93**	0.85**	1.00				
<i>nosZ</i>	10	0.72**	0.59*	0.71**	0.75**	0.90**	0.82**	0.92**	0.85**	0.97**	1.00			
16S rRNA	11	0.78**	0.78**	0.80**	0.71**	0.93**	0.68*	0.98**	0.92**	0.96**	0.95**	1.00		
		1	2	3	4	5	6	7	8	9	10	11		

p*<0.05; *p*<0.01; ^aAnnual N₂O emission in 2012-2013 winter wheat-summer maize rotation

^bTotal nitrogen concentration in the soil; ^cTotal organic carbon

^dPotential nitrification rate; ^ePotential denitrification rate

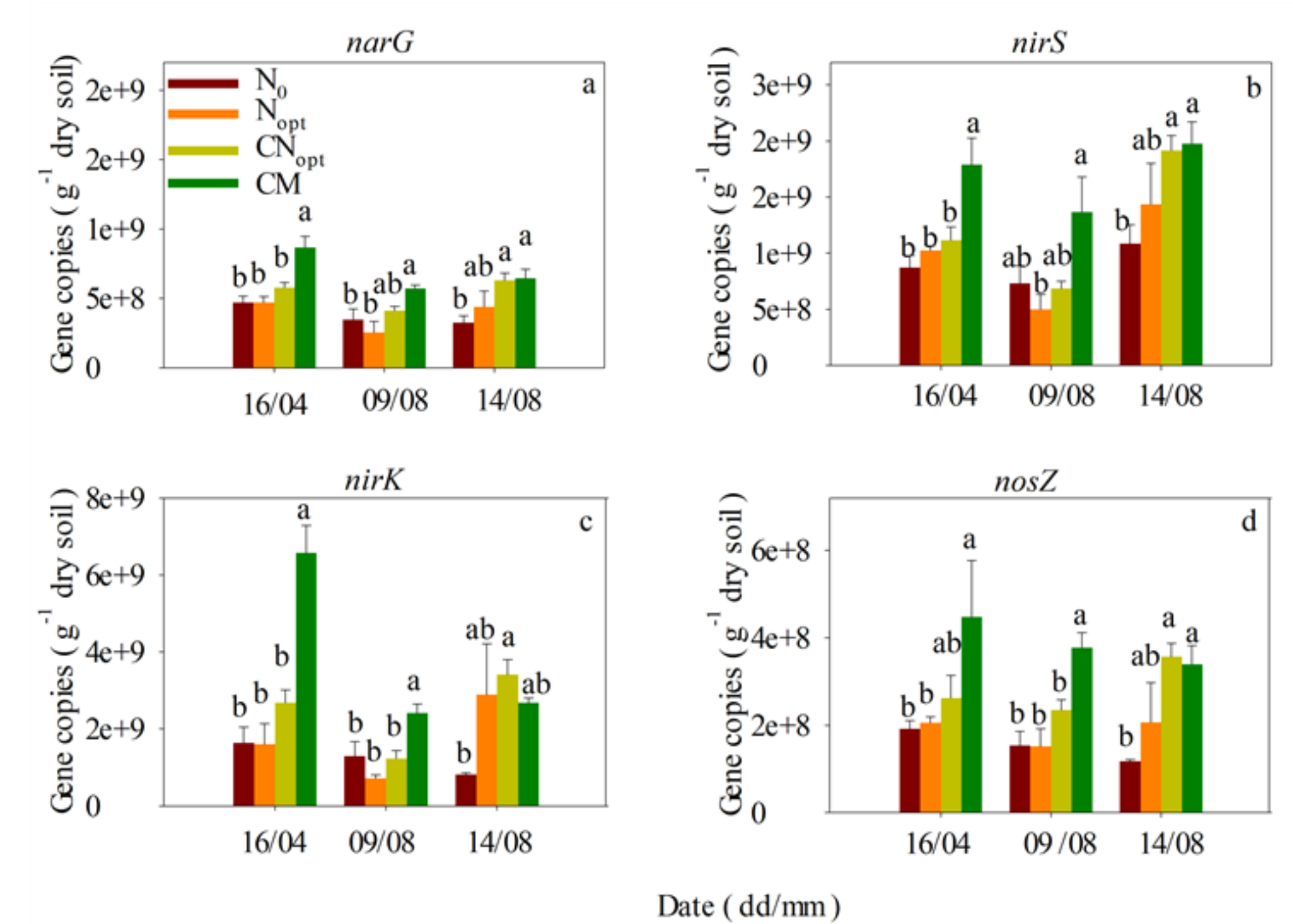


Fig. 3 Gene copies of the nitrate reductase gene (*narG*), nitrite reductase genes (*nirS*) and (*nirK*) and the N₂O reductase gene (*nosZ*) of different treatments in 0-20cm soil depth in sampling dates in 2013. Different letters indicate significant difference (*P* < 0.05) among treatments.

Conclusion

Our study highlights the linkage of instant high N₂O emission peaks with the abundance of the bacterial *amoA* gene for nitrification and of annual N₂O emissions and small N₂O pulse after rainfall or irrigation with the abundance of denitrification genes, providing insight into the mechanism of N₂O production and the factors controlled by distal and proximal drivers in this intensively managed calcareous fluvo-aquic soil. These findings will help to draw the pertinence measures for mitigating N₂O emissions in this 'hotspot' region.

References

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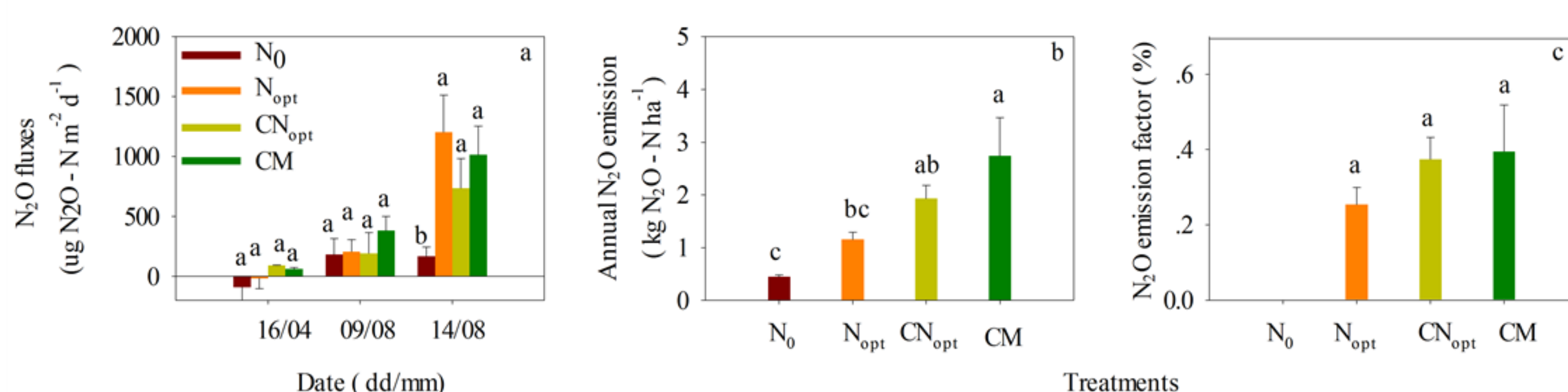


Fig. 1. N₂O fluxes on the sampling dates in 2013 (a); N₂O data from the study year in the 2012-2013 winter wheat-summer maize rotation (b); and N₂O emission factor (c). Different letters indicate significant difference (*P* < 0.05) between pairs of treatments.

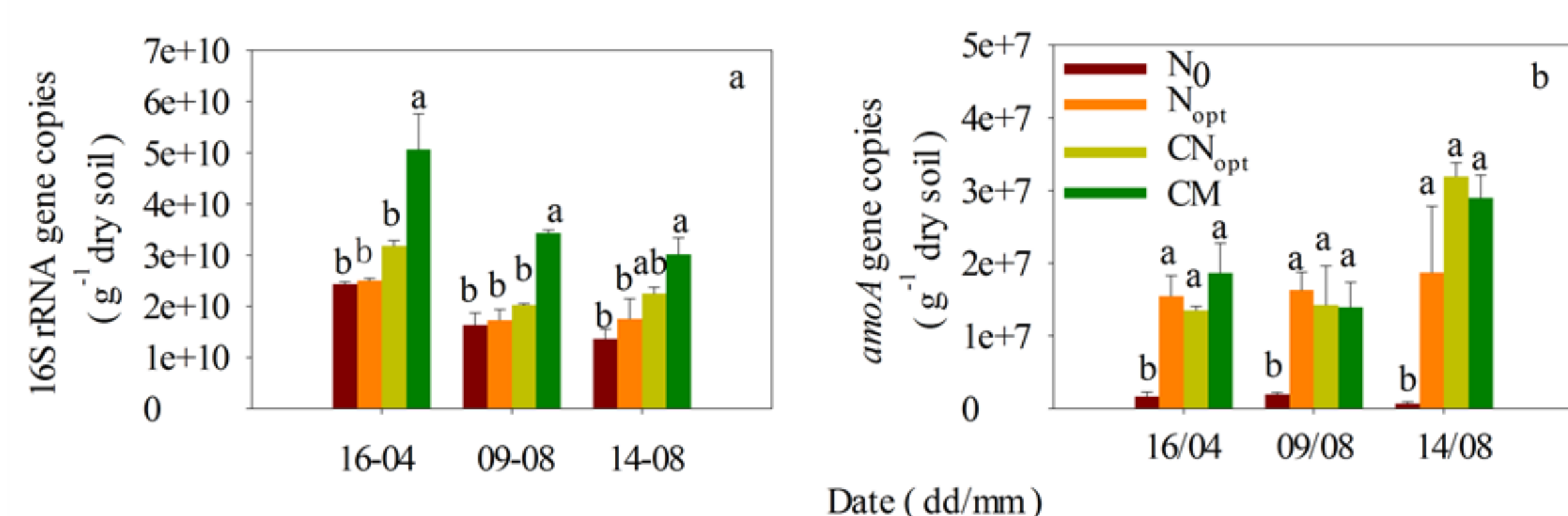


Fig. 2. Gene copies of 16S rRNA (a) and ammonia monoxygenase gene (*amoA*) of bacteria (AOB) (b) of different treatments in 0-20cm soil depth in sampling dates in 2013. Different letters indicate significant difference (*P* < 0.05) among treatments