

Supplementary information

Investigation on the feasibility of straw incorporation to improve soil fertility without obviously increasing global warming potential

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Table S1 Primer sets and thermal programs for qPCR

Target gene		Primers (5'→3')	Expected size bp	Ta °C	Primer μM	Reference
Bacterial 16S rRNA	1369F	CGGTGAATACGTTTCYCGG	123	58	0.3	(Eden et al., 1991; Weisburg et al., 1991; Suzuki et al., 2000)
	1492R	GGWTACCTTGTTACGACT				
Fungal 18S rRNA	nu-SSU-0817	TTAGCATGGAATAATRRATAGGA	382	56	1.2	(Borneman and Hartin, 2000)
	nu-SSU-1196	TCTGGACCTGGTGAGTTTCC				
<i>mcrA</i>	mcrAF	GGTGGTGTMGGATTCACACARTAYGCWACAGC	491	56	0.3	(Springer et al., 1995; Luton et al., 2002)
	mcrAR	TTCATTGCRTAGTTWGGRTAGTT				
<i>pmoA</i>	A189F	GGNGACTGGGACTTCTGG	470	56	0.3	(Holmes et al., 1995; Costello and Lidstrom, 1999)
	mb661R	CCGGMGCAACGTCYTTACC				
<i>nirS</i>	cd3aF	GTSAACGTSAAGGARACSGG	423	60	0.3	(Michotey et al., 2000; Throbäck et al., 2004)
	R3cd	GASTTCGGRTGSGTCTTGA				
<i>nosZII</i>	nosZII-F	CTIGGICCIYTKCAYAC	748	56	1.0	(Jones et al., 2013)
	nosZII-R	GCIGARCARAAITCBGTRC				

Ta = Annealing temperature. Thermal program: Step 1, pre-denaturation, 95°C, 2 min. Step 2, denaturation, 95°C, 15 s; annealing, Ta, 30 s; extension, 72°C, 30 s (for

bacterial 16S rRNA, denaturation, 95°C, 5 s; annealing, Ta, 20 s; extension, 72°C, 20 s). Step 3, melting curve, 95°C, 15 s; 60 or 65°C, 15 s; 95°C continuous

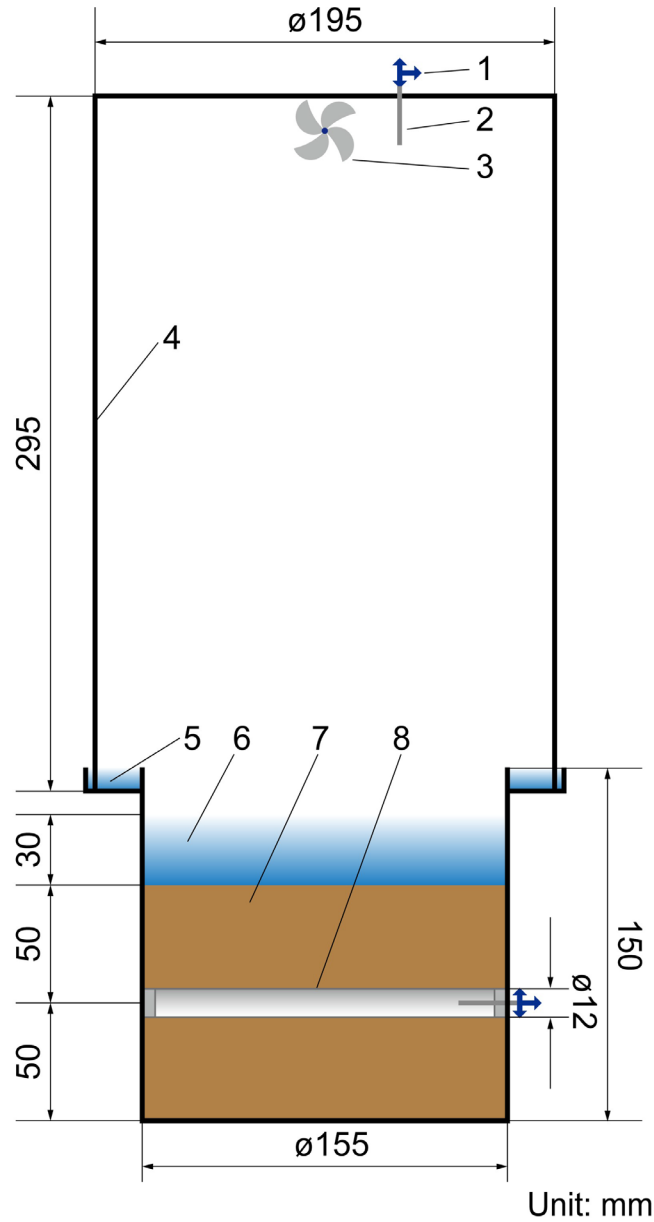


Fig. S1 Simplified diagram of the gas sampling pot. 1, three-way stopcock; 2, stainless steel tube; 3, electric fan; 4, static chamber; 5, water for sealing; 6, overlying water (during flooding); 7, soil; 8, gas-permeable silicone tube (with silicone rubber stoppers at both ends).

References

- Borneman, J. and Hartin, R. J.: PCR primers that amplify fungal rRNA genes from environmental samples, *Appl. Environ. Microbiol.*, 66, 4356-4360, <https://doi.org/10.1128/aem.66.10.4356-4360.2000>, 2000.
- Costello, A. M. and Lidstrom, M. E.: Molecular characterization of functional and phylogenetic genes from natural populations of methanotrophs in lake sediments, *Appl. Environ. Microbiol.*, 65, 5066-5074, <https://doi.org/10.1128/aem.65.11.5066-5074.1999>, 1999.
- Eden, P. A., Schmidt, T. M., Blakemore, R. P., and Pace, N. R.: Phylogenetic analysis of *aquaspirillum magnetotacticum* Using polymerase chain reaction-amplified 16S rRNA-specific DNA, *Int. J. Syst. Evol. Microbiol.*, 41, 324-325, <https://doi.org/10.1099/00207713-41-2-324>, 1991.
- Holmes, A. J., Costello, A., Lidstrom, M. E., and Murrell, J. C.: Evidence that participate methane monooxygenase and ammonia monooxygenase may be evolutionarily related, *FEMS Microbiol. Lett.*, 132, 203-208, <https://doi.org/10.1111/j.1574-6968.1995.tb07834.x>, 1995.
- Jones, C. M., Graf, D. R. H., Bru, D., Philippot, L., and Hallin, S.: The unaccounted yet abundant nitrous oxide-reducing microbial community: a potential nitrous oxide sink, *ISME J.*, 7, 417-426, <https://doi.org/10.1038/ismej.2012.125>, 2013.
- Luton, P. E., Wayne, J. M., Sharp, R. J., and Riley, P. W.: The *mcrA* gene as an alternative to 16S rRNA in the phylogenetic analysis of methanogen populations in

landfill, Microbiology (Reading), 148, 3521-3530, <https://doi.org/10.1099/00221287-148-11-3521>, 2002.

Michotey, V., Méjean, V., and Bonin, P.: Comparison of methods for quantification of cytochrome *cd₁*-denitrifying bacteria in environmental marine samples, Appl. Environ. Microbiol., 66, 1564-1571, <https://doi.org/10.1128/AEM.66.4.1564-1571.2000>, 2000.

Springer, E., Sachs, M. S., Woese, C. R., and Boone, D. R.: Partial gene sequences for the a subunit of methyl-coenzyme M reductase (*mcrI*) as a phylogenetic tool for the family *Methanosarcinaceae*, Int. J. Syst. Bacteriol., 45, 554-559, <https://doi.org/10.1099/00207713-45-3-554>, 1995.

Suzuki, M. T., Taylor, L. T., and DeLong, E. F.: Quantitative analysis of small-subunit rRNA genes in mixed microbial populations via 5'-nuclease assays, Appl. Environ. Microbiol., 66, 4605-4614, <https://doi.org/10.1128/AEM.66.11.4605-4614.2000>, 2000.

Throbäck, I. N., Enwall, K., Jarvis, Å., and Hallin, S.: Reassessing PCR primers targeting *nirS*, *nirK* and *nosZ* genes for community surveys of denitrifying bacteria with DGGE, FEMS Microbiol. Ecol., 49, 401-417, <https://doi.org/10.1016/j.femsec.2004.04.011>, 2004.

Weisburg, W. G., Barns, S. M., Pelletier, D. A., and Lane, D. J.: 16S ribosomal DNA amplification for phylogenetic study, J. Bacteriol., 173, 697-703, <https://doi.org/10.1128/jb.173.2.697-703.1991>, 1991.