

Who produces N₂O in cropland fields?

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Agricultural fields are one of the largest anthropogenic sources of atmospheric N₂O. A wide phylogenetic range of microbes including bacteria, archaea and fungi are involved in N₂O production through nitrification and denitrification. However, most of the previous studies on the microbial N₂O production in agricultural fields have focused on the proteobacterial denitrifiers and nitrifiers. We have recently developed the molecular technique which allows the detection of the phylogenetically-diverse denitrifiers including non-proteobacteria, archaea and fungi. Thus, the objective of this study is to revise the microbial ecology of the N₂O emission in agricultural fields.

The study field is a cropland located in Niigata, Japan. N₂O flux in the field after fertilizations of organic matter or urea was measured every week during the cultivation period. Total RNA was extracted from the soil and marker genes for the production and reduction of N₂O (i.e. proteobacterial and non-proteobacterial nirK and nirS, fungal nirK, bacterial and archaeal amoA, and bacterial nosZ) were quantified using RT-qPCR to estimate the contribution of each microbial functional group to the N₂O emission.

Two N₂O flux peaks were observed after the moderate and heavy rainfalls in the field amended with the organic fertilizer. The transcript abundances of the previously unaccounted bacterial nirK, bacterial and archaeal amoA, and bacterial nosZ increased at the first peak and the abundance of the fungal nirK increased at the second peak. On the other hand, only one N₂O flux peak was observed after the heavy rainfall in the field with the urea fertilizer. Then, the transcript abundances of the fungal nirK and bacterial amoA increased. These results show that more diverse microbes than previously considered contribute the N₂O emissions in croplands and the main contributors can sequentially change and differ according to the type of fertilizers.

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