

Research Highlight

A Novel Function of Controlled-Release Nitrogen Fertilizers

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Nitrogen is the most important essential nutrient that plays a major role in achieving maximum crop yield in agriculture. Therefore, nitrogen fertilizers such as ammonium sulfate and urea have been extensively used in modern agriculture. These fertilizers are generally oxidized to nitrate via nitrite by nitrifying microorganisms in the agricultural field (4, 10, 11). The serious environmental problems associated with the use of nitrogen fertilizers are nitrate contamination of ground and surface water due to nitrate leaching and loss from the agricultural field (15). For these reasons, controlled-release nitrogen fertilizers have been developed to enable a slow release of nitrogen into the soil during the crop-growing season. The use of controlled-release nitrogen fertilizers is mainly based on the principle of nitrogen utilization efficiency for crop production. However, in the current issue, Ikeda *et al.* report that the controlled-release nitrogen fertilizer urea-formaldehyde unexpectedly modifies the microbial community structure in the phytosphere of crops (8).

Controlled-release nitrogen fertilizers consists of three major types: biologically or chemically degradable organic nitrogen, nitrogen coated with a physical barrier, and lowly soluble nitrogen. Controlled-release nitrogen fertilizers have recently received increased attention because of their potential N₂O emission-reducing properties (1). Nitrous oxide, which is produced by nitrification and denitrification (4, 10, 11), is an effective earth-warming gas with a 298-fold higher efficiency than carbon dioxide. Nitrogen fertilizers such as urea, ammonium sulfate, and ammonium nitrate are sources of N₂O. Recent studies have revealed that slow-release nitrogen fertilizers reduce N₂O emissions from the agricultural field (1, 24). The urea-formaldehyde fertilizer, which is a representative controlled-release nitrogen fertilizer, is synthesized from urea and formaldehyde in the presence of a catalyst at various temperature conditions (2).

The urea-formaldehyde fertilizer is degraded by soil microorganisms, resulting in the gradual release of urea into the soil, which is then further metabolized by soil microorganisms into plant available nitrogen forms such as ammonium and nitrate (12, 13). Urea-formaldehyde fertilizers contain short-chain and long-chain methylene urea polymers. The nitrogen release rates of the fertilizer into the soil are dependent on the content ratio of the long-chain polymers. Previous studies on the influence of microorganisms on urea-formaldehyde fertilizers in soils have examined the processes of urea-formaldehyde degradation and urea release rate to evaluate its nutrient efficiency for crop production (2, 12). PCR-denaturing gradient gel electrophoresis (DGGE)

analysis has detected differences in bacterial community structure between urea-treated and methylene urea-treated soils (3). *Ochrobactrum anthropi* (14), *Ralstonia paucula* (13), and *Agrobacterium tumefaciens* (17) have been identified as the major microorganisms that degrade urea-formaldehyde fertilizers. These bacteria produce different types of urea-formaldehyde-hydrolyzing enzymes that produce ammonia, urea, and formaldehyde. The urea-formaldehyde-degrading enzyme purified from *O. anthropi* hydrolyzes different lengths of methylene urea oligomers into ammonium, formaldehyde, and urea.

The interface between plants and the external environment is called the phytosphere, which consists of the phylloplane, rhizosphere, and rhizoplane (22). The microbial community in the phytosphere plays important roles in the defense against plant pathogens (16, 20, 25) and environmental stresses, as well as in essential reactions of nutrient dynamics (9, 19). Molecular ecological methods have been recently employed to investigate the community structure of microorganisms in the phytosphere (22). Previous studies by Ikeda and coworkers have shown that tissues (*i.e.*, leaves, stems, roots, and tubers) (26), crop species (23), various environmental factors and agricultural management (5, 6, 27) could negatively or positively affect the diversity and abundance of microorganisms in the phytosphere. For example, nitrogen fertilizer (urea) application levels affected the bacterial community structure in the rhizosphere of rice in paddy fields (7). Low-level nitrogen fertilizers shifted the community structure including important microorganisms for plant associations and methane metabolism in the paddy soil and rice. Additionally, microorganisms in the phytosphere have been reported to improve crop growth and prevent plant pathogen infection (19, 28).

Ikeda *et al.* conducted field experiments to evaluate the effect of urea-formaldehyde fertilizers on the microbial community in the underground tissues of crops. They observed that the application of urea-formaldehyde fertilizers to onion bulbs and the main roots of sugar beet changed the diversity of the microbial community and the abundances of certain bacterial species. This unexpected effect could be thought to be beneficial to crop growth because these bacterial strains were identified as plant growth-promoting bacteria based on the analysis of their 16S rRNA gene sequences. Another interesting result is the increase in the number of bacterial strains that are capable of metabolizing C1 compounds, which are the metabolites of urea-formaldehyde fertilizers. They expected that urea-formaldehyde fertilizers were not only an effective nitrogen source but also a useful driving force for the control of the microbial community structure in the phytosphere. These studies have thus shown that specific

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fertilization practices (*i.e.*, types of fertilizer and level and frequency of fertilization) are important factors that shape the microbial community structure in the phytosphere.

Nitrogen fertilizers have been increasingly used as a nutrient source for crops consumed by the growing human population. The current global consumption of nitrogen fertilizers is estimated to be approximately 100 million tons per year. Based on these circumstances, controlled-release nitrogen fertilizers are considered a good nitrogen source for crops. Ikeda *et al.* clearly demonstrated that fertilizers played an additional function, which is the improvement of the microbial community in the rhizosphere. Their findings provide fresh insights into the direction of research on agricultural microbial ecology and fertilization management. It is expected that their research will eventually confirm the positive effects and mechanisms associated with the changes in the microbial community caused by the application of nitrogen fertilizers to crops. Recent advances in molecular ecological technologies (18, 30) and sequencing methods (21, 29) will also facilitate a better understanding of these issues. Further studies on the role of fertilizers on the microbial community in the phytosphere could lead to innovative changes in fertilization practices in modern agriculture.

Reference

- Akiyama, H., X. Yan, and K. Yagi. 2010. Evaluation of effectiveness of enhanced-efficiency fertilizers as mitigation options for N₂O and NO emissions from agricultural soils: meta-analysis. *Glob. Change Biol.* 16:1837–1846.
- Alexander, A., and H.-U. Helm. 1990. Ureaform as a slow release fertilizer: a review. *J. Plant Nutr. Soil Sci.* 153:249–255.
- Garcia-Tejreiro, R., D.A. Lightfoot, and J.D. Hernandez. 2009. Effect of a chemical modified urea fertilizer on soil quality: soil microbial populations around corn roots. *Commun. Soil Sci. Plant Anal.* 40:2152–2168.
- Hayatsu, M., K. Tago, and M. Saito. 2008. Various players in the nitrogen cycle: diversity and functions of the microorganisms involved in nitrification and denitrification. *Soil Sci. Plant Nutr.* 54:33–45.
- Ikeda, S., M. Anda, S. Inaba, *et al.* 2011. Autoregulation of nodulation interferes with impacts of nitrogen fertilization levels on the leaf-associated bacterial community in soybeans. *Appl. Environ. Microbiol.* 77:1973–1980.
- Ikeda, S., T. Okubo, T. Kaneko, S. Inaba, T. Maekawa, S. Eda, S. Sato, S. Tabata, H. Mitsui, and K. Minamisawa. 2010. Community shifts of soybean stem-associated bacteria responding to different nodulation phenotypes and N levels. *ISME J.* 4:315–326.
- Ikeda, S., K. Sasaki, T. Okubo, *et al.* 2014. Low nitrogen fertilization adapts rice root microbiome to low nutrient environment by changing biogeochemical functions. *Microbes Environ.* 29:50–59.
- Ikeda, S., K. Suzuki, M. Kawahara, M. Noshiro, and N. Takahashi. 2014. An assessment of urea-formaldehyde fertilizer on the diversity of bacterial communities in onion and sugar beet. *Microbes Environ.* 29:231–234.
- Inaba, S., F. Ikenishi, M. Itakura, M. Kikuchi, S. Eda, N. Chiba, C. Katsuyama, Y. Suwa, H. Mitsui, and K. Minamisawa. 2012. N₂O emission from degraded soybean nodules depends on denitrification by *Bradyrhizobium japonicum* and other microbes in the rhizosphere. *Microbes Environ.* 27:470–476.
- Ishii, S., S. Ikeda, M. Minamisawa, and K. Senoo. 2011. Nitrogen cycling in rice paddy environments: past achievements and future challenge. *Microbes Environ.* 26:282–292.
- Isobe, K., and N. Ohte. 2014. Ecological perspectives on microbes involved in N-cycling. *Microbes Environ.* 29:4–16.
- Jahns, T., H. Ewen, and H. Kaltwasser. 2003. Biodegradability of urea-aldehyde condensation products. *J. Polym. Environ.* 11:155–159.
- Jahns, T., and H. Kaltwasser. 2000. Mechanism of microbial degradation of slow release fertilizers. *J. Polym. Environ.* 8:11–16.
- Jahns, T., R. Schepp, and H. Kaltwasser. 1997. Purification and characterization of an enzyme from a strain of *Ochrobactrum anthropi* that degrades condensation products of urea and formaldehyde (urea form). *Can. J. Microbiol.* 43:1111–1117.
- Ju, X.T., G.X. Xing, X.P. Chen, S.L. Zhang, L.J. Zhang, X.J. Liu, Z.L. Cui, B. Yin, P. Christie, and Z.L. Zhu. 2009. Reducing environmental risk by improving N management in intensive Chinese agricultural systems. *Proc. Natl. Acad. Sci. U.S.A.* 106:3041–3046.
- Kawaguchi, A. 2013. Biological control of crown gall on grapevine and root colonization by nonpathogenic *Rhizobium vitis* strain ARK-1. *Microbes Environ.* 28:306–311.
- Koivunen, M.E., C. Morisseau, W.R. Horwath, and B.D. Hammock. 2004. Isolation of a strain of *Agrobacterium tumefaciens* (*Rhizobium radiobacter*) utilizing methylene urea (ureaformaldehyde) as nitrogen source. *Can. J. Microbiol.* 50:167–174.
- Kubota, K. 2013. CARD-FISH for environmental microorganisms: technical advancement and future applications. *Microbes Environ.* 28:3–12.
- Lin, L., Z. Li, C. Hu, X. Zhang, S. Chang, L. Yang, L.Y. Li, and Q. An. 2012. Plant growth-promoting nitrogen-fixing enterobacteria are in association with sugarcane plants growing in Guangxi, China. *Microbes Environ.* 27:391–398.
- Mallaiah, M., V. Manchanahally, and B. Shivanna. 2011. Fungal assemblages in the rhizosphere and rhizoplane of grasses of the subfamily *Panicoideae* in the Lakkavalli region of Karnataka, India. *Microbes Environ.* 26:228–236.
- Okubo, T., S. Ikeda, A. Yamashita, K. Terasawa, and K. Minamisawa. 2012. Pyrosequence read length of 16S rRNA gene affects phylogenetic assignment of plant-associated bacteria. *Microbes Environ.* 27:204–208.
- Saito, A., S. Ikeda, and K. Minamisawa. 2007. Microbial community analysis of the phytosphere using culture-independent methodologies. *Microbes Environ.* 22:93–105.
- Sasaki, K., S. Ikeda, T. Ohkubo, C. Kisara, T. Sato, and K. Minamisawa. 2013. Effects of plant genotype and nitrogen level on bacterial communities in rice shoots and roots. *Microbes Environ.* 28:391–395.
- Smith, K.A., I.P. McTaggart, and H. Tsuruta. 1997. Emissions of N₂O and NO associated with nitrogen fertilization in intensive agriculture, and the potential for mitigation. *Soil Use Manag.* 13:296–304.
- Someya, N., T. Morohoshi, T. Ikeda, K. Tsuchiya, and S. Ikeda. 2012. Genetic diversity and ecological evaluation of fluorescent pseudomonads isolated from the leaves and roots of potato plants. *Microbes Environ.* 27:122–126.
- Someya, N., Y. Ohdaira Kobayashi, S. Tsuda, and S. Ikeda. 2013. Molecular characterization of the bacterial community in a potato phytosphere. *Microbes Environ.* 28:295–305.
- Sugawara, M., and M.J. Sadowsky. 2013. Influence of elevated atmospheric carbon dioxide on transcriptional responses of *Bradyrhizobium japonicum* in the soybean rhizoplane. *Microbes Environ.* 28:217–227.
- Toyota, K., and T. Watanabe. 2013. Recent trends in microbial inoculants in agriculture. *Microbes Environ.* 28:403–404.
- Unno, Y., and T. Shinano. 2013. Metagenomic analysis of the rhizosphere soil microbiome with respect to phytic acid utilization. *Microbes Environ.* 28:120–127.
- Wang, Y., M. Hayatsu, and T. Fujii. 2012. Extraction of bacterial RNA from soil: challenges and solutions. *Microbes Environ.* 27:111–121.