

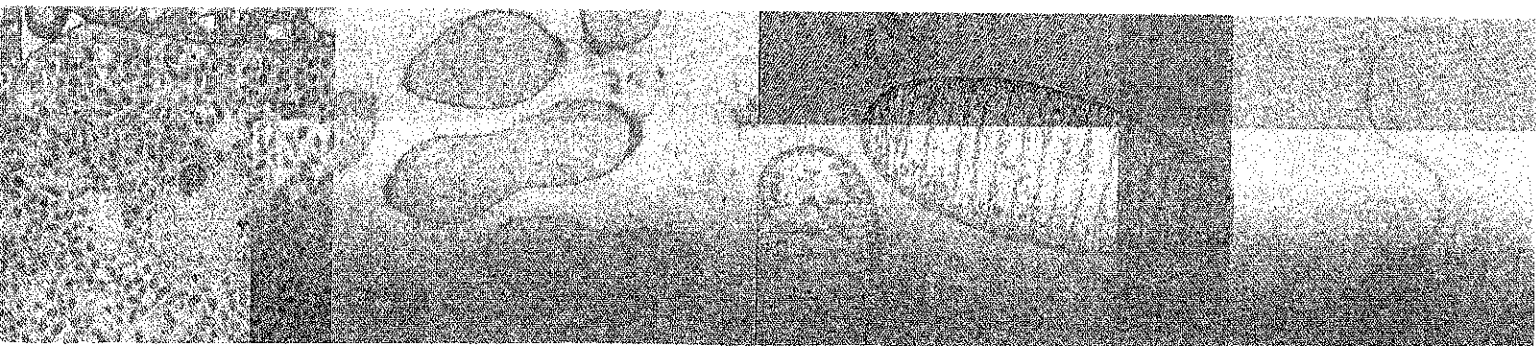
2013年度 東京大学生物生産工学研究センター シンポジウム

# 微生物機能をどう探る・どう使う？

～ Bacterial Functions for Environmental Challenges ～

## 要 旨 集

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東京大学弥生講堂一条ホール



## **N-cycling: Bridging microbial community ecology and terrestrial ecosystem functioning**

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Microbial communities have a central role in ecosystem processes by driving the Earth's biogeochemical cycles (Falkowski et al. 2008). However, the importance of microbial diversity for ecosystem functioning is still debated. Indeed, studies using natural microbial diversity gradients or manipulating microbial diversity in microcosms, either by assembling communities or diluting natural communities, have not resulted in a consistent view on the link between microbial biodiversity and ecosystem functioning. This seminar will highlight how trait-based approaches can help understanding the role of microbial diversity in ecosystem functioning. For this purpose, denitrification, a microbial process involved in N-cycling, will be used as a model functional trait. Denitrification is a microbial respiratory process during which soluble nitrogen oxides are used as alternative electron acceptor when oxygen is limiting (Zumft, 1997). Denitrification can result in considerable losses of nitrogen, which is the most limiting nutrient for crop production in agriculture. It is also responsible for emissions of nitrous oxide, a major greenhouse gas considered by the Kyoto protocol. In addition to natural variations, agroecosystems are characterized by the use of numerous practices, such as fertilization and tillage, which influence N-fluxes by denitrification. This has been widely documented in the literature, mirroring the complexity of the underlying mechanisms regulating this process. During the last decade, application of molecular biology approaches has given the opportunity to look behind denitrification rates and study the ecology of the microorganisms involved in this process, the denitrifying community. This seminar will provide examples of experiments combining molecular approaches and geostatistical modeling to explore spatial patterns of the denitrifying community at different scales (Bru et al. 2011) and of diversity-manipulation experiments (Hallin et al. 2012; Philippot et al. 2013) to illustrate how to bridge microbial community ecology, microbial processes and ecosystem functioning (Figs. 1 and 2).

Falkowski et al. 2003. The microbial engines that drive earth's biogeochemical cycles. *Science* 320: 1034

Zumft. 1997. Cell biology and molecular basis of denitrification. *Microb Mol Biol Rev.* 61:533

Bru D et al. 2011. Determinants of the distribution of nitrogen-cycling microbial communities at the landscape-scale. *The ISME J.* 5: 532-542

Hallin S et al. 2012. Microbial biodiversity affects soil functional operating range. *PlosOne.* 7(12): e51962.

Philippot L et al. 2013. *ISME J.* Loss in microbial diversity affects nitrogen-cycling in soil. *ISME J.* 7, 1609–1619

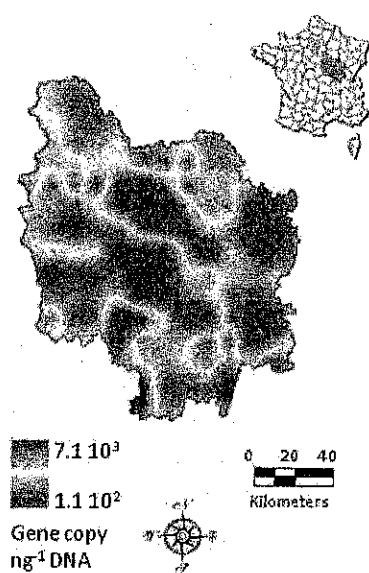


Fig. 1. Map of the denitrifier distribution at the landscape scale.

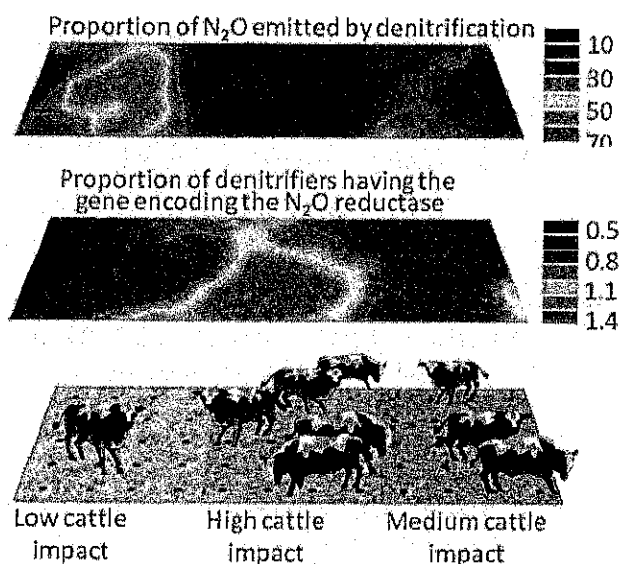


Fig. 2. Spatial distribution of the proportion of greenhouse gas  $N_2O$  emitted by denitrification in relation to the proportion of denitrifiers genetically capable to reduce  $N_2O$  in a grassland field subjected to different cattle impacts.

**Speaker:** Laurent Philippot is Director of Research at the French National Institute for Agronomic Research (INRA), France and vice head of the Agroecology department in Dijon. He is a microbial ecologist and his main research interest is in bridging microbial community ecology, microbial processes and ecosystem functioning using a trait-centered approach. He has developed this line of research with a focus on microbial guilds involved in nitrogen cycling and greenhouse gas emissions such as the denitrifiers. He is currently involved in several EU-projects (e.g. Metaexplore, EcoFINDERS, NORA) and has published more than 100 articles in peer-reviewed journals and several book chapters. Laurent is also editorial board member of the several journals in microbial ecology (e.g. *Applied and Environmental Microbiology*, *ISME J.*, and *FEMS Microbiology Ecology*).