Mapping spatial patterns of denitrifiers for bridging community ecology and microbial processes along environmental gradients

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Background: While there is ample evidence that microbial processes can exhibit large variations at a field scale, very little is known about the spatial distribution of the communities mediating these processes.

Objectives: To explore spatial patterns of size and activity of the denitrifying community, a functional guild involved in N-cycling, in a grassland field subjected to different cattle grazing regimes.

Methods: We used geostatistical modeling to map the distribution of size and activity of the denitrifier community in the pasture. Size of the denitrifier community was estimated by PCR quantification of the denitrification gene copy numbers while its activity was estimated by measuring potential denitrification activity and potential N₂O emissions.

Results: Non-random distribution patterns of the size and of the activity of the denitrifier community were observed with a field-scale spatial dependence. The soil properties, which were strongly affected by presence of cattle, imposed significant control on potential denitrification activity, potential N₂O production but not on the size of the denitrifier community. The relative abundance of bacteria possessing the nosZ gene encoding the N₂O reductase within the total bacterial community was a strong predictor of the N₂O/N₂ ratio.

Conclusions: The high correlation between the N₂O/N₂ ratio and the nosZ/16S rRNA ratio strongly suggests bacterial community composition could be important for ecosystem processes.