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

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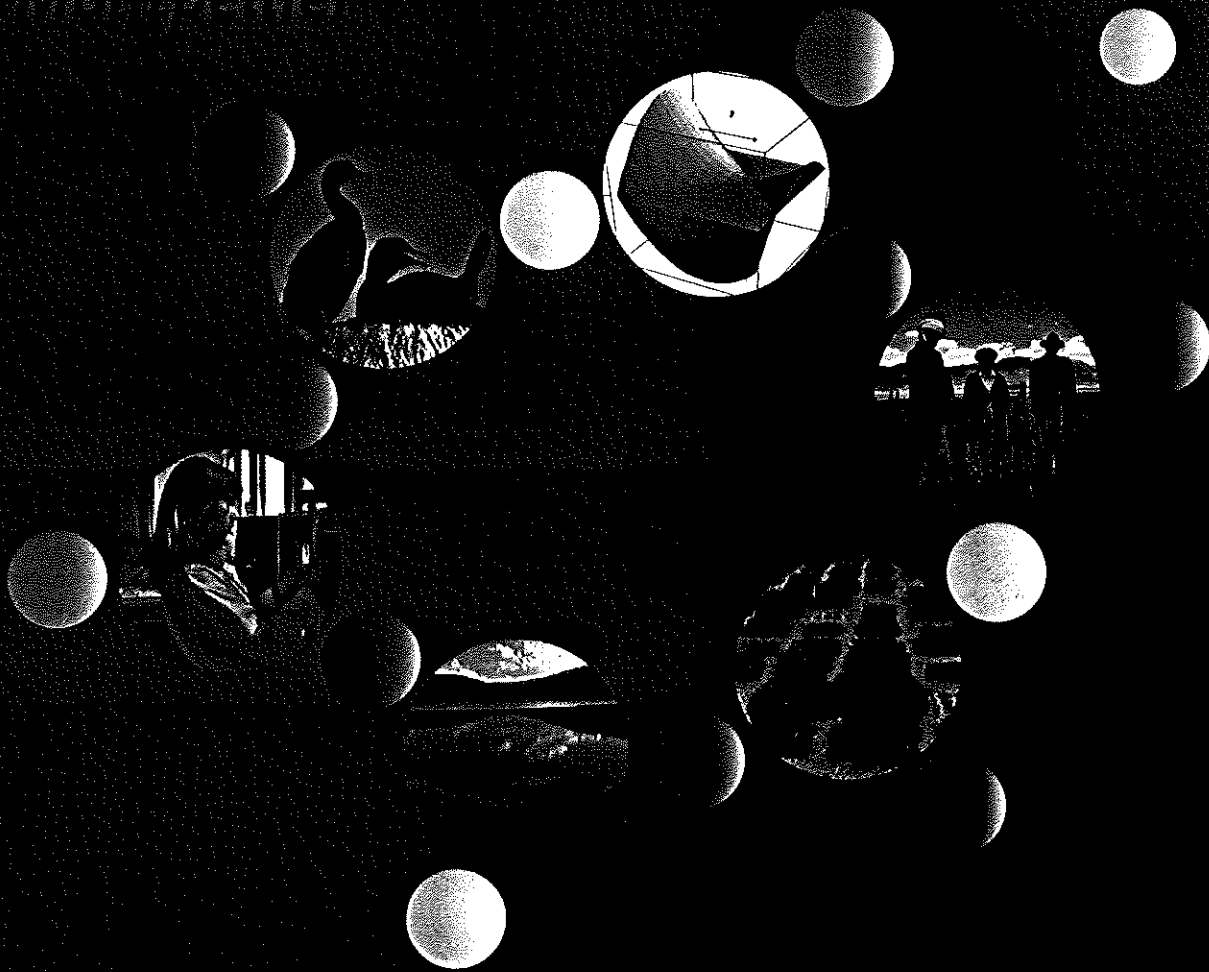
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# Posters

**Session 05 : Biodiversité, fonctionnement et services dans les écosystèmes terrestres**

**P05/01 Titre : Mapping spatial patterns of denitrifiers for bridging community ecology and microbial processes along environmental gradients**

*David Bru - Laurent Philippot - Jiri Cuhel - N.P.A. Saby - Dominique Cheneby - Dominique Arrouays - Fabrice Martin-Laurent - Miloslav Simek*

**Posters Session 05**

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. 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. 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 emissions of the greenhouse gas N<sub>2</sub>O. 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 N<sub>2</sub>O production but not on the size of the denitrifier community. The relative abundance of bacteria possessing the nosZ gene encoding the N<sub>2</sub>O reductase within the total bacterial community was a strong predictor of the N<sub>2</sub>O/N<sub>2</sub> ratio. Our results clearly indicated that patterns of distribution of the abundance of denitrifiers can be modelled at a field scale. Characterization of such pattern at a field-scale constitutes the first step in modelling distribution of functional bacterial communities at a scale compatible with land management strategies. The absolute abundance of most denitrification genes was not correlated with potential denitrification activity or potential N<sub>2</sub>O production. However, the relative abundance of bacteria possessing the nosZ gene in the total bacterial community was a strong predictor of the N<sub>2</sub>O/(N<sub>2</sub>+N<sub>2</sub>O) ratio, providing evidence for a relationship between ecosystem processes and bacterial community composition.

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**P05/02 Titre : Stabilité des communautés écologiques et architecture des réseaux mutualistes et trophiques**

*Colin Fontaine - Elisa Thébaud*

La recherche sur la relation entre l'architecture des réseaux écologiques et la stabilité des communautés s'est principalement focalisée sur les interactions trophiques, négligeant les autres types d'interaction tels que les interactions mutualistes. En utilisant une approche théorique pour montrer que l'architecture favorisant la stabilité diffère entre réseaux mutualistes et réseaux trophiques. Les fortes connectances et les architectures emboîtées favorisent la stabilité des réseaux mutualistes alors que la stabilité des réseaux trophiques est accrue par de faibles connectances et une architecture compartimentée. Ces prédictions théoriques sont confortées par une méta-analyse sur l'architecture de réseaux empiriques de pollinisation et d'herbivorie. Nos résultats indiquent que la stabilité contraint l'architecture des réseaux mutualistes et antagoniste vers des architectures opposées.

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