



HAL
open science

Mapping and predictive variations of soil microbial richness, bacterial and archaeal phyla across France

Sébastien Terrat, Battle Karimi, Walid Horrigue, Samuel Dequiedt, Nicolas Saby, Mélanie Lelièvre, Virginie Nowak, Julie Tripied, Tiffanie Régnier, Claudy Jolivet, et al.

► To cite this version:

Sébastien Terrat, Battle Karimi, Walid Horrigue, Samuel Dequiedt, Nicolas Saby, et al.. Mapping and predictive variations of soil microbial richness, bacterial and archaeal phyla across France. 4. International Conference on Microbial Diversity 2017 (MD 2017), Oct 2017, Bari, Italy. pp.209-211. hal-02738142

HAL Id: hal-02738142

<https://hal.inrae.fr/hal-02738142>

Submitted on 2 Jun 2020

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

MAPPING AND PREDICTIVE VARIATIONS OF SOIL MICROBIAL RICHNESS, BACTERIAL AND ARCHAEAL PHYLA ACROSS FRANCE

TERRAT Sébastien (1), KARIMI Battle (1), HERRIGUE Walid (1),
DEQUIEDT Samuel (1), SABY Nicolas P.A (2), LELIEVRE Mélanie (3),
NOWAK Virginie (1), TRIPIED Julie (3), REGNIER Tiffanie (3),
JOLIVET Claudy (2), ARROUAYS Dominique (2), WINCKER Patrick
(4), CRUAUD Corinne (4), BISPO Antonio (5), CHEMIDLIN PREVOST-
BOURRE Nicolas (1) MARON Pierre-Alain (1), RANJARD Lionel (1)*.

(1) Agroécologie, AgroSup Dijon, INRA, Univ. Bourgogne Franche-Comté,
21000 Dijon, France

(2) INRA Orléans, US 1106, Unité INFOSOL, Orléans, France

(3) Agroécologie - Plateforme GenoSol, BP 86510, F-21000 Dijon, France

(4) CEA / Institut de Biologie François Jacob / Genoscope, 2, Rue Gaston
Crémieux, CP 5706, 91057 Evry cedex, France

(5) ADEME, Service Agriculture et Forêt, 20, Avenue du Grésillé - BP
49006, 49004 Angers Cedex 01, France

*Corresponding Author: lionel.ranjard@inra.fr

Introduction

Numerous studies performed over the last two decades in the field of
microbial ecology have focused on variations of the soil microbial diversity
under different environmental conditions to better understand its regulation
and predict the impact of perturbations (O'Brien *et al.*, 2016; Trivedi *et al.*,
2016). Indeed, soil microbial community as a whole and how it varies has
already been examined over regional, territorial or continental scales by
several studies (Delgado-Baquerizo, Maestre, *et al.*, 2016; Delgado-
Baquerizo, Reich, *et al.*, 2016). However, most of the studies that compared
microbial diversity and composition were conducted in very different
ecosystems and soils (generally chosen with *a priori*), which could
facilitated community discrimination and exacerbated the relationship

with contrasting environmental filters. Moreover, few studies have focused on the distribution and determinism of the *taxa* constituting this community, limiting our knowledge of drivers and ecological attributes borne by these (Hermans *et al.*, 2017). In fact, some microbial *taxa* are cosmopolitan and can be found in a large range of environmental conditions, whereas other microbial *taxa* are more specialized and depend on a far more restricted range of environmental conditions (Barberan *et al.*, 2012). Unfortunately, the environmental drivers that shape these differences across microbial *taxa* remain unidentified to date, which hampers our ability to predict their fluctuations in a changing environment. To tackle these limitations, it is crucial to better integrate all the dominant and minor *taxa* constituting the community as well as the heterogeneity of a wide range of environmental parameters such as soil types, land management, climate, and geography. To attain this goal, we used an extensive set of 1,798 soils across France to obtain a holistic understanding of the spatial distribution of: (i) microbial richness (*i.e.* Operational Taxonomic Unit number), (ii) and bacterial and archaeal *phyla*. Geostatistics was applied to these data to provide the first comprehensive maps of soil microbial richness and composition variation along the environmental gradients encountered in France. Moreover, we identified the ecological processes involved in their distributions using variance partitioning analysis.

Material and Methods

Soil samples were obtained from the French Soil Quality Monitoring Network (RMQS) which is a soil monitoring network based on a 16 km regular grid across the 550,000 km² French territory (Arrouays *et al.*, 2002). All sites have been geo-positioned with a precision <0.5m and the soil profile, site environment, climatic factors, vegetation and land use are described. Microbial DNA was extracted and purified from 1 g of the soil sampled in each RMQS site, using a procedure described previously (Terret *et al.*, 2015). A 16S rRNA gene fragment targeting the V3-V4 regions to characterize bacterial diversity was then amplified using a protocol described recently to prepare sequencing libraries. Pyrosequencing was then carried out on a GS FLX Titanium (Roche 454 Sequencing System) by Genoscope (Evry, France).

Bioinformatic analyses were done using the GnS-PIPE pipeline (Terrat *et al.*, 2015). From the 49,794,516 raw reads obtained, the preprocessing steps lead to the conservation of 32,634,692 high-quality reads. The number of

high-quality reads for each sample was then normalized (*i.e.* 10,000 high-quality reads) by random selection to allow efficient comparison of the datasets and avoid biased community comparisons. All reads from all samples were then: (i) merged, aligned and clustered at 95% of similarity into OTUs, and (ii) compared to a dedicated reference database originated from Silva using similarity approaches (USEARCH). A geostatistical method was then used to map microbial richness and *phyla* and to characterize their spatial variations. The relative contributions of environmental parameters were evaluated by performing a variance partitioning for microbial richness and *phyla*. The explanatory variables were selected to reduce the auto-correlation in the models and to obtain the most parsimonious models.

Results and Discussion

Mapping of microbial richness (minimum: 938, average: 2,422, maximum: 3,562 OTUs per sample) revealed a heterogeneous spatial distribution, structured into patches of about 111 km of radius, mainly driven by proximal filters such as soil characteristics and land use (both supporting a selection process), but also significantly influenced by spatial descriptors (supporting dispersal limitation in microbial populations, derived from neutral theory) (see Figure 1). This wide spatial scale was also shown to be relevant for evaluating overall land use in the context of a sustainable use of soil resources.

Regarding microbial *phyla* in French soils, twenty of the 35 *phyla* detected were cosmopolitan and abundant with heterogeneous spatial distributions, structured in patches sizing from 43 km to 260 km radius. Sixteen *phyla* were mainly influenced by environmental selection whereas 4 were ascribed to spatial descriptors involving neutral processes such as dispersal limitation. The hierarchy of the environmental drivers was: soil pH > land use > soil texture > soil nutrients > climate.