



Contrasting Spatial Patterns and Ecological Attributes of Soil Bacterial Taxa across French National Territory

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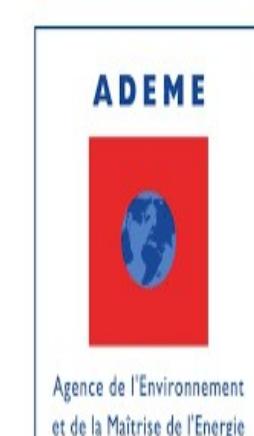
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Contrasting Spatial Patterns and Ecological Attributes of Soil Bacterial Taxa across French National Territory



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GENOSCOPE



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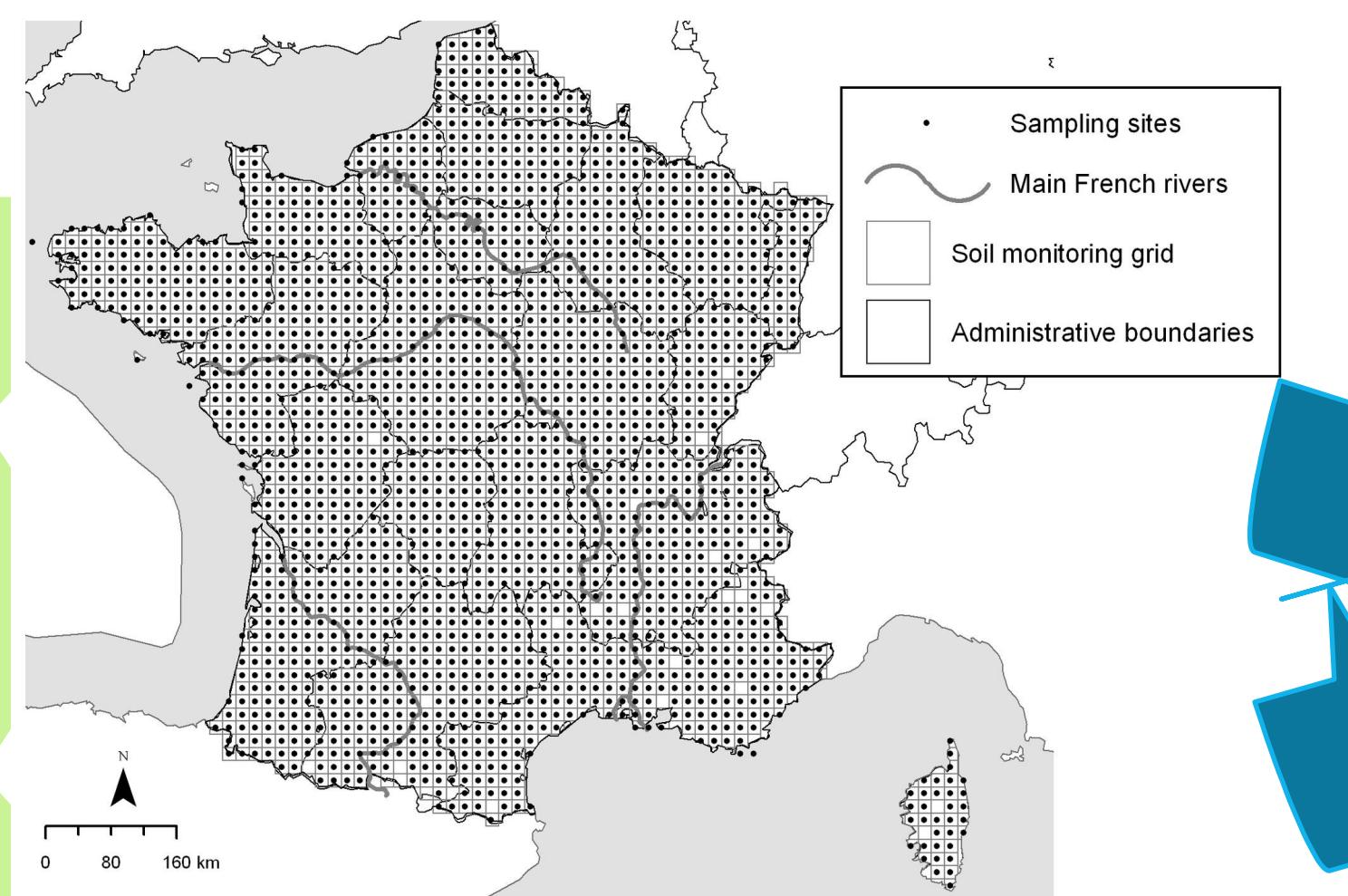
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Although soil bacteria have a key role in ecosystem services and are the most abundant organisms on Earth, the ecological processes and filters regulating their distribution at large scale remain poorly understood. Recent studies have clarified the influence of environmental filters on bacterial community diversity and concluded that soil pH, texture and C are the main drivers selecting an higher diversity. However, the filters constraining bacterial populations variations remain unclear. In consequence, our ability to understand the ecological attributes of soil bacteria and to predict microbial community response to environmental stress is therefore limited.

Based on the framework of the French Soil Quality Monitoring Network (RMQS, Réseau de Mesure de la Qualité des Sols), the objectives were to:

- (i) Identify the bacterial and archaeal community composition at the scale of French National Territory
- (ii) Determine the spatial patterns of the main phyla at a large scale
- (iii) Rank the ecological processes and environmental filters most influencing the distribution of these phyla.



RMQS = French Soil Quality Monitoring Network
16 km regular grid across the 550 000 km² territory
2137 monitoring sites

Environment characterization

- Climatic factors
- Spatial location
- Land management
- Soil physico-chemical properties

Microbial community characterization

- Pyrosequencing approach targeting 16S rRNA genes
- GnS-PIPE processing and taxonomic assignment

Descriptive Statistics

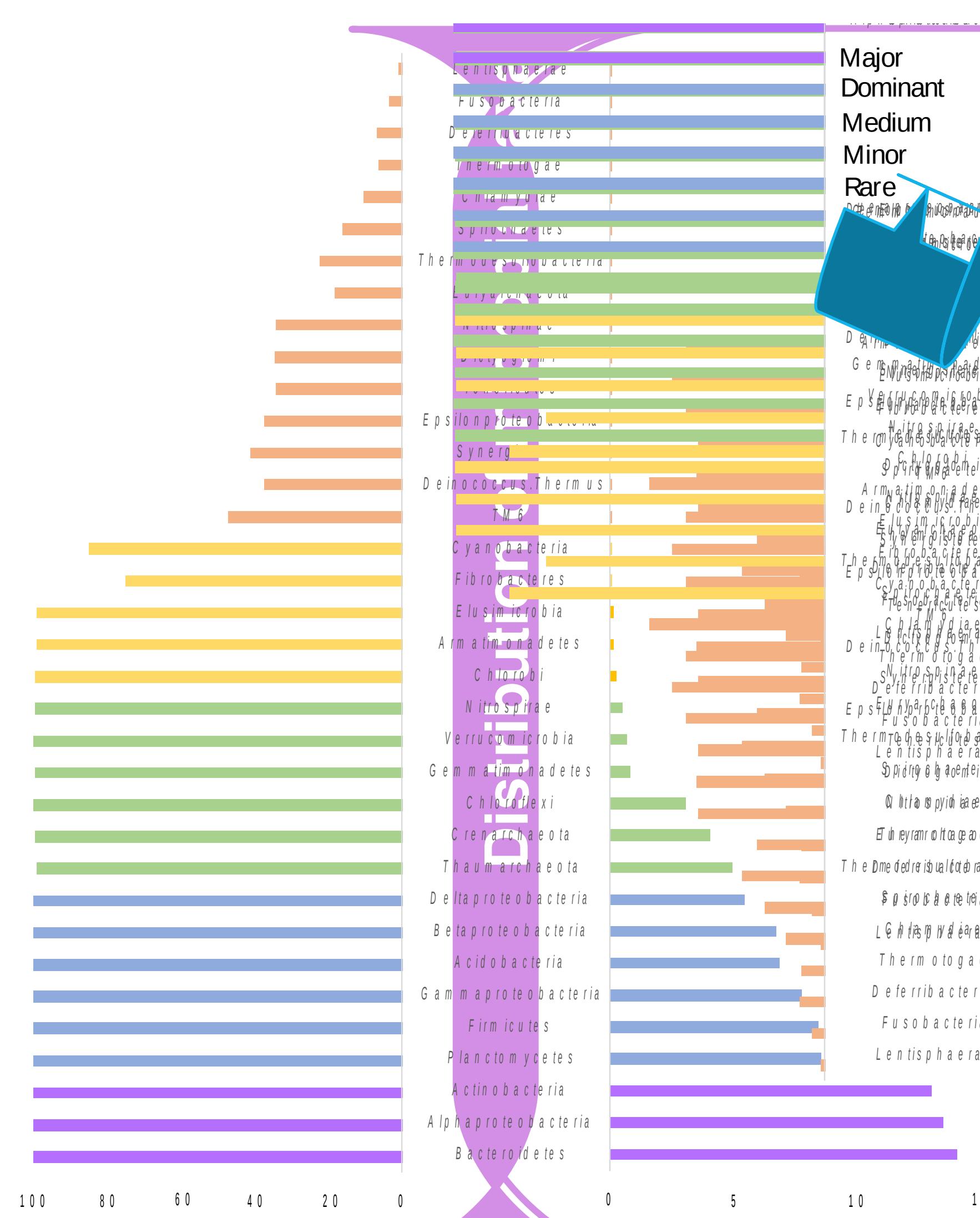
- Occurrence
- Average relative abundance

Geostatistical approach

- Kriging and Mapping

Variance partitioning

- Ranking ecological processes
- Identifying environmental filters

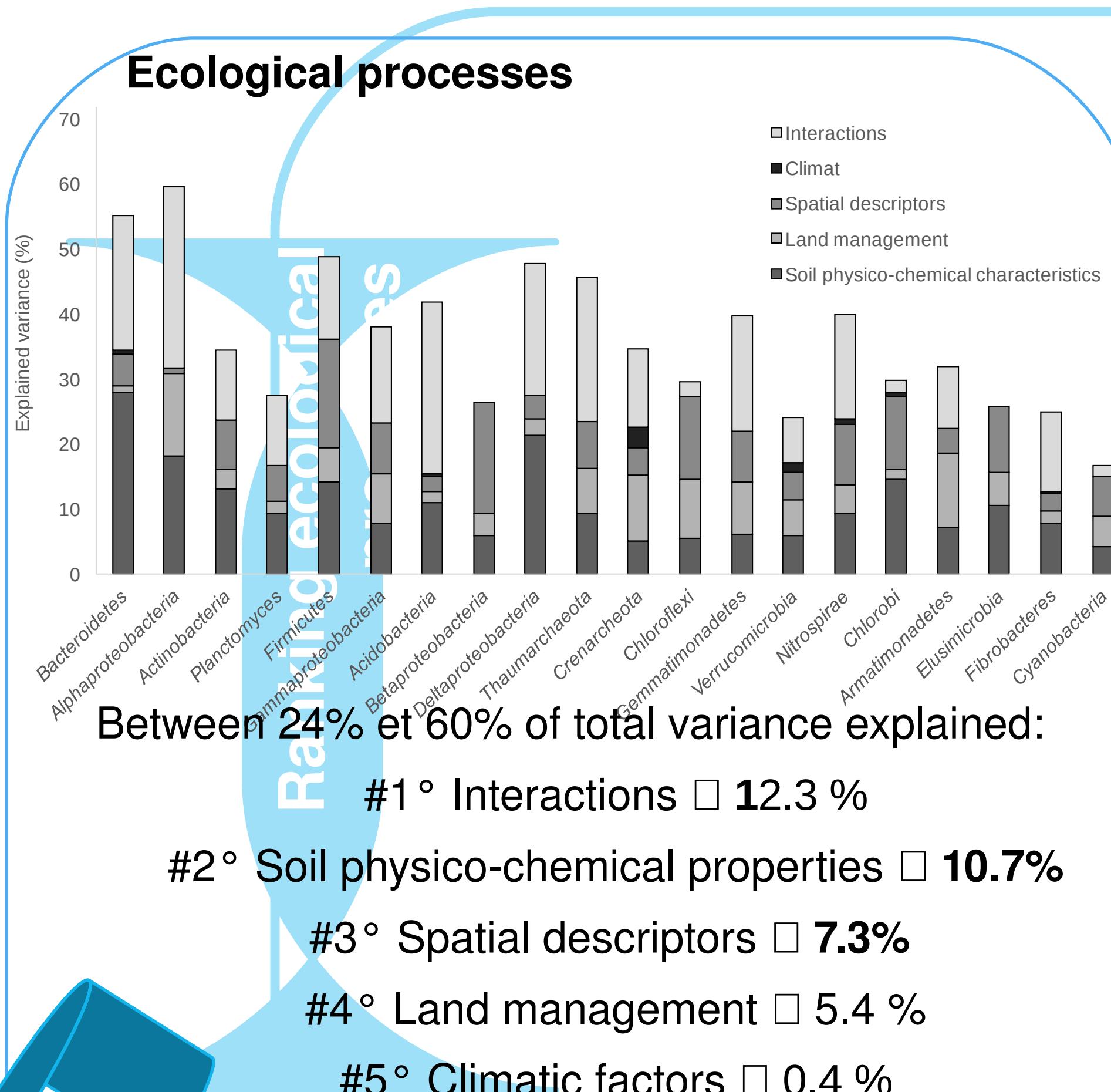


Descriptive Statistics
18 cosmopolitan phyla (in all sampling sites)
15 rare phyla (<50% of sites)

12 phyla represented each more than 3% of sampling

4 spatial patterns with different patch size (radius)

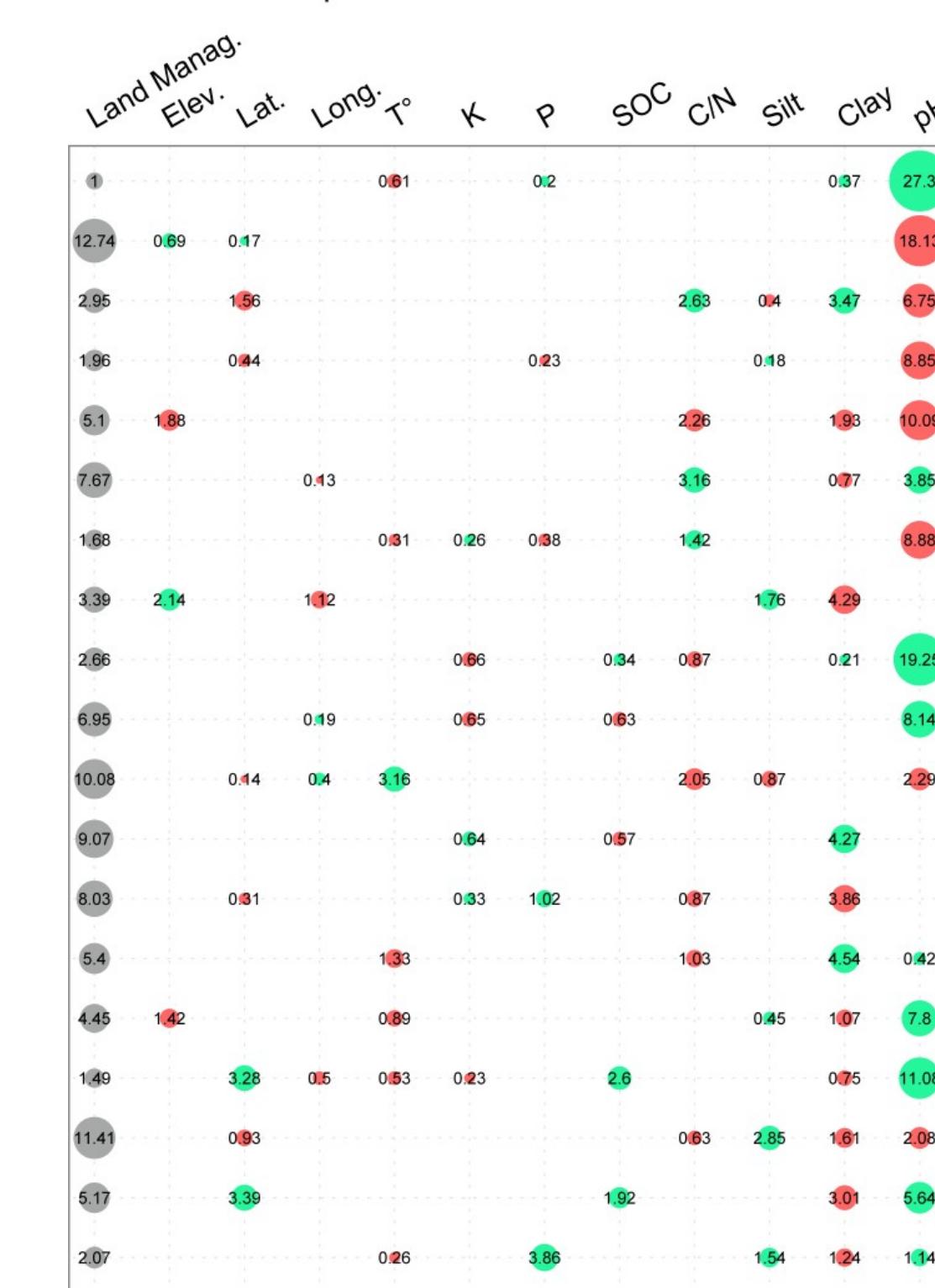
- Fine (~50km)
Chloroflexi, Fibrobacteres, Cyanobacteria
- Medium (~100km)
Bacteroidetes, Alphaproteobacteria, Acidobacteria, Deltaproteobacteria, Thaumarchaeota, Crenarchaeota
- Coarse (~150km)
Planctomycetes, Gemmatimonadetes, Verrucomicrobia, Armatimonadetes
- Large (~200km)
Actinobacteria, Firmicutes, Chlorobi, Gammaproteobacteria, Nitrosipirae, Elusimicrobia



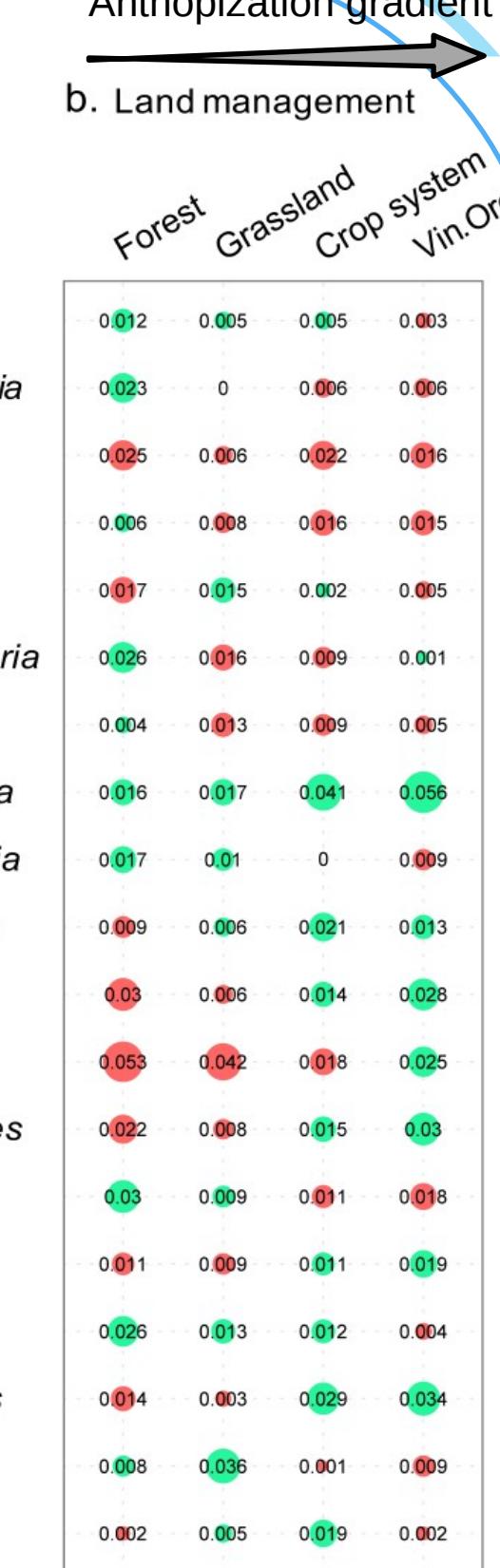
Selection and dispersal limitation are the main drivers involved in the bacterial phyla determinism.

Contribution and effects of environmental filters

a. Environmental parameters



b. Land management



Soil physico-chemical properties

pH and texture are the main filters

Land management

3 different responses to the anthropization gradient

- Positive relation e.g. Betaproteob., Chloroflexi
- No relation e.g. Firmicutes, Fibrobacteres
- Negative relation e.g. Alphaproteob., Deltaproteob.

Spatial descriptors

Two scales of geographical filters

Response depend on the phylum

