Innovative tools to diagnose the impact of land use practices on soil microbial communities

Sébastien Terrat*[1], Walid Horrigue[1], Battle Karimi[1], Samuel Dequiedt[1], Nicolas Chemidlin Prévost-Bouré[1], Dominique Arrouays[2], Bispo Antonio[3], Patrick Wincker[4], Pierre-Alain Maron[1], and Lionel Ranjard[1]

[1]UMR 1347 Agroécologie – Institut National de la Recherche Agronomique : UMR1347, Université de Bourgogne, Institut National Supérieur des Sciences Agronomiques, de lÁlimentation et de lÉnvironnement, Institut National Supérieur des Sciences Agronomiques, de lÁlimentation et de lÉnvironnement, Institut National Supérieur des Sciences Agronomiques, de l'Alimentation et de l'Environnement – 17 rue Sully 21000 Dijon, France

[2]Unité INFOSOL (ORLEANS INFOSOL) – Institut National de la Recherche Agronomique : UA1106 – France

[3]Agence de lÉnvironnement et de la Maîtrise de lÉnergie - ADEME – Agence de l'Environnement et de la Maîtrise de l'Energie - ADEME – France

[4]Genoscope - Centre national de séquençage [Evry] (GENOSCOPE) – Commissariat à l'énergie atomique et aux énergies alternatives : DSV/IG – 2, rue Gaston Crémieux CP5706 91057 EVRY Cedex, France

Abstract

Preservation and sustainable use of soil biological communities represent major challenges in the current agroecological context. Indeed, most of soil ecosystem services results from biological functions mainly driven by taxonomic and functional assemblages of microbiological communities (*i.e.* nutrient cycling, soil aggregation, depollution, etc.). Consequently, soil microbial communities are logical candidates as effective indicators of soil quality and sustainability. But, good biological indicators must be associated with references that encompass an operating range of measured values that are positioned in order to perform the desired diagnosis. Even if numerous studies have focused on soil microbial communities over the last two decades, due to the variety of ecosystems, sampling designs and methods, we still lack reference databases and diagnosis tools allowing the robust evaluation of agricultural practices impact on soil microbial communities. To attain this goal, we used an extensive set of samples originated from the French Soil Quality Monitoring Network (RMQS). This monitoring network is based on a 16-km regular grid across the 550,000 km2 French territory representative of its pedoclimatic diversity. We determined: (i) the microbial biomass by quantifying the DNA extracted from soils, and (ii) the bacterial taxonomic richness. Both measures are good microbial indicators as they satisfy technical, practical and economic prerequisites. Based on the database encompassing thousands of values, two diagnosis tools were developed, using statistical predictive models according to environmental parameters (soil physico-chemical, climatic characteristics). Indeed, they provide reference values fitted for a given pedoclimatic condition, which is to be compared to the corresponding measured

*Speaker

data for a robust diagnosis of soil biological quality. These tools were validated on external datasets and their applicability directly in the field was demonstrated on a farm network. In conclusion, these innovative tools providing reference values for a given pedoclimatic condition allow a robust diagnosis of soil biological quality.