Effect of organic fertilizers on genetic and functional diversity of soil micro-organisms

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Farms recycle very diverse organic matter which, for the majority, comes from their own activities or urban waste such as green waste, the composting of household refuse and sewage sludge (of which 60 % is spread in agriculture). The use of this organic matter in a more environmentally respectful agriculture, requires the follow-up of the consequences of these additions on the biological quality of the soil, in particular on the microflore, one of the essential factors in the dynamics of the organic matter.

In this context, BioSol Laboratory of ESITPA joined a multi-field program entitled: "Agronomic modalities and environmental effects of organic material spreading on the plain of Caen".

At present published works show a great diversity in the methodological approaches. We chose to follow the repercussion in kinetics of four types of improvement : sewage sludge, poultry manure, compost and mineral processing on the microbial population of the soil during crop rotation. The analyses are done by considering the microbial biomass by measuring microbial carbon and quantification of total DNA, the genetic diversity of the population by molecular method ARDRA (Amplified Ribosomal DNA Analysis Restriction) and the functional diversity of the populations by BIOLOG system. Work initially consisted of developing effective and reproducible tools for analysis. There is no standardized use of BIOLOG system for microbial population analyses ; so, several types of preparation of the sample such as several inoculation techniques of the plates have been tested. Thus, a protocol of cells extraction have been elaborated by shaking 5 g of soil samples in 45 ml of physiological water in vortex for 3 min. The development also made it possible to show that suspended matter had to be limited to the maximum while the greatest number possible of the microbial species present in the soil should be preserved. Thus 5 minutes of moderate centrifugation at 1000 rpm enders, after inoculation, reproducible results and in-between plot variance lower than 20%. During development, the first results still seem to indicate a concomitant evolution of microbial carbon and total DNA quantity.

Homogeneity of the plots before spreading could be highlighted compared : to a quantitative point of view the estimated total microbial biomass is around an average value of 146µg + /- 35 µg of C/g of dry soil, 6.6 µg + /- 0,6 µg of total DNA/g of dry soil for each plot and from a qualitative point of view with similar catabolic profiles with a number of positive wells bordering the 48 wells for GN plate at 48 hours and 59 wells for GP plates at 60 hours. Evolution of the microbial communities in the three months after spreading seems to be a function of the type of improvement, in particular the evolution of the total DNA quantity shows a peak at 1 month with compost and with the manure of poultry. It is untimely to say if those alterations are transient or sustainable. It will thus be necessary to follow the evolution of the microbial population of these sites for one more significant length of time and especially during all the crop rotation to know the real impact of the organic improvement on this soil population.