



Spatiotemporal evolution of bacterial community structure in agricultural soils.

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This multidisciplinary program aiming to establish an index of soil biological status consists in an evaluation of genetic and functional diversity of microbial communities.

Two experimental sites located in Normandy with contrasted agricultural practices (meadow and crop fields) have been chosen to follow the spatiotemporal evolution of bacterial community structure and determine the prevalence of natural or anthropic impacts in order to establish a bioindicator. This work reports the results for bacterial community structure obtained by two different approaches:

- a global approach (i) enumeration of culturable bacteria (ii) enumeration of total bacteria by flow cytometry and 16S rDNA quantification (real time qPCR) (iii) measurement of bacterial catabolic diversity (CLPP) and (iiii) T-RFLP on 16S rDNA.
- a more specific approach using *P. fluorescens* as a biomarker for populations with *oprF* as a specific gene.

Whatever the quantitative method: (i) intra-field variability is higher for the meadow, (ii) total telluric bacteria are at least twice as high in the meadow as in the crop field, (iii) culturable bacteria account for 0,2% of the total bacteria in meadows against 0,5% in crop fields. Moreover, variance of total bacteria is explained by agricultural practices (75% when estimated by 16S rDNA and 44% by FMC) and is independent of season, while culturable bacteria and CLPP-AWCD seem more influenced by season.

Such multidisciplinary approach shows the importance of new tools to access to total bacterial biomass (culturable or not) and enables to determine the pertinence of different methods according to the objectives of the study.