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Search for indicators of soil suppressiveness to soil-borne diseases: functional genomics approach

Soils which are suppressive to soil-borne diseases are soils in which pathogens, although present, sometimes in large inoculum density, cannot carry their infectious activity. In most cases, biotic factors are responsible for this inhibition, although the abiotic environment regulates these factors.

Currently, only bioassays under controlled conditions can be used to assess the level of soil suppressiveness to a given disease and its development but they have no generic value for different diseases, and are often time, space and energy consuming, which limits their role as actual indicators or predictive indicators (in relation with agricultural activities) of the phytosanitary quality of soils.

Metagenomic approaches using DNA extracted from soil have been proposed to evaluate without any a priori knowledge the functional diversity of genes associated with soils suppressiveness. Activity based metagenomics typically leads to the establishment of huge gene libraries and the production of thousands of clones, which can be expression screened to test the involvement of these genes, or corresponding gene products, in the mechanisms of disease suppression. Despite the development of relevant procedures to address the metagenomic analysis of soil and the provision of those libraries of multiple and exploitable genes in many areas else than soil suppressiveness, this approach remains partially biased because it relies primarily on the exploration of prokaryotic genomes, because of the predominant availability of prokaryotic expression systems and technical challenges posed by the analysis of eukaryotic genomes present in soil. In this thesis, we propose to conduct an intermediate approach between the metagenomic analysis of soil suppressiveness to diseases and the search for fungi whose activities contribute to the inhibition of infectious pathogens. The aim is to define a set of fungal genes a priori associated with mechanisms reflecting the suppressiveness of given soils to a disease and to check whether these genes are common to all the suppressive soils to different types of disease regardless of the taxonomic biodiversity present in these soils. Bioassays were conducted in both suppressive and conducive soils, DNA was extracted from the rhizosphere of susceptible plants grown in these soils, 454 sequencing of prokaryotic and eukaryotic DNA is in progress and tools to manage the data are being setting up in the frame of the UE project EcoFINDERS FP7-ENV-2010-264465.