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Impact of agricultural practices and global climate changes on the taxonomic and functional diversity of soil eukaryotic microbes in the Mediterranean area -An environmental genomics study

The aim of my PhD project is to assess the impact of land use and of simulated climate changes on soil eukaryotic biodiversity in Mediterranean ecosystems. Investigations will focus on soil organic matter degradation (one of the major steps in the global carbon cycle and one of the main factors controlling soil fertility), a process essentially performed by eukaryotic organisms (fungi). Studies will be performed in longterm environmental observatories, one in Sardinia (Berchidda) and one in southern France, north of Montpellier (Puéchabon). The site of Berchidda is dedicated to the study of the impact of land use on soil processes in Mediterranean area. It encompasses a range of agricultural practices, from traditional managed permanent pasture land with scattered cork oak trees, to different vineyards and cork oak forests. The site of Puéchabon is a unique Holm oak forest site where a severe 30% rain exclusion regime has been imposed over the last 8 years to evaluate the potential effects of forecasted climate changes on ecosystem functioning (<http://www.cefe.cnrs.fr/fp/fe/puechabon/welcom.htm>).

Taxonomic and functional diversity of soil eukaryotes are appreciated using environmental genomics approaches (metatranscriptomics) and Next Generation Sequencing (NGS) technologies. Taxonomic diversity is appreciated using soil-extracted DNA used as template to amplify and sequence ITS sequences. In term of functional diversity the work will focus on genes involved in soil organic matter degradation, essentially performed by fungi. Examples of such genes are the different classes of cellulases, hemicellulose or peroxidases necessary to the hydrolysis of cellulose hemicelluloses and lignin, respectively. PCR primers have been developed to amplify fragments of several of these gene families. To take into account the active fraction of the microbial community, gene amplification is performed not on soil-extracted DNA but on reverse-transcribed soil RNA.

Obtained results will allow us to visualize the impact of different environmental factors on the molecular mechanisms of organic matter degradation in soils. Results will serve to define guidelines for soil and ecosystem conservation. Besides understanding the impact of agricultural practices and of climate change on microbial diversity, additional outcomes of the project could also be the characterization of novel enzyme of biotechnological potential.