Geophysical Research Abstracts
Vol. 19, EGU2017-7385, 2017
EGU General Assembly 2017

Agroforestry management in vineyards: effects on soil microbial communities

Virginie Montagne (1), Virginie Nowak (1), Charles Guilland (2), Laure Gontier (3), Thierry Dufourcq (4), Josépha Guenser (5), Juliette Grimaldi (6), Emilie Bourgade (7), and Lionel Ranjard (1)

(1) INRA, UMR1347 Agroécologie, BP 86510, F-21000 Dijon, France (virginie.montagne@inra.fr), (2) Université de Bourgogne, UFR SVTE, 6 boulevard Gabriel, F-21000 Dijon, France, (3) IFV pôle sud Ouest, V'innopole, BP22, F-81310 Lisle sur Tarn, France, (4) IFV pôle Sud-ouest, Château de Mons, F-32100 Caussens, France, (5) VITINNOV, 1 cours du Général de Gaulle, F-33170 Gradignan, France, (6) CESBIO, UMR 5126, 24 rue d'Embaquès, F-32000 Auch, France , (7) Arbre et Paysage, 93 route de Pessan, F-32000 Auch, France

Some vineyard practices (tillage, chemical weeding or pest management) are generally known to impact the environment with particular negative effects on the diversity and the abundance of soil microorganisms, and cause water and soil pollutions. In an agro-ecological context, innovative cropping systems have been developed to improve ecosystem services. Among them, agroforestry offers strategies of sustainable land management practices. It consists in intercropping trees with annual/perennial/fodder crop on the same plot but it is weakly referenced with grapevine. The present study assesses the effects of intercropped and neighbouring trees on the soil of three agroforestry vineyards, in south-western France regions.
More precisely soils of the different plots were sampled and the impact of the distance to the tree or to the neighbouring trees (forest) on soil microbial community has been considered. Indigenous soil microbial communities were characterized by a metagenomic approach that consisted in extracting the molecular microbial biomass, then in calculating the soil fungi/bacteria ratio – obtained by qPCR - and then in characterizing the soil microbial diversity – through Illumina sequencing of 16S and 18S regions.
Our results showed a significant difference between the soil of agroforestry vineyards and the soil sampled in the neighbouring forest in terms of microbial abundance and diversity. However, only structure and composition of bacterial community seem to be influenced by the implanted trees in the vine plots. In addition, the comparison of microbial co-occurrence networks between vine and forest plots as well as inside vine plots according to distance to the tree allow revealing a more sensitive impact of agroforestry practices. Altogether, the results we obtained build up the first references for concerning the soil of agroforestry vineyards which will be interpreted in terms of soil quality, functioning and sustainability.