



Impact of different transgenic crops on rhizospheric microbial activity and soil organic matter

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One of the least understood areas in the environmental risk assessment of genetically modified crops is their impact on soil quality and microbial communities. In the last years the recognition that these interactions could change microbial biodiversity and affect ecosystem functioning has stimulated a limited number of studies. Novel proteins have been shown to be released from roots of transgenic plants into the soil ecosystem, and their presence can influence the biodiversity of the rhizospheric microbial community by selectively stimulating the growth of organisms that can use them. Although differences in both the genetic structure and the metabolic function of the microbial communities associated with some transgenic plant lines have been established, it remains to be seen whether these differences have an ecological impact on the soil microbial communities. Alterations in the diversity of the microbial community could affect soil health and ecosystem functioning, and therefore, the impact that plant variety may have on the activity of the rhizosphere microbial populations and on ecosystem sustainability, requires further study.

In this work we report the results obtained in the study we conducted on a single experimental site where rhizosphere samples associated with transgenic Actinidia, Olive and Cherry varieties with their relative wild types were sampled. Community-level physiological profiles, microbial biomass determination, microbial respiration rate and soil organic matter characterization of rhizosphere samples were performed to identify and compare differences of the rhizospheric microbial activity and soil biological fertility between the transgenic and the conventional plants. Principal-component analysis showed that there was variation in the microbial activity associated with different plant varieties but not between different genetic modifications within the same variety.