



## **Tillage system affects microbiological properties of soil**

A. Delgado (1), A. de Santiago (2), M. Avilés (1), and F. Perea (3)

(1) University of Seville, Sevilla, Spain (adelgado@us.es, +34954486436), (2) Instituto de Investigación La Orden-Valdesequera, Badajoz, Spain, (3) IFAPA, Junta de Andalucía, Spain

Soil tillage significantly affects organic carbon accumulation, microbial biomass, and subsequently enzymatic activity in surface soil. Microbial activity in soil is a crucial parameter contributing to soil functioning, and thus a basic quality factor for soil. Since enzymes remain soil after excretion by living or disintegrating cells, shifts in their activities reflect long-term fluctuations in microbial biomass. In order to study the effects of no-till on biochemical and microbiological properties in comparison to conventional tillage in a representative soil from South Spain, an experiment was conducted since 1982 on the experimental farm of the Institute of Agriculture and Fisheries Research of Andalusia (IFAPA) in Carmona, SW Spain (37°24'07"N, 5°35'10"W). The soil at the experimental site was a very fine, montomorillonitic, thermic Chromic Haploxerert (Soil Survey Staff, 2010). A randomized complete block design involving three replications and the following two tillage treatments was performed: (i) Conventional tillage, which involved mouldboard plowing to a depth of 50 cm in the summer (once every three years), followed by field cultivation to a depth of 15 cm before sowing; crop residues being burnt, (ii) No tillage, which involved controlling weeds before sowing by spraying glyphosate and sowing directly into the crop residue from the previous year by using a planter with double-disk openers. For all tillage treatments, the crop rotation (annual crops) consisted of winter wheat, sunflower, and legumes (pea, chickpea, or faba bean, depending on the year), which were grown under rainfed conditions. Enzymatic activities ( $\beta$ -glucosidase, dehydrogenase, aryl-sulphatase, acid phosphatase, and urease), soil microbial biomass by total viable cells number by acridine orange direct count, the density of cultivable groups of bacteria and fungi by dilution plating on semi-selective media, the physiological profiles of the microbial communities by BiologR, and the Shannon ( $H'$ ) and Gini (1-G) diversity index of microbial communities were determined in soil samples (0–10 cm depth) taken in autumn 2009. All the enzymatic activities and the biomass estimated by viable cell counting were significantly higher under no-till than under conventional tillage. However, only fluorescent pseudomonas population was increased under no-till, meanwhile oligotrophic bacteria and actinomycetes populations were higher with conventional tillage than with no-till. Overall, there was a higher use of all the group of carbon sources used in the BiologR test with conventional tillage than with no-till, by except amines and phenols which showed non-significant differences. This reveals different physiological profiles in the microbial communities under both tillage systems. The Gini diversity was significantly lower with no-till than with conventional tillage. It can be concluded that no-till increases microbial biomass in soil and subsequently enzymatic activities likely ascribed to an increased organic matter content. Under low availability of hydrocarbon sources in soil due to conventional tillage, which promotes a decrease in the organic matter content of the soil, populations of oligotrophs and the diversity of microbial communities are increased. Under these conditions, there must not be dominant carbon sources promoting the selection of microorganisms with a given physiological profile. The reduced hydrocarbon availability and the higher diversity contribute to explain the increased use of carbon sources used in Biolog with conventional tillage than with no-till.