



Soil microbial community composition changes according to the tillage practice and plant development stage

Florine Degrunne (1,2), Marc Dufrière (3), Gilles Colinet (3), Bernard Taminiau (4), Marie-Pierre Hiel (1,2), Georges Daube (4), and Micheline Vandenberg (1)

(1) Université de Liège, Gembloux Agro-Bio Tech, Department of Chemistry and Bio-Industry, Gembloux, Belgium (florine.degrunne@ulg.ac.be), (2) Université de Liège, AgricultureIsLife.be, Gembloux, Belgium, (3) Université de Liège, Gembloux Agro-Bio Tech, Department of Biosystems Engineering, Gembloux, Belgium (gilles.colinet@ulg.ac.be), (4) Université de Liège, Faculté de médecine vétérinaire, Belgium (bernard.taminiau@ulg.ac.be)

Soil microorganisms are abundant and diverse and can have both beneficial and adverse effects on crop growth. Some, such as plant-growth-promoting rhizobacteria and mycorrhizae, are well known to favor crop productivity and plant health. They are notably involved in key processes such as improving plant nutrient acquisition, and they also play major roles in stimulating plant growth and protecting plants against pathogens by producing bioactive substances. Conversely, both agricultural practices and the plant development stage are known to influence the physical and chemical properties of the soil and hence the abundance and diversity of soil microorganisms.

Here we investigated the impact of both tillage practice (conventional versus reduced tillage) and plant development stage (germination versus flowering) on the microbial community composition of an agricultural soil supporting a faba bean crop. Samples were taken at a depth of 15-20 cm from a silty soil in Belgium.

For bacteria, we observed significant shifts in community composition according to both factors. Some changes were strongly related to the plant development stage and others to the tillage practice. Some taxa, including Gemmatimonas, Xanthomonadaceae, and Sinobacteraceae, showed a higher relative abundance at the flowering stage than at the germination stage, but no effect of tillage practice. Other taxa, including Flovobacterium, Chitinophaga, and Luteolibacter, showed a higher relative abundance under conventional tillage than under reduced tillage, but no change according to the stage of plant development.

For fungi, significant shifts in community composition were observed according to the plant development stage. No effect of tillage practice was observed. The relative abundances of certain taxa, including Chaetomium and Clavicipitaceae, were higher during germination than during flowering, whereas other taxa, including Minimedusa and Teberdinia, showed a higher relative abundance during flowering.

For both bacteria and fungi, the observed patterns appeared to be explained by differences in soil conditions between conventional and reduced tillage and between germination and flowering: the soil nitrate content and humidity were higher during germination than during flowering, and the P and K contents were higher under conventional than reduced tillage.