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STUDY OF BACTERIAL DIVERSITY IN AN AGRICULTURAL SOIL

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Bacterial growth in soil is dependent on soil characteristics. In this experiment, we have studied the evolution of bacterial diversity during a winter wheat crop and the impacts caused by the tillage and residue incorporation. Three growth stages of wheat was chosen for this work : germination, tillering and booting. The analyse of bacterial diversity in these conditions was performed by the Next Generation Sequencing technology. Results obtained by this method indicate that the soil is composed, in average, by 38,02 ($\pm 4,81$)% Proteobacteria; 19,71($\pm 3,88$)% Actinobacteria; 7,77($\pm 1,44$)% Firmicutes; 6,94($\pm 1,58$)% Fibrobacteres/Acidobacteria group; 5($\pm 3,21$)% Bacteroidetes/Chlorobi group; 3,89($\pm 1,36$)% Chloroflexi; 2,96($\pm 0,67$)% Planctomycetes; 2,87($\pm 1,58$)% Verrucomicrobia; 1,42($\pm 0,41$)% Cyanobacteria and 15,38($\pm 2,64$)% others. The tillage influences mostly the Deltaproteobacteria, Gammaproteobacteria, Actinobacteridae, Bacteroidetes/Chlorobi group and Verrucomicrobia. Residue incorporation has an impact on Betaproteobacteria, Gammaproteobacteria, Actinobacteridae, Acidimicrobidae, Firmicutes and Bacteroidetes/Chlorobi group. The wheat growth stages affect especially Betaproteobacteria, Deltaproteobacteria, Actinomycetales, Acidibacteria, Fibrobacteres and Bacillales. The results will be presented and discussed on the poster.