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Conference Topic : Microbial community diversity and ecosystem function

Study of bacterial diversity in the topsoil and below the hardpan in an agricultural soil by metagenomics following by two analysis pipelines

Stroobants Aurore¹, Lambert Christophe², Degruene Florine¹, Portetelle Daniel¹, Vandebol Micheline¹

¹ Unité de Microbiologie et Génomique, Université de Liège, Gembloux Agro-Bio Tech, Avenue Maréchal Juin 6, 5030 Gembloux, Belgium, e-mail: aurore.stroobants@ulg.ac.be

² Progenus SA, Rue des Praules 2, 5030 Gembloux, Belgium

On earth, Bacteria are ubiquitous and even present in extreme environments (pH, temperature,...). In soils in particular, bacteria are very abundant (up to 10^9 cells per gram of soil) but still poorly characterized. Thus, it is of paramount importance to use relevant study and analysis procedures to ensure that the results obtained closely reflect the real-life conditions. In the present work, we analyze the bacterial diversity in the topsoil and below the hardpan in an agricultural soil using the metagenomics approach, with the Ion Torrent PGM sequencer. The soil samples were collected at three depths : 10 cm (topsoil), 25 cm (topsoil above the hardpan) and 45 cm (below the hardpan), in a tilled and a no tilled plot. The taxonomic analysis of the reads obtained are carried out according to two different procedures with the RDP classifier program and with a confidence score threshold of 0 and 0.99. The 0 threshold is used to assign a species to all reads, each read being therefore assigned to its most closest known species. The threshold of 0.99 enables us to focus on reads being assigned to a species with a high degree of confidence. In this case, each read is assigned to the most specific rank having a confidence score higher than 0.99. The bacterial diversity was then compared between the different conditions. Results obtained demonstrate that the bacterial communities were not the same in the two horizons. For example, some classes of *Acidobacteria* were up to 11 fold more numerous in topsoil while others were until 12 fold more represented below the hardpan. The biomass and the bacterial diversity (Shannon index) were also greatly different between the two depths.