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Streszczenie rozprawy doktorskiej w języku angielskim

Summary

The aim of this research was to determine the diversity of microorganisms (bacteria and fungi) in eight different soil types on two levels: structural and functional. The experimental object was over 130 years of microplots experiment, in which various soil types were collected and separated from each other by concrete walls. The location of all the plots in one place eliminated all external factors, such as weather, timing of sampling, latitude, allowing to investigate the soil type as the main factor.

The tests were carried out on the basis of modern high-throughput methods. The structural diversity was determined by the next generation sequencing (NGS) taking into account the hypervariable regions of the 16S rRNA (bacteria) and ITS-1 (fungi).

Functional diversity was analyzed using Biolog ECO and FF approaches and dehydrogenases activity measurement as a sensitive method of determining general metabolic activity. The results of the study were subjected to a wide spectrum of statistical and bioinformatics analyses with the use of the latest computer tools.

As a result, it was determined that the composition of bacteria and fungi is closely related to the physicochemical properties of the soils studied. Unique microorganisms for each of the eight soils were determined and core microorganisms for different soil groups and common for all soils were selected. It was found that the assessment of microbial biodiversity through genetic and bioinformatics analysis can be a very sensitive and precise indicator of soil quality.