



Chitinolytic and pectinolytic community of soils and terrestrial ecosystems of different climatic zones

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Structural and functional features of the complex microbial degradation of biopolymers one of the most important direction in microbial ecology. But there is no a lot of data concerns degradation in vertical structure of terrestrial ecosystems. Microbial complexes of natural areas were analyzed only as humus horizons (A1) of the soil profile. Only small part of microbial community could be studied with this approach.

The breakdown of chitin and pectin was studied. The aim was to provide a characterization of microorganisms involved in chitin and pectin degradation in the soils and terrestrial ecosystems in different climatic zones: steppe zone, deciduous forests and taiga.

Samples of leaves, soils and litter were studied and compared.

Quantity of eukaryote and prokaryote organisms increased in samples with chitin and pectin comparing with control samples. Increasing of eukaryote in samples with pectin was more then in samples with chitin. Also should be noted the significant increasing of actinomycet's quantity in the samples with chitin in comparison with samples with pectin.

Further prokaryote community was investigated by method FISH (fluorescence in situ hybridization). FISH is a cytogenetic technique developed that is used to detect and localize the presence or absence of specific DNA sequences on chromosomes. Quantity of Actinomycetes and Firmicutes was the largest among identified cells with metabolic activity in both types of the samples. Should be noted significant increasing of the quantity of Acidobacteria and Bacteroidetes in pectinolytic community and Alphaproteobacteria in chitinolytic community soils.

The difference between climatic zones was studied and the mathematical model was created. The mathematic model could be use in different aims, such as prognosis of microbial community composition and their classification.