

9<sup>th</sup> Edition of International Conference on **Environmental Science & Technology**  
 &  
 48<sup>th</sup> World Congress on **Microbiology**  
 &  
 50<sup>th</sup> International Congress on **Nursing Care**

June 24-25, 2019 Moscow, Russia

## Analysis of the taxonomic structure of the bacterial community of organic enriched black soil by the method of RT-PCR

Anastasiia I Nechaeva, Konstantin S Boyarshin, Violetta V Klueva, Yuliia N Kurkina, Valentina V Skorbach, Alexander A Sirotnin and Irina V Batlutskaia  
 Belgorod State University, Russia

In ensuring fertility of soils an important factor is the proper functioning of microbial communities in them. Despite the active development of powerful methods for the analysis of soil microbial communities based on metagenomic and metaproteomic approaches, taxon-specific RT-PCR remains and the most convenient for wide practical use, as the fastest and cheapest method. In this study, a technique was developed for using a set of taxon-specific primers in the taxonomic analysis of the bacterial component of the soil microflora using the example of black soil enriched with regular application of organic fertilizers. Samples of the orable black ground were taken from a depth of ~5 cm after defrosting in March and stored for three weeks at room temperature with abundant moistening to activate the microbiota. For the study, a set of taxon-specific primers was used, which includes pairs specific to six types and one class of bacteria, as well as to the Bacteria domain as a whole. According to the data obtained (Fig. 1) Firmicutes and Bacteroidetes phyla were found in large numbers in the studied sample. The Actinobacteria phylum and the Gammaproteobacteria class, belonging to the Proteobacteria phylum were represented in a smaller amount and the Verrucomicrobia phylum in very small amount. The types Deferribacteres and Tenericutes were not detected. The selection of taxon-specific pairs of primers for analysis was based on literature data indicating the presence of selected taxa in the soil microflora. A significant proportion of bacteria belonging to the types Bacteroidetes, Actinobacteria, and the Gammaproteobacteria class are consistent with the data presented in these sources. A high percentage of representatives of the type Firmicutes may be associated with the application of organic fertilizers, since the microorganisms belonging to this taxon dominate in the manure of farm animals.

### Recent Publications

1. Yang Y W, Chen M K, Yang B Y, Huang X J, Zhang X R, He L Q, Zhang J and Hua Z C (2015) Use of 16S rRNA Gene-targeted group-specific primers for real-time PCR analysis of predominant bacteria in mouse feces. *Applied and Environmental Microbiology* 81:6749-6756.
2. Zarraonaindia I, Owens M, Weisenhorn P, West K, Hampton-Marcell J, Lax S, Bokulich N, Mills D, Martin G, Taghavi S, van der Lelie D and Gilbert J (2015) The soil microbiome influences grapevine-associated microbiota. *mBio* 6:e02527-14.
3. Kim Y and Liesack W (2015) Differential assemblage of functional units in paddy soil microbiomes. *PLoS ONE* 10(4): e0122221.
4. Zhang L, Li L, Pan X, Shi Z, Feng X, Gong B, Li J and Wang L (2018) Enhanced growth and activities of the dominant functional microbiota of chicken manure composts in the presence of maize straw. *Front Microbiol.* 9:1131.

### Biography

Anastasiia I Nechaeva is a specialist of a wide profile in the field of industrial and soil Microbiology. Her track record includes participation in the development of an innovative pilot plant for the bioconversion of hydrogen into methane based on the autotrophic microbial consortium. Currently, she is engaged in the analysis of soil microbial communities for the needs of soil fertility restoration.

nechayeva@list.ru