Identification of 3 unknown bacterial strains, characterization of copper oxidase genes

M. Plotnikova

Voronezh State University, Department of Genetics, Cytology and Bioengineering, Voronezh, Russia e-mail: j.mariia@rambler.ru

Key words: copper oxidase, genome sequence, 16R RNA, identification of strains

Motivation and Aim: The purpose of this research is identification of unknown strains of microorganisms and characterization of Copper Oxidase Genes in their genomes.

Methods and Algorithms: Objects of research are unknown strains from RCM (Russian Collection of Microorganisms, Pushchino). Bacterial cells were provided by the staff of the RCM department (http://www.vkm.ru) of the Scryabin Institute of Biochemistry and Physiology of Microorganisms, Russian Academy of Sciences. DNA strains were isolated using the Genomic DNA Purification Kit (Thermo Fisher Scientific) by the manufacturer's procedure with modifications: treatment with lysozyme cells before lysis solution was applied. The fragment of the 16s rRNA gene was amplified using specific primers 27F (AGA GTT TGA TCC TGG CTC AG) and 1492R (ACG GYT ACC TTG TTA CGA CTT). Polymerase chain reaction included denaturation of the matrix in the first cycle at 95 °C for 5 min and 35 cycles of amplification in the following regime: 95 °C – 30 s, 55 °C – 30 s, 72 °C – 1 min. PCR products were analyzed in a 1.3 % agarose gel with ethidium bromide (0.0002 %). PCR products of about 1500 bp were purified from the gel using the Cleanup Mini kit (Eurogen, Russia) and transferred to Eurogen to determine the nucleotide sequence.

Results: Using the methods of molecular biology, we identified 3 unknown strains of microorganisms from RCM. After analysis of the nucleotide sequence, it was found that the strains studied belong to the following species: strain 1 – Cellulosimicrobium cellulans (99 %); strain 2 – Cellulosimicrobium funkei (98 %).

Conclusion: The strains of microorganisms from the RCM were identified. Nowadays, we research the expression of Copper Oxidase Genes in these genomes (Cellulosimicrobium cellulans, Cellulosimicrobium funkei).

Acknowledgements: Supported by the Voronezh State University and Scryabin Institute of Biochemistry and Physiology of Microorganisms, Russian Academy of Sciences.