



BIOINFORMATIC ANALYSIS OF 16S rRNA GENE SEQUENCES OF DESULFOVIBRIO CLOSE RELATED SPECIES

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The bacterial species identification based on the complex of morphological, physiological, biochemical and genetic characteristics although when metagenomic researches carry out only 16S rDNA sequencing takes into consideration. It seemed that 16S sequences were exploited to distinguish even strains based on the single nucleotide polymorphisms within the gene. To identify and differentiate bacterial species both a whole 16S rRNA gene sequences and sequences of several variable regions of the gene can be used.

Desulfovibrio species are sulfate-reducing bacteria that can be found in the various econiches, for instance, soil, water, animals, human. An integrative characterization of bacteria implies a complex of specific features and properties that are grounded on the accurate species identification of these bacteria.

The present study aimed to perform analysis of 16S rDNA nucleotide sequences of two taxonomic closed species belonging to *Desulfovibrio* genus, *D.termitidis* and *D.oryzae*, using a bioinformatic approaches. 16S rRNA gene sequences were downloaded from GenBank: 5 sequences of *D.termitidis* and 7 sequences of *D.oryzae*, and programs MEGA 6.0 and BioEdit version 7.0.5.3 were used to carry out the sequences and phylogenetic analyses.

Results of the analysis showed that the length of *D.termitidis* and *D.oryzae* 16S rRNA gene fragments deposited in GenBank was varied from 522 to 1540 nucleotides with the average of 750 nucleotides for *D.termitidis* and 738 – for *D.oryzae*. Among



D. oryzae strains 14 nucleotide sites were revealed variable though only two were observed within overlapping region for all strains. These values were three and one if *D. termitidis* strains were analyzed. The number of variable sites among all 12 strains of both species amounted to 28 and only two of them were located within overlapping region. It should be noted that 14 sites were specific only for *D. termitidis* and 7 ones - for *D. oryzae*.

Thus, results of 16S rRNA gene sequences of two close related *Desulfovibrio* species suggested that the longer size of gene sequence the more precise distinguishing between species representatives, the bacterial species might be identified on the base of 500-600 nucleotides but for strain differentiation should be sequenced more than 900 nucleotides.