Rep-PCR FINGERPRINTING AS A TOOL FOR THE ANALYSIS OF GENOMIC DIVERSITY OF ESCHERICHIA COLI STRAINS ISOLATED FROM A WATER ENVIRONMENT

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Genetic diversity of bacteria is a fact. The mechanisms of the generation of genetic variability have not been fully elaborated on. There is a need to determine the variability in bacteria species in different environments. Escherichia coli is an important object of such types of investigation. Most E.coli are present as comensal organisms found among intestinal microflora of humans and animals. E.coli can periodically appear in water environments. It is necessary to characterize the highest possible number of strains to describe the genetic diversity of the microbiological environment. Molecular biology methods are helpful in qualitative analysis. One such methods which can be useful in examining the genomic diversity of an E.coli population is rep-PCR fingerprinting. This technique involves amplifying the genomic DNA located between repetitive sequences to obtain strain-specific DNA fingerprints. The aim of this study was to analyse the genomic diversity of E.coli strains collected from the Wojnowskie Wschodnie and Wojnowskie Zachodnie lakes. Samples of the lakewater were drawn from appointed sample drawing stand, from the bottom and subsurface zones, once a month. The samples were analysed microbiologically to obtain E.coli strains. 102 E.coli strains were isolated. The DNA derived from the isolates was analysed by means of rep-PCR fingerprinting with the use of primers specific for ERIC or REP repetitive sequences. The PCR products were separated electrophoretically. The products obtained using specific primers for REP-type repetitive sequences revealed a higher complication of genomic fingerprints than found for products of reaction rep-PCR with primers of the ERIC-type. The obtained genomic fingerprints were analysed with BioGene software, which enabled the determination of the rate of the inter-strain similarity/relatedness. Dendrograms were constructed using the Jaccard similarity coefficient. The analysis revealed the diversity in the distribution of REP- and ERIC-type repetitive sequences in E.coli strains. The similarity of the strains was compared, and related to collection time. The groups of similarity in dendrograms, obtained using REP and ERIC primers, were mainly formed by the strains isolated in the same given month in the case of the subsurface sample drawing stand. Such a tendency was not observed in the bottom zone.

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