

A GENOMIC APPROACH IN MICROBIAL RESEARCH: FROM TAXONOMY TO BIOTECHNOLOGY

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The beginnings of microbial genomics date back to 1995, when the complete sequences of two human pathogens were published, *Haemophilus influenzae* (1,78 Mbp) and *Mycoplasma genitalium* (0,57 Mbp), promptly followed by the first sequenced genome of an archaeon *Methanococcus* (later *Methanocaldococcus*) *jannaschii* [1, 2]. Over the next 4 years, the collection of bacterial and archaeal genomes grew exponentially and laid the basis for a comprehensive comparative analysis [3]. During the following years, various computational methods and databases were developed, that allow comparing genomes and predicting genes. The genomic approach has found application in many areas of microbiological research.

For many years, the 16S rRNA gene has been used as a reliable genetic marker in microbial identification and taxonomy but due to an extremely slow rate of development, it shows significant evolutionary limitation. As a result, different bacterial species can share identical or very similar 16S rRNA gene sequences but show high variability at the whole-genome level (e.g. genera *Pseudomonas*, *Streptomyces*, *Acinetobacter*). Thus, genomic analyzes enable more reliable identification and classification of microorganisms as well as the study of their evolution. For these purposes, it is possible to use the construction of phylogenetic trees [4], digital DNA:DNA hybridization [5], calculation of average nucleotide identity or average amino acid identity values [6], as well as core and pangenome analysis based on the orthologous gene determination [7, 8].

Genomic analyzes enable the study of metabolic pathways and biochemical processes in prokaryotic cells, even in non-cultivable species. The identification of coding sequences and regulatory genes enables a better understanding of components and their functions in the physiological processes of the cell. The knowledge can be used in the fight against various diseases (e.g. genetic disorders, cancer) or to determine target sites for the development of new antimicrobial agents against pathogenic microorganisms (viral, bacterial and fungal diseases) [9].

The genomic approach enables the study of adaptation mechanisms of microorganisms to various environmental conditions (such as enzymatic equipment or production of secondary metabolites). The identification of genetic determinants enabling the survival of organisms in special/inhospitable/extreme conditions (e.g. low/high temperature, pH, pressure, presence of heavy metals or other toxic substances) is

important for understanding the interactions of microorganisms with their environment, as well as microorganisms with each other. In addition, it is important for the study of evolutionary processes of microorganisms. Microorganisms living in harsh conditions are often characterized by the production of enzymes and secondary metabolites that are very valuable for various biotechnological applications (e.g. industry, bioremediation, bioplastics production); the genomic approach allows to predict the trait of interest and evaluate the biotechnological potential of the microorganism without using expensive tests [10].

In conclusion, the genomic approach can be applied in various areas of human activity, from basic biological research through medicine to the biotechnological use of microorganisms.

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