

The thesis describes the history of development of sequencing methods with special focus on the modern effective parallel sequencing methods and their application in microbiology. The development and improvements of sequencing systems lead to the acceleration of the process and considerable decrease of price, which consequently allow wider spectrum of applications. Each of the sequencing systems has its characteristic features including drawbacks stemming from the principle of the respective method. Not every method suitable for all the applications. In the thesis the sequencing methods are compared and examined with respect to their appropriateness for certain application fields in microbiology. The currently available sequencing methods are usually categorized into three "generations", distinguished by sets of typical features. First generation methods include the systems of Sanger and Maxam-Gilbert; "next generation" is represented by methods 454, Illumina, SOLiD and Helicos; and finally SMRT, Ion Torrent and the commercially not yet available nanopore sequencing are usually called "next-next generation". Now the sequencing becomes a standard technology of molecular biology, not only in the basic microbiological research, but it is also widely applied in medicine (quick identification of pathogens, metagenomic studies of the human body metabiomes).