

Abstract

The nasopharyngeal swab is a very heterogeneous easily available sample which is used to diagnose infectious diseases of the upper respiratory tract.

Recently, the swab is increasingly used in biomedical research. The nasopharynx is the place of contact between the external and internal surrounding of an individual and the first immune response to the intrusion of pathogens. Mucosal damage initiates inflammatory and regenerative processes. The nasopharyngeal mucosa is permanently inhabited by a large group of microorganisms which influence the process of the disease. Therefore, the nasopharyngeal swab is a very rich source of host cells and its microbiome.

The introduction of the method of massive parallel sequencing, has developed and automated methods for DNA and RNA isolation. It also led to a significant reduction in the cost of their analysis and provides an information about the host genome, the presence of microorganisms and the current level of expression of host and pathogen genes as well. Thanks to the introduction of the single cell sequencing method, it is possible to monitor the interactions of individual cell types under physiological conditions and during the immune response.

The aim of this work is to provide an overview of the biological function of the nasopharynx, its cellular composition and RNA sequencing method, which lead to the diagnosis of the disease and a better understanding of biological processes.