optimizing the therapy of Helicobacter-associated diseases and continuing the use of standard eradication therapy.

VIRUS-VIRUS INTERACTION

[1]Seniuk I.V., [2]Nodar Sulashvili

[1]National University of Pharmacy, Kharkiv, Ukraine

citochrom@gmail.com

[2]Tbilisi Open University, International School of Medicine, Tbilisi, Georgia

n.sulashvili@ug.edu.g e

Introduction. Several respiratory viruses can circulate during the same period and can concurrently or sequentially infect the respiratory tract, leading to virus–virus interactions. At the host level, the course of infection of 1 virus might be influenced by prior or concurrent infection by another virus. Infection by a first virus could enhance or reduce infection and replication of a second virus, resulting in positive (additive or synergistic) or negative (antagonistic) interaction.

Positive virus–virus interaction corresponds to a co-infection that might result in an increased disease severity and pathogenesis (e.g., severe acute respiratory syndrome coronavirus 2 [SARS-CoV-2] and influenza A[H1N1]). Negative virus-virus interaction can be homologous or heterologous depending on whether the 2 viruses belong to the same family or to different serotypes or families. Homologous virus-virus interaction implies that cross-reactive immunity against a first virus prevents infection with a second virus (e.g., among different influenza subtypes or lineages). Heterologous viral interference relies on induction of a nonspecific innate immune response by a first virus that reduces or prevents infection and replication of a second virus (e.g., influenza A virus [IAV] and respiratory syncytial virus [RSV]). The type of virus-virus interaction (negative or positive) is probably dependent on the respiratory viruses involved, the timing of each infection, and the interplay between the response of the host to each virus. In this perspective, we focus more specifically on viral interference.

Materials and Methods. A literature search was conducted in Google Scholar, PubMed, Scopus and Web of Science databases.

Results and Discussion. The more probable mechanism of negative viral interactions relies on the induction of a transient innate immunity by the interfering virus. Structural components of viruses are sensed by pattern recognition receptors in epithelial and immune cells. This recognition triggers the expression of interferon (IFN) – stimulated genes (ISGs) and type I (i.e., IFN-α/β) and type III (i.e., IFN-λ) IFNs. The IFN-α/β receptor is expressed on most cell types, whereas the IFN-λ receptor is predominantly present on epithelial cells of the gastrointestinal and respiratory tracts. Secreted IFNs bind to receptors present at the surface of infected and neighboring cells to amplify the expression of ISGs. This process leads to an antiviral defense program consisting in the

production of effectors that directly inhibit viral replication, as well as cytokines and chemokines.

Induction of ISGs by a first virus might limit infection and replication of a second virus, especially if they show a differential ability to induce an IFN response or different degrees of susceptibility to immune mediators. To evade the immune system, respiratory viruses have developed a series of mechanisms that counteract the induction and antiviral action of IFNs, which might influence the type of virus–virus interactions. Influenza viruses and SARS-CoV-2 have developed a broader range of multifaceted strategies to escape IFN induction and signaling than RSV, human metapneumovirus (HMPV) and human rhinovirus (HRV).

At the cellular level, blocking or reduction of cell surface receptors and competition for cellular resources and factors were suggested as mechanisms of negative virus–virus interaction. For instance, the expression of neuraminidase in 293T cells infected with influenza A(H1N1) or A(H3N2) viruses can prevent a subsequent infection with retroviruses pseudotyped with a range of hemagglutinin molecules or a second IAV by removing sialic acid from the cell surface. Furthermore, replication of RSV was inhibited during co-infection with IAV in MDCK cells by competition for viral protein synthesis and budding from infected cells.

Other mechanisms leading to reduced or increased viral replication include the down-regulation or up-regulation of the gene promotor of a virus by a gene product of an interfering virus, but these mechanisms have not been yet demonstrated for respiratory viruses. Positive virus-virus interaction could result from the formation of syncytia. For instance, the cell-cell fusion activity of human parainfluenza virus type 2 was shown to enhance the growth of IAV *in Vero cells*. Co-infection could also increase disease severity through an overzealous production of IFNs or proinflammatory cytokines or through a reduced secretion of noninflammatory mediators, such as interleukin 10.

Defective viral genomes (DVGs) are produced during replication of RNA viruses and are believed to play a role in adaptation, viral escape, and persistence. DVGs have severe genomic truncations/modifications and require a full-length helper virus to replicate. DVGs are packaged, forming virus particles that are biochemically and morphologically similar to standard virus. DVGs might hamper the cytopathic effects induced by a wild-type virus. DVGs also rapidly produce cytopathic effects and interfere with replication of other co-infecting homologous or heterologous viruses. DVGs resulting from influenza virus replication can mediate homologous interference by competing with viral genomes for replication or packaging. DVGs might also mediate heterologous interference through production of IFN-I and IFN-III.

The role of DVGs in viral interference is not clearly established, but it is suggested that they could be used as therapeutic interfering particles against respiratory virus infections. In this respect, a first infection of mice with influenza A-based defective interfering virus, which was derived by a single central deletion from the full-length

genomic segment 1 of influenza virus isolate A/PR/8/34 (H1N1), prevented disease caused by a second infection with a heterologous IBV. Protection against IBV was partially alleviated in mice that did not express a functional type I IFN receptor. Furthermore, a first infection with influenza A-based defective interfering virus also protected mice against a second infection with pneumonia virus, a genetically unrelated respiratory virus.

Conclusions. Recent viral infections of the respiratory tract might induce a refractory period during which the host is less likely to be infected by another respiratory virus. This viral interference requires closely spaced virus co-exposures, implying that both viruses share common ecologic conditions (e.g., cold weather). Factors that could predict an interference between respiratory viruses include the capacity of the interfering virus to induce a rapid IFN response; the degree of susceptibility of the second virus to immune mediators; the extent to which the different viruses counteract the induction and antiviral effects of IFN; and the differential innate immune response patterns triggered by each viruses in the upper and lower respiratory tracts.

BIOLOGICAL METHODS TO IDENTIFY MICROORGANISMS

Seniuk I.V., Shcherbak O. A., El Hajjami Nada
National Pharmaceutical University, Kharkiv, Ukraine
citochrom@gmail.com

Introduction. Two factors determine the potential use of microorganisms in biotechnological processes, and also the pathogenicity of other strains are their genetic features and biochemical abilities. In the near future, industrial application as well as treatment of infection, will be possible after characterization, identification, and following taxonomic classification of the biological material. It is necessary to emphasize that taxonomy and systematics, very often used interchangeably, are in fact two different terms. Although systematics deals with the diversity of organisms, relationships, and possible interactions, taxonomy is a classification of organisms in a hierarchical structure of homogeneous groups that consist of descendants of the nearest common ancestor. Despite a high degree of phenotypic similarity, every assemblage of an individual shows some degree of phenotypic diversity due to genotypic variation. The greater the differences at the genetic level, the farther the related organisms are. Commonly known and used examples of hierarchical classification are the kingdom, division, class, family, genus, species, and finally, strain. Research works in the field of classification, systematics, and identification of microorganisms are interconnected and have an impact on each other. Accurate identification affects taxonomic classification of microorganisms as well as their systematics, and vice versa. Therefore, the broader the research aimed at the characterization of an individual microorganism, the more precise its identification, and thus the classification and systematics. Accordingly, the