



Virus in Human Health

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Editorial

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Abstract

Virus discovery as submicroscopic entities, data from the end of the 19th century, which marked the beginning of a new research discipline, the viruses study. Since then, the presence of viruses has been found in cancer and in multiple diseases whose origin was unknown. Viruses have shown their great potential in triggering infections, causing pandemics at a high cost to society as the Spanish Flu in 1918. The challenge of acting at the health emergency due to the outbreak of diseases caused by new viruses, has led to research with the application of new technologies, in order to find strategies, diagnostic methods, treatment and development of vaccines.

Keywords: Virus; Cancer; Classification; Pandemic; Coronavirus

Editorial

Presence of virus in plants and animals is dated since the end of nineteenth century with Dimitri Ivanovsky to whom credit is given to recognize a filterable and submicroscopic entity as the cause of tobacco mosaic disease [1,2]. In 1903 Borrel propose the virus theory of cancer [3] and few years later (1908) an avian leukemia virus was discovered [4]. In 1911 Peyton Rouse reported the isolation of “filterable agent” that was later called the Rouse Sarcoma Virus [5,6]. The following studies around the Rouse sarcoma virus marked an important starting point in virus research [7]. Finally in a mammary cancer in mice the interaction of three etiological factors (genetic background, hormones and virus) was proposed as clinical disease [8].

Since then, researchers have looked for cancer-related viruses in animals, such as rabbit papilloma-carcinoma, rabbit fibroma and myxoma, murine mammary carcinoma, bovine ocular carcinoma, canine mast cell sarcoma and sheep adenomatosis [8]. In a study of cancer incidence related to infectious agents in the year of 2002, it was founded an association with human papilloma viruses (5.2%), the hepatitis B and C viruses (4.9%), Epstein-Barr virus (1%),

human immunodeficiency virus (HIV) together with the human herpes virus 8 (0.9%) and human T-cell lymphotropic virus type I (0.03%) [9]. It has been estimated that between 15% - 20% of all cancers are related with oncogenic viruses [10].

In human, viruses like particles were identified in pre-cancerous, cancerous tissues and serum by electron microscopy, which allowed its morphological description [11-17]. Currently viral particles are analyzed by different imaging techniques as fluorescence, transmission and scanning electron microscopy, electron tomography, focused ion beam/scanning (FIB/SEM), single molecule tracking, structured illumination microscopy, stimulated emission depletion, stochastic optical reconstruction microscopy, photoactivation localization microscopy, ground state depletion and correlative light electron microscopy (Figure 1) [18]. In clinical samples virus can be identified by viral cultures, ELISA test, immunoprecipitation, *in situ* hybridization, end point PCR, multiplex PCR, real time PCR, flow cytometry, ViriChip method, and Next-generation sequencing (NGS) [19-21].

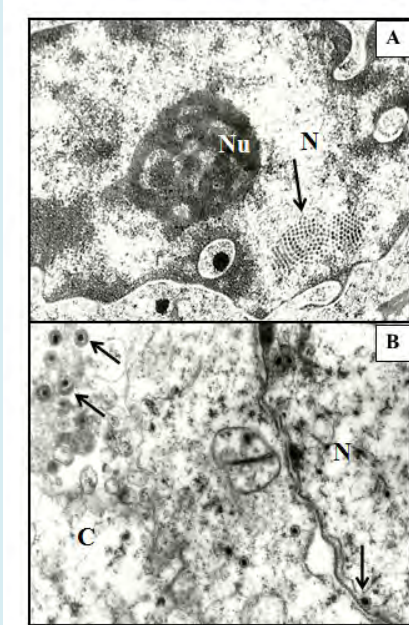


Figure 1: Electron micrograph of viruses. A) Nucleus inclusion of papilloma virus in crystalline arrangement in epidermal cell (arrows; 19,680X); B) Cytoplasmic and nucleus inclusions of Pseudorrabia virus in kidney cells (arrows; 24,000 X). C: cytoplasm; N: Nucleus; Nu: nucleolus. Uranyl acetate and Lead citrate. Archive photomicrographs from the Experimental Neuropathology Laboratory.

Virus classification has been established by the International Committee on Taxonomy of viruses (ICTV) since 1966; the classification is organized into taxonomic levels that have changed over time according to the knowledge that is being acquired due to technological and molecular advances that have better tools to investigate viruses in more detail [22]. At the beginning ICTV recognized only genera and families, later virus classification developed into a five-rank hierarchy (species, genus, subfamily, family and order) which staying until 2017. In 2019 the virus classification evolved to fifteen-rank structure, which also includes genomic properties and comparative sequences analysis of conserved genes and proteins. In the last decades of the 20th century, other classification was proposed according to their genome type (double- stranded DNA, single-stranded DNA, double-stranded RNA, positive-sense RNA, negative-sense RNA, reverse-transcribing RNA and reverse-transcribing DNA) [2].

The human viroma, which is part of the microbiome, is distributed in different compartments in the body, harboring viral communities that changing during lifespan and in response to environment [23]. It has been estimated that more than ten permanent viral infections are chronically present in the human body [24], which can lead to

oncogenesis [10]. In a metagenomics sequencing analysis from human samples only 14% - 87% sequences have been classified [25]. In human, DNA viruses have been found throughout the body in healthy asymptomatic subjects and in illness symptomatic conditions, such as those of the *Herpesviridae* family (*Cytomegalovirus*, *Lymphocryptovirus*, *Rhadinovirus*, *Roseolavirus*, *Simplexvirus*), *Papillomaviridae* family (*Alphapapillomavirus*, *Betapapillomavirus*, *Gammapapillomavirus*) and *Polyomaviridae* family (*Alphapolyomavirus*, *Betapolyomavirus*, *Deltapolyomavirus*), among others. Other human viruses with specific distribution in human body have been reported, as is the case of the *Coronaviridae* family, *Paramyxoviridae* family, *Pneumoviridae* family, *Orthomyxoviridae* family, *Parvoviridae* family, *Astroviridae* family, *Reoviridae* family, *Caliciviridae* family, *Picornaviridae* family, *Picobirnaviridae* family, and *Flaviviridae* family, among others. Unlike DNA virus, RNA virus tends to cause acute infections. [23].

It has been proposed that virus spread could be by means of horizontal (within a species by postnatal contact), vertical (neonatal or prenatal transmission within a species from mother to young) and by exogenous spread (transmission of virus from one species to another with or without the aid of insect vectors) [8] and it has been observed that individuals that recover from some acute infections can still carry the pathogenic viruses for varying periods of time [26,27].

Threats to human health due to infections by microorganisms have always been present, which have been controlled by advances in scientific knowledge, however, threats of zoonotic infections have emerged, which have become epidemics and have spread widely, becoming pandemics such as the Spanish Flu in 1918, Asian Flu H2N2 in 1957, Hong Kong Flu H3N2 in 1968, Hantavirus pulmonary syndrome in 1993, SARS CoV-2 in 2002-2003, the Influenza A H1N1 pdm09 in 2009, MERS-CoV in 2012, the polio resurgence in 2014, the Ebola epidemic in West Africa in 2014, the emergence of Zika virus in the Americas in 2016 and currently the SARS-CoV-2 (2019-2020) [28,29].

Zoonotic virus, severe acute respiratory syndrome-related coronavirus 2 (SARS-CoV-2) according to the ICTV classification, belongs to the order of the Nidovirales, Coronavirineae suborder, Coronaviridae family, Orthocoronavirinae subfamily, Betacoronavirus genus, and Sarbecovirus subgenus, with a positive-sense single-stranded RNA genome. This novel type of coronavirus made its appearance in late december 2019 in Wuhan China, and from there the infection spread rapidly by human to human transmission [2,30]. The clinical manifestations of COVID-19 disease are diverse related with respiratory (fever, headache, fatigue, sore throat, nasal congestion, cough, dyspnea, and acute respiratory stress) and neurological

disorders, in addition to nausea, vomiting and diarrhea that have also been reported. This pandemic is a new challenge for humanity, but due to the technological advances, the genomic characterization was obtained by next-generation sequencing in patient samples and the scientific community has focused on investigating the origin, structure, genome and biological behavior of this new virus, as well as finding efficient, fast and reliable diagnostic methods, treatments and in vaccines development [31-33].

The appearance of new infectious diseases is the result of development and globalization, in which the economic exchange between countries, travel, and the invasion and contact with different ecological niches, have confronted humans with new microorganisms, which in turn, due to environmental changes caused by man, have undergone mutations that make them more capable of invading new environments.

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