










Nanotechnology based solutions to combat zoonotic viruses with special attention to SARS, MERS, and COVID 19: Detection, protection and medication

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Highlights

- Brief information's on previous zoonotic viral disease outbreaks
- Reviewed the use of nanotechnology for zoonotic virus management
- Discussed the development of nano-based materials for the treatments and vaccines development

Abstract

Zoonotic viruses originate from birds or animal sources and responsible for disease transmission from animals to people through zoonotic spill over and presents a significant global health concern due to lack of rapid diagnostics and therapeutics. The Corona viruses (CoV) were known to be transmitted in mammals. Early this year, SARS-CoV-2, a novel strain of corona virus, was identified as the causative pathogen of an outbreak of viral pneumonia in Wuhan, China. The disease later named corona virus disease 2019 (COVID-19), subsequently spread across the globe rapidly. Nano-particles and viruses are comparable in size, which serves to be a major advantage of using nano-material in clinical strategy to combat viruses. Nanotechnology provides novel solutions against zoonotic viruses by providing cheap and efficient detection methods, novel, and new effective rapid diagnostics and therapeutics. The prospective of nanotechnology in COVID 19 is exceptionally high due to their small size, large surface-to-volume ratio, susceptibility to modification, intrinsic viricidal activity. The nano-based strategies address the COVID 19 by extending their role in i) designing nano-materials for drug/vaccine delivery, ii) developing nano-based diagnostic approaches like nano-sensors iii) novel nano-based personal protection equipment to be used in prevention strategies. This review aims to bring attention to the significant contribution of nanotechnology to mitigate against zoonotic viral pandemics by prevention, faster diagnosis and medication point of view.

Introduction

Zoonotic viruses were identified as life-threatening pathogens for the past three decades and associated with a global disease outbreak. Zoonotic viruses were predominantly found in wild species and capable of transmitting to humans and other domestic animals through direct or indirect contact with infected populations [1]. Direct contact includes coming into contact with body fluids such as saliva, blood, urine, mucous, and faeces. Meanwhile, the indirect contact includes exposure to habitat, surface or food accessed by the infected animals and studies have shown that zoonotic viruses were capable of transmitting through insect vectors, food, and water [2], as illustrated in Fig. 1.

The symptoms on the infected host also showed varying degrees of symptoms depending on the virus types. As the animals and birds play an essential role in the global economy and environmental impact, it is essential to study and keep tracking Zoonotic diseases to prevent pandemic and epidemic outbreaks. In the last three decades, we have evidence of a noticeable spike in emerging zoonotic diseases in humans (70% of infectious diseases were Zoonotic diseases) [3]. However, due to the loss of natural habitats, lifestyle, human behaviour, and food habits, increasingly, these viruses are emerging from wild species. Zoonotic pathogens were noticed in humans for a very long time and historically featured as human diseases, and evidence showed that most of these diseases have come from domestic animals, poultry and livestock sources [4].

The Bats (*Chiroptera*) were identified as reservoirs of viral pathogens and identified as an initial host for diseases such as Severe acute respiratory syndrome (SARS), Ebola hemorrhagic fever, and COVID 19 disease [5]. The zoonotic viruses such as Paramyxoviruses, Coronaviruses, Filoviruses, astroviruses, adenoviruses and herpesviruses were previously reported in bats [6]. The health threat of these viruses to the public remains unclear and may range from mild to severe illness; it would be necessary to keep tracking Zoonotic diseases for potential spill over events. Although bats were identified as the reservoirs of zoonotic viral pathogens, recent events showed non-bat origin zoonotic viruses exist. For example, the West Nile virus (WNV) was first identified in Uganda in 1937, and the first outbreak was noticed in the United States in the summer of 1999. The studies showed that WNV gets transmitted from birds to humans through mosquito bites [7]. Chikungunya virus (ChV) belongs to the genus *Togaviridae* is another zoonotic virus transmitted to humans by infected *Aedes aegypti* and *Aedes albopictus*. Although the ChV infection is nonlethal, it is a major concern as it left patients with chronic joint pain (arthralgia) [8].

The Corona viruses (CoV) were known to be transmitted in animals for a long time (since 1964), and the first animal-human transmission and pathogenicity was observed as a severe acute respiratory syndrome (SARS, 2002) in the East Asian region and the Middle East respiratory syndrome (MERS, 2012) in the Middle East region [9,10]. The SARS outbreak recorded more than 8000 confirmed cases and 800 deaths approximately, and the fatality rate for MERS ranges between 40 and 50%. In general, six CoV strains were known to infect humans, including human CoV 229E (HCoV-229E), HCoV-OC43, HCoV-NL63, HCoV-HKU1, SARS-CoV, and MERS-CoV. As of April 2020, there are no potential vaccines or drugs that have been shown to prevent or cure both SARS and MERS [11,12]. However, researchers and pharmaceutical companies have conducted clinical trials with both western and traditional medicines against CoV strains. The World Health Organization is effectively involved in coordinating efforts to develop vaccines and drugs against CoV related diseases.

Recently, a novel coronavirus strain has posed a public health threat and responsible for an ongoing pandemic globally; the strain was named severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) by the International Committee on Taxonomy of Viruses (ICTV) and identified as a causative pathogen for the disease COVID-19. The pandemic was tracked to Huanan South China Seafood Market in Wuhan, China. Initially, the SARS-CoV-2 spread rapidly within China and later on spread to many countries [13]. The genomic analysis of the SARS-CoV-2 strain suggests that it is closely related to bat-SL-CoVZXC21 and bat-SL-CoVZC45 strains and genetically distinct from MERS-CoV (nearly 50%) and SARS-CoV (79% similarity) [14].

The genomic and sequence information of SARS-CoV-2 strains were freely available in ViPR [15] and NCBI databases [16]. The phylogenetic analysis of SARS-CoV-2 strains obtained from the Indian population was performed to analyze the evolution and spread of the virus across different Indian states [17]. The cladograms of SARS-CoV-2 genomic RNA from different countries were illustrated in Fig. 2. The genome analysis suggests that during the transmission, the SARS-CoV-2 has differentiated into many clades globally and is continuously evolving [18]. The clinical data suggest that the reported COVID-19 cases have ranged from asymptomatic to severe respiratory infection, which leads to death, and the symptoms can include fever, cough, shortness of breath. Considering the severity of this disease and the spreading potential on a global scale, World Health Organization (WHO) declared a global health emergency on January 31, 2020 and a pandemic situation on March 11, 2020, subsequently [13]. At present, there are no potential vaccines or drugs that have been shown to prevent or treat COVID-19 effectively, and most countries are currently trying to prevent the spreading of the SARS-CoV-2 virus by implementing control and preventive strategies.