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REVIEW ARTICLE

Perspective on therapeutic and diagnostic potential of camel nanobodies for coronavirus disease- 19 (COVID- 19)

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Abstract

In this paper, we focus on the camelid nanobodies as a revolutionary therapy that can guide efforts to discover new drugs for Coronavirus disease (COVID-19). The small size property makes nanobodies capable of penetrating efficiently into tissues and recognizing cryptic antigens. Strong antigen affinity and stability in the gastrointestinal tract allow them to be used via oral administration. In fact, the use of nanobodies as inhalant can be directly delivered to the target organ, conferring high pulmonary drug concentrations and low systemic drug concentrations and minimal systemic side effects. For that, nanobodies are referred as a class of next-generation antibodies. Nanobodies permit the construction of multivalent formats that may achieve ultra-high neutralization potency and then may prevent mutational escape and can neutralize a wide range of SARS-CoV-2 variants. Due to their distinctive characteristics, nanobodies can be of great use in the development of promising treatment or preventive strategies against SARS-CoV-2 infection. In this review, the state-of-the-art of camel nanobodies design strategies against the virus including SARS-CoV-2 are critically summarized. The application of general nanotechnology was also discussed to mitigate and control emerging SARS-CoV-2 infection.

Keywords Antibodies engineering · Coronavirus disease (COVID-19) · Heavy chain antibodies · Pandemic · Single- domain antibody

Introduction

The coronavirus disease 2019 (COVID-19) is spreading rapidly since its first appearance in Wuhan, China, in December 2019. The occurrence of COVID-19 has been reported from more than 200 countries worldwide. On 16 December 2020, the number of confirmed cases has reached 73,476,721 including 1,635,464 deaths (https://coronavirus.jhu.edu/map.html). Coronavirus was referred to as severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) and belongs to the beta-CoV genus of the Coronaviridae family (Lu et al. 2020). Phylogenetic analysis showed that SARS-CoV-2 genome has shared the highest nucleotide sequence identity to severe acute respiratory syndrome coronavirus

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