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Journal of Antivirals & Antiretrovirals

Editorial

Editorial Note on RNA Viruses

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DESCRIPTION

RNA viruses pose serious threats to human health. Their success relies on their capacity to generate genetic variability and, consequently, on their adaptive potential. We describe a strategy to attenuate RNA viruses by altering their evolutionary potential. We rationally altered the genomes of Coxsackie B3 and influenza A viruses to redirect their evolutionary trajectories towards detrimental regions in sequence space. Specifically, viral genomes were engineered to harbor more serine and leonine codons with nonsense mutation targets: codons that could generate Stop mutations after a single nucleotide substitution. Indeed, these viruses generated more Stop mutations both in vitro and in vivo, accompanied by significant losses in viral fitness. In vivo, the viruses were attenuated, generated high levels of neutralizing antibodies and protected against lethal challenge. Our study demonstrates that cornering viruses in 'risky' areas of sequence space may be implemented as a broad-spectrum vaccine strategy against RNA viruses.

Vaccines remain the most successful means of controlling morbidity and mortality caused by RNA viruses, yet relatively few viral vaccines exist. In recent years, several severe outbreaks have occurred: chikungunya and Zika viruses in the Americas, coronaviruses in the Middle East, and Ebola virus in West Africa.

Consequently, there is a need for rationally designed and broadly applicable vaccine strategies. Given their high mutation rates, large population sizes and short generation times, RNA viruses can evolve rapidly, and strategies to control RNA viruses should take into account this adaptive potential. Due to their mutation rates, RNA viruses generate networks of closely related genetic variants, linked through mutation , that allow them to escape from selective pressures and adapt to different

Environments Ultra deep characterization of single Rna nucleotide polymorphisms of viral populations reveals thousands of variants heterogeneously distributed throughout the genome.

This 'genetic architecture' suggests that certain mutations might be more or less accessible depending on the original nucleotide.

Codon, thereby defining different mutational neighborhoods within The same sequence space In evolutionary biology, sequence space refers to every combination of a given sequence and theoretically is a vast multidimensional hypercube connecting all possible combinations.

The important concern taken into account to treat viral infections. The oral and parenteral routes of drug administration have several shortcomings, however, which could lead to the search for formulating better delivery systems. Now, a day's Novel Drug Delivery Systems (NDDS) proved to be a better approach to enhance the effectiveness

Localization of a virus population in sequence space, defined by its starting sequence, should then determine which mutational neighborhoods are accessible. It is thus proposed that access to certain neighborhoods will determine the potential of reaching beneficial mutations to facilitate adaptation.

Viruses have the property to replicate very fast in host cell. It can attack any part of host cell. Therefore, the clinical efficacy of antiviral drugs and its bioavailability is more of the antivirals and improve the patient compliance and decrease the adverse effect.

CONCLUSION

Despite their dramatic impact on the reduction of infectious diseases, vaccines are viewed skeptically by some, and modern vaccines are subject to ever-tightening safety requirements. Many successful vaccines are attenuated strains that undergo limited replication in the vaccine. These live-attenuated vaccines offer advantages over inactivated agents, subunit or virus-like particles that do not replicate in the host, including a typically low cost of manufacture and the induction of rapid and long-lived hum oral and cell-mediated immunity after a single dose. Vaccines for polio, smallpox, and yellow fever are a few examples of highly successful, live-attenuated viral vaccines. However, these vaccines have a low but significant risk for reactogenicity and can sometimes produce life-threatening disease.

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Received: December 04, 2020; **Accepted:** December 18, 2020; **Published:** December 28, 2020

Citation: Karimulla, SK (2020) Editorial Note on RNA viruses. J Antivir Antiretrovir.S13:e001