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MINI-REVIEW

CRISPR-Cas system: from diagnostic tool to potential antiviral treatment

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Abstract

This mini review focuses on the diagnosis and treatment of virus diseases using Crisper-Cas technology. The present paper describes various strategies involved in diagnosing diseases using Crispr-Cas-based assays. Additionally, CRISPR-Cas systems offer great potential as new therapeutic tools for treating viral infections including HIV, Influenza, and SARS-CoV-2. There are several major challenges to be overcome before this technology can be applied routinely in clinical settings, such as finding a suitable delivery tool, toxicity, and immunogenicity, as well as off-target effects. This review also discusses ways to deal with the challenges associated with Crisper-Cas technology.

Key points

- *Crisper technology is being applied to diagnose infectious and non-infectious diseases.*
- *A new generation of CRISPR-Cas-based assays has been developed which detect pathogens within minutes, providing rapid diagnosis of diseases.*
- *Crispr-Cas tools can be used to combat viral infections, specifically HIV, influenza, and SARS-CoV-2.*

Keywords HIV · Influenza · SARS-CoV-2 · Crispr-Cas

Introduction

The clustered regularly interspaced short palindromic sequence repeats-Cas (CRISPR-Cas) system has emerged as a promising tool for next-generation pathogen diagnosis, gene editing, drug discovery, and therapeutics. It forms a part of natural adaptive immune response in many species of archaea and bacteria, against foreign bacteriophage and plasmid infections by cleaving their nucleic acid (Brouns et al. 2008; Horvath et al. 2010; Garneau et al. 2010; Barrangou et al. 2007). Research investigations now focus on optimizing Crispr-Cas system to be utilized in Humans (Cebrian-Serrano et al. 2017; Hendel et al. 2015; Kumar et al. 2019; Moorthy et al. 2020; Naeem et al. 2020).

Rapid detection of disease-causing pathogens enables accurate and quick treatment and helps in preventing the spread of disease. While conventional diagnostic methods such as restriction enzymes, recombinases, nucleases, sequencing-based methods, PCR/qPCR-based methods, and isothermal amplification-based techniques (Yang and Rothman 2004; Zhao et al. 2015; Scheler et al. 2014) are time-consuming, have low specificity and sensitivity, and are expensive, requires technical expertise, and sophisticated

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