

Advancements in modern biotechnological approaches for combating HIV infection

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ABSTRACT

Human immunodeficiency virus (HIV) continues to pose a major global health threat, affecting millions of individuals. While antiretroviral therapy (ART) has made substantial progress in managing the infection, a complete cure remains elusive. This review focuses on the latest advancements in biotechnological strategies aimed at combating HIV. Promising approaches include the development of therapeutic vaccines, monoclonal antibodies, and RNA interference. Therapeutic vaccines are being designed to enhance immune responses, while monoclonal antibodies, particularly broadly neutralizing ones, target viral replication. RNA interference, utilizing small interfering RNA (siRNA), is being explored to silence essential viral genes and reduce viral burden. Furthermore, gene-editing tools such as CRISPR-Cas9 offer potential for the targeted removal of HIV from infected cells. This review highlights the mechanisms and ongoing research surrounding these innovative technologies, evaluating their potential to overcome the challenges of current HIV treatments and bringing us closer to a cure.

Keywords: *Human immunodeficiency virus (HIV), antiretroviral therapy (ART), therapeutic vaccines, monoclonal antibodies, RNA interference, CRISPR-Cas9*

Introduction

HIV/AIDS is a major public health concern worldwide more than 30 years after HIV was identified as the cause of acquired immunodeficiency syndrome (AIDS). With over 2 million new infections and 1 million AIDS-related deaths annually, there are currently over 36 million individuals living with HIV (Auclair et al. 2018). HIV infection causes a significant reduction in host immunity through the death of CD4⁺ T-cells, which throws off the balance between the host immune response and the human microbiome (Li et al. 2023). Although the primary method of transmission in adults is heterosexual, mother-to-child transmission (MTCT) during pregnancy, labor, and delivery, as well as postpartum breastfeeding, accounts for the majority of pediatric infections (Amin et al. 2021). HIV is a retrovirus with a lipid-based envelope that is around 100 nm in diameter. The envelope contains 72 trimers of the Env proteins, gp120 and gp41. Within the envelope is a conical capsid that contains two copies of positive-sense single-stranded RNA that code for structural and regulatory proteins. The HIV genome encodes several regulatory proteins, including the transactivator protein (Tat) and the RNA splicing regulator (Rev), which are necessary for viral replication (Cohen et al. 2010). The initial viral proteins to participate in the replication cycle are the Env proteins; gp120 and gp41 mediate the binding to the cell and the fusing to the cellular membrane, respectively (Arrildt et al. 2012). It is believed that infected monocytes act as “Trojan Horses” to pass the blood-brain barrier and allow HIV to enter the brain. The virus spreads throughout the brain when the monocytes develop into macrophages and create fresh HIV virions (Gaskill et al. 2017). Perivascular macrophages, microglia, and astrocytes are the main targets of HIV infection (Joseph et al. 2015). However, it is still unknown how astrocytes enter these cells and what part they play in HIV neuropathogenesis overall (Luo et al. 2015; Joseph et al. 2015). Numerous inflammatory host and viral factors, including as cytokines, chemokines, and viral proteins, are produced and secreted by infected cells, mainly macrophages, monocytes, and microglia. Chronic neuroinflammation is the outcome of these factors (Hong et al. 2015; Zayyad et

al. 2015). Antiretroviral treatment (ART) quickly lowers the plasma viral load to values below the detection limit when HIV-1 infection is treated (Palella et al. 1998). HIV eradication is hampered by the existence of a long-lasting reservoir of latently infected cells carrying proviral HIV-1 DNA, even while therapy with ART stops viral replication (Robb et al. 2016). After stopping ART, this reservoir – which was created early in the infection – continues to act as a source of viral reproduction. Peripheral CD4⁺ T cell levels of HIV-1 DNA dramatically drop when ART is started during acute infection; those treated at the earliest stage of acute infection show the largest reduction (Ananworanich et al. 2016; Ananworanich et al. 2012). Advances in HIV therapy and prevention have been made possible by contemporary biotechnological techniques like gene editing, HIV vaccines, recombinant viral vectors, and enhanced drug delivery systems (Pantaleo et al. 2010). This review attempts to investigate these contemporary biotechnology methods, evaluate their present state, and look into their prospective applications in the future.

Biotechnological techniques in HIV management

Gene editing technology (CRISPR-cas System)

Gene-editing techniques that are related to the clustered regularly interspaced short palindromic repeat (CRISPR)-associated nuclease 9 (Cas9) have been created and marketed as efficient treatments for HIV-1 infection in recent years. However, new gene-targeting techniques that are based on or work similarly to CRISPR/Cas9, such as prime editing, base editor, SHERLOCK, DETECTR, PAC-MAN, ABACAS, and pfAGO, have been created and optimized for the identification of pathogens and the correction of disorders (Zhang et al. 2022).

Table. 1: Application of CRISPR-cas system

CRISPR-cas system	Delivery	Target	Cell type/organisms	Animal Model	Ref.
SpCas9	Lentivirus, Adenovirus, Electroporation & Transfection,	LTR, Rev, Gag, Pol, Env, CCR5, CXCR4, Restriction factors,	HEK293T, 293T-CD4-CCR5, 293 Primary T cells, HeLa, TZM-b1, Jurkat, SupT1, K562, hPSC, iPSC, , U937, JLat10.6, J.Lat FL, CEMss, C8166, Ghost, pMoHIV, CHO, human CD34+ HSPCs, CHME5	Mouse	Ebina et al. 2013; Hu et al. 2014; Liao et al. 2015; Wang et al. 2014; Wang et al. 2016; Lebbink et al. 2017; Cho et al. 2013; Li et al. 2015
SaCas9	AAV, Lentivirus & Transfection	TR, Gag, proviral HIV DNA, CCR5, CXCR4,	HEK293T, TZM-bl, C11, Ghost, Jurkat, primary CD4+ T, human CD34+ HSPCs, J-Lat 6.3	Tg26 transgenic mouse, SIV-infected macaques	Xiao et al. 2019a; Olson et al. 2020; Zhang et al. 2022
CRISPRa	Transfection, Lentivirus & Electroporation	LTR, APOBEC3G, APOBEC3B, T5, T6,	TZM-b1, J-Lat, CHME5 microglial cell, C11, HEK293T, ACH2, J1.1, CEM LCHIT 3.2, HeLa, U1	No	Zhang et al. 2022
CRISPRi	Lentivirus	PSMD 1, PSMD 3, PSMD 8, Spt4, Spt5, host factors (FTSJ3, TMEM178A, NICN1)	Jurkat 2D10	No	Krasnopolsky et al. 2021; Zhang et al. 2022)

CPF1	Adenovirus & Lentivirus	CCR5, LTR, Gag, Vpr, Tat, Rev	TZM-b1, SupT1-R5, Primary CD4+T cells, HEK293T	No	Zhang et al. 2022; Gao et al. 2020)
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Even if the use of CRISPR/Cas gene editing to treat HIV-1 has advanced and improved, DSB still causes some unavoidable flaws in the NHEJ and HDR processes that could result in uncontrollable adverse effects. Alexis et al. created a unique genome editing method known as “base editor” to prevent DSB. It consists of a DNA-modifying enzyme, such cytidine deaminase, and a programmable DNA-binding protein, like catalytically impaired Cas9, which is incapable of cleaving DNA, or nickase Cas9 Cytosine base editor (CBE) is a “base editor” that can be effectively modified. Its “active window” is usually bases 4–8 of the protospacer, where PAM is counted as 21–23 bases. As a result, it can successfully fix a variety of point mutations linked to human illnesses (Komor et al. 2016). Base editors can successfully install four transition mutations (C→T, G→A, A→G, and T→C), but at this point, the remaining eight conversions (C→A, C→G, G→C, G→T, G→T, A→C, T→A, and T→G) cannot be generated. By combining reverse transcriptase with catalytically damaged Cas9 (H840A), a novel gene-editing method known as Prime Editing (PE) was created to address this issue. Using a primary editing guide RNA (pegRNA), which binds specifically to the target site and encodes for the necessary editing sequence, new genetic information is directly written into the designated DNA spot in the PE system (Anzalone et al. 2019).

HIV-1 genomic RNA and inbound RNA in infected cells can be targeted by Cas13a. For quick, easy, and sensitive target gene detection, specific high-sensitivity enzymatic reporter unlocking (SHERLOCK) was proposed by combining the Cas13a enzymology of RNA cleavage with nucleic acid preamplification of isothermal recombinase polymerase or reverse transcription recombinase polymerase (Kellnar et al. 2019) (Gootenberg et al. 2017). Similar to SHERLOCK, the Cas12a derived DNA endonuclease-targeted CRISPR trans reporter (DETECTR) can cause DSB, which induces nonspecific

DNA cleavage (Li et al. 2019). Therefore, DETECTR can break the ssDNA reporter with fluorescence and quenching groups linked at either end. It may detect HIV-1 provirus DNA in AIDS patients using DETECTR with specific gRNA/Cas12 (Li et al. 2019). The prophylactic antiviral CRISPR approach in human cells (PAC-MAN), which is also used to manage HIV-1/AIDS, was created by Abbott et al. in response to the COVID-19 pandemic caused by SARS-CoV-2 in the previous year. It is based on Cas13d and targets SARS-CoV-2 and all sequenced coronavirus strains (Abbott et al. 2020). The antibody and CAS fusion (ABACAS) technique was created by fusing Cas13 with a particular antibody of the primary viral structural proteins, namely S protein, in order to target SARS-CoV-2 more precisely. Since HIV-1 can also enter target cells by endocytosis, combining ABACAS with Cas13 and an HIV-1 antibody may increase the virus's selectivity and RNA cleavage efficiency (Zhang et al. 2022).

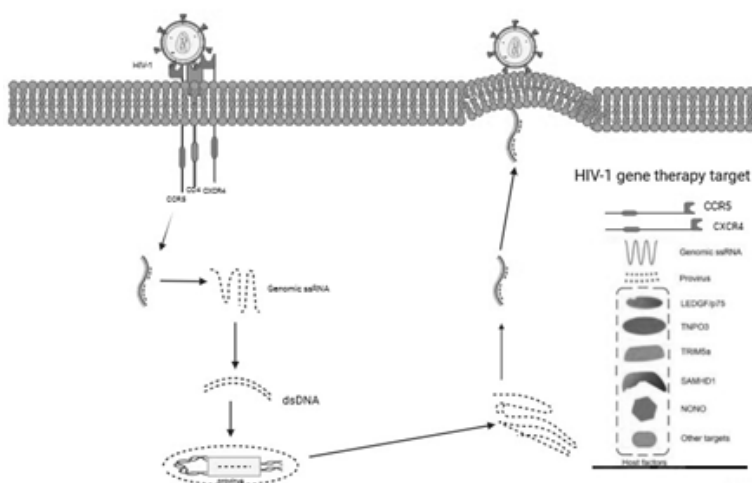


Fig. 1. Gene Editing Targets in the HIV-1 Life Cycle: HIV-1 gene therapy targets can be categorized into four main areas: **1. HIV-1 Co-Receptors:** Since HIV-1 invades immune cells via the CCR5 and CXCR4 co-receptors, gene-editing technologies can be employed to silence or mutate these co-

receptors, thereby rendering cells resistant to HIV-1 infection.

2. HIV-1 RNA Genome or Provirus: CRISPR-Cas systems like Cas12a and Cas13a can target and degrade HIV-1 RNA. Additionally, proviral DNA can either be excised using gene-editing tools or reactivated through CRISPRa as part of the “shock and kill” approach. **3. Essential Host Factors:** Host proteins like LEDGF/p75 and TNPO3, which are crucial for the HIV-1 life cycle, can be disrupted through gene-editing strategies to inhibit viral replication within host cells. **4. HIV-1 Restriction Factors:** Gene-editing tools or CRISPRa can be used to upregulate restriction factors such as TRIM5 α , SAMHD1, and NONO, or to create enhanced variants that bolster cellular defences against HIV-1 (Zhang et al. 2022).

RNA interference (rnaï) therapies for HIV:

The endoribonuclease Dicer recognizes and cleaves intracellular long double-stranded RNA (dsRNA) intermediates or endogenous microRNAs (miRNA) into small interfering RNAs (siRNAs) of 21–23 nucleotides, which starts the conventional route of RNA interference (Ding et al. 2007). An essential part of the RNA-induced silencing complex (RISC) is the Argonaute protein, more especially Ago2 in mammals. After one of the siRNAs is loaded onto Ago2, RISC uses the loaded siRNA’s guide strand to locate and cleave the complementary mRNA in the center of the siRNA:mRNA duplex. In the meantime, the loaded siRNA’s non-targeted (passenger) strand is removed (Svoboda et al. 2020). Artificial miRNA can be manufactured and expressed intracellularly from a transgenic construct, or synthetic mature siRNA or short shRNA can be utilized to create artificial dcrRNA, which can be transfected into the cell (Zeng et al. 2002).

Anti-HIV⁻¹-SiRNAs:

Anti-HIV-1 siRNAs may have an advantage over existing treatments in that their sequences may be modified to specifically target a patient’s unique viral strains, offering a more individualized therapeutic strategy. Additionally, they would create a number of new targets for HIV-1 combination medication therapy (Mizrahy et al. 2017). A major challenge for the development of anti-HIV-1 siRNAs

is that lymphocytes, which represent the major cell-type for HIV-1 replication, are widely distributed in the body and extremely difficult to penetrate with existing siRNA delivery technologies. Anti-HIV-1 siRNAs must be oral, have a long shelf life, and reduce viral loads to undetectable levels with at least one dose per day in order to compete with existing HIV-1 medication regimens (Scarborough et al. 2017).

Anti-HIV-1-ShRNAs

Three extensive siRNA screens have been carried out to find human genes involved in HIV-1 replication. Nevertheless, only three genes (MED7, MED8, and RELA) shared characteristics throughout the investigations, and none of them included well-known co-factors of HIV-1 replication like LEDGF/p75 (Brass et al. 2008; Zhou et al. 2008; Eekels et al. 2011). 30 human genes that have been linked to HIV-1 replication in the past, and various shRNAs target these genes (Eekels et al. 2011). They determined that TRBP, ALIX, and AGT6 were the most appropriate genes for long-term suppression of HIV-1 replication in shRNA-transduced T lymphocyte cell lines with low toxicity. CCR5 was not evaluated because it was already shown that it was a viable target for shRNA treatment. It would be extremely difficult for HIV-1 to become resistant to the reduction of a crucial component required for its reproduction if the mRNAs of cellular proteins essential in HIV-1 replication were targeted (Scarborough et al. 2017). Every coding and non-coding area of HIV-1 RNA can be targeted by shRNAs, and one shRNA that targets the overlapping tat/rev exon 1 reading frame has progressed to clinical trials. The fact that the target location of shRNAs targeting HIV-1 RNA is conserved across circulating HIV-1 strains is the most crucial factor in their design (Scarborough et al. 2017). Additionally, HIV-1 can evade shRNAs by acquiring mutations in sequences beyond the target site that affect its accessibility, most likely as a result of RNA structural alterations. RNA structural conservation may potentially be just as crucial for the creation of shRNAs as sequence conservation (Herrera-Carrillo et al. 2015; Westerhout et al. 2008).

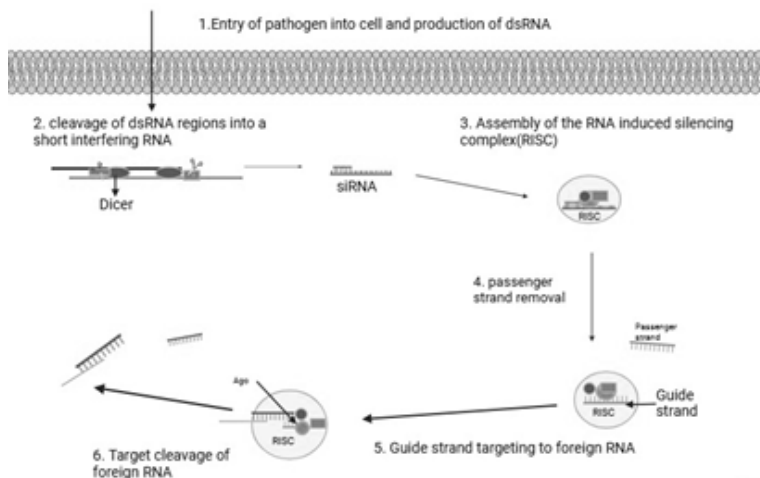


Fig. 2. Human micro-RNA (miRNA) pathway (Scarborough et al. 2017)

Monoclonal antibodies

Over the past few decades, a great deal of information has been gathered about monoclonal antibodies that target the HIV envelope (Env) glycoprotein. Both HIV-infected people with chronic progressive infection and people who control HIV without antiretroviral medication have been found to have a wide variety of antibodies with exceptional neutralizing potency and breadth against vast panels of cross-clade viruses (Freund et al. 2017; Walker et al. 2011). The CD4 binding site antibodies VRC01, 3BNC117, and VRC07-523LS; the V3-loop-directed antibodies PGT121 and 10-1074; the V1/V2 loop antibodies PGDM1400 and CAP256-VRC26.25; and the membrane-proximal region (MPER)-specific antibody 10E8 are among the monoclonal antibodies in clinical development for treatment and prevention (Doria-Rose et al. 2014; Sok et al. 2014). These antibodies target multiple epitopes on the surface of Env. In phase 1 and 2 studies, these antibodies—which were chosen for their capacity to bind and kill virions—have demonstrated encouraging outcomes by lowering plasma viremia and postponing viral rebound after

treatment interruptions for antiretroviral therapy (Rudicell et al. 2014; Rossignol et al. 2021). However, a broadly neutralizing monoclonal antibody's capacity to bind firmly to highly conserved areas of the viral envelope is a crucial factor in determining its capacity to induce neutralization (Lu et al. 2016a; Gautam et al. 2016). Rather, both Fab- and Fc-mediated processes are necessary for the removal of HIV reservoir cells. In order to eliminate the antibody-opsonized target, antibodies must recognize an infected cell and use Fc receptors (FcγRs) expressed on the cell to attract innate effector cells including neutrophils, monocytes, and natural killer cells (Ren et al. 2018; Rossignol et al. 2021). While earlier research has shown that broadly neutralizing antibodies (bNAb) may identify and eradicate infected cells, these antibodies only target neutralizing epitopes on the Env trimer, which could not fully represent the epitope landscape on the surface of the infected cell (Moore et al. 2006).

Vaccine development

Current strategies for preventing and treating HIV/AIDS include antiretroviral therapy (ART) and pre-exposure prophylaxis (PrEP), which have transformed AIDS into a manageable chronic condition. However, these treatments are costly, require strict adherence, may cause side effects, and face challenges like drug resistance. A prophylactic vaccine remains crucial to ending the epidemic, with recent advances in HIV immunogen design and mRNA vaccine technology offering promising developments (Mu et al. 2021). The basis of an mRNA vaccination is the mRNA encoding one or more immunogens, which are then translated into proteins when they are delivered into host cells. A possible new method of delivering antigens is using RNA-based vaccinations (Bloom et al. 2021).

Non-amplifying mRNA, encoding only the immunogen, offers a straightforward and cost-effective approach to mRNA vaccine development. Initially, such mRNAs were used alone or in liposomes as immunogen sources. Recent advancements, including codon optimization, 3' and 5' untranslated region modifications, nucleoside alterations, poly-A tail enhancements, and improved purification

methods, have significantly boosted their immunogenicity and safety (Petsch et al. 2012; Alameh et al. 2022).

Self-amplifying RNAs (saRNAs) are engineered replicons derived from RNA viruses that encode both the immunogen and replication machinery. Once inside the cell, saRNAs replicate, increasing immunogen production compared to non-amplifying RNAs. This allows saRNAs to achieve comparable immunogenicity at lower doses. They can be delivered directly or as viral replicon particles (VRPs), offering versatile approaches for vaccine development (Geall et al. 2013; Bloom et al. 2021).

Nanotechnology based drug delivery

A new and innovative approach to treating complicated illnesses is nanomedicine. With its high drug-loading capacity, ability to deliver medications to targeted diseased tissues, and increased biocompatibility, nanomedicine has numerous advantages over traditional medicine (Patra et al. 2018). Nanoparticles can also increase drug stability and control the release of the drug. Nanoparticles typically range from 1 to 100 nanometers. In addition, the composition of nanoparticles can be inorganic or organic. Nanoparticles can have a variety of shapes to meet the experiment's needs. Several nanomaterials, including dendrimers, liposomes, micelles, and nanosuspensions, have been studied for their potential application in HIV-1 infection (Fletcher et al. 2014).

Repeatedly branching molecules that radiate from a central core make up dendrimers. Their dynamic interior voids, restricted molecular weight distribution, and overall homogeneity make them very distinctive. By conjugating or absorbing pharmaceuticals onto their surface or by encapsulating them in their interior cavities, dendrimers can be utilized as nanocarriers (Dutta et al. 2007).

Micelles are lipid molecules that cluster spherically in aqueous solutions; pharmaceuticals can be encapsulated in the hydrophobic core of a micelle by forming a sort of shell around the water-soluble exterior (Chiappetta et al. 2010).

One or more phospholipid bilayer membranes around an aqueous center form the spherical structures known as liposomes. Liposomes offer many advantages as drug carriers owing to their nontoxic, non-immunogenic, biocompatible and biodegradable nature. The transdermal delivery of Indinavir – a protease inhibitor – was significantly enhanced by use of ethanolic liposomes (Dubey et al. 2010).

Colloidal dispersions of medication particles that are nanosized and usually stabilized by a surfactant to prevent agglomeration are known as nanosuspensions. Cellulosics, lecithin, poloxamer, and polysorbates are popular stabilizers used in nanosuspensions. Drugs that are broken down or not absorbed in the GI tract (GIT) and/or have demonstrated only modest increases in bioavailability by stabilizing with surfactants are more suited for injectable nanosuspensions. Numerous antiretroviral nanosuspensions have produced prolonged release characteristics that could enable reduced dosage frequency and enhanced adherence (Roy et al. 2015).

Challenges and limitations

CRISPR-cas9

This is still a problem for HIV-1/AIDS gene therapy in clinical research employing CRISPR/Cas9. In order to improve the practice in future applications, we should: (1) create more specific gRNA and Cas9 mutants to minimize off-target effects; (2) create single- or multi-functional base editors that can edit bases directly and accurately without DSB-induced NHEJ or HDR; (3) create Cas9 variants with flexible PAM sequences to increase the use of CRISPR/Cas9; (4) investigate new vehicles for the safe and effective delivery of gene-editing tools; and (5) optimize the HIV-1/AIDS animal models and conduct more in vivo gene therapy experiments, which will set the groundwork for clinical use. With the aforementioned developments, genome editing technologies like CRISPR/Cas9 could lead to interesting and optimistic advancements in HIV-1/AIDS gene therapy (Zhang et al. 2022).

RNAi

Gene therapy employing nucleotide-related drugs including ribozyme, antisense oligonucleotides, and siRNA has advanced significantly during the last 20 years. The therapeutic use of siRNA/shRNA in the treatment of HIV infections is, however, constrained by three factors. These three problems are the ineffectiveness of delivering nucleotide-derived medicines to target cells, the toxicities of RNA interference because of off-target effects, and the challenges of validating possible treatment leads from un vitro screening using an in vivo model (Zhang et al. 2007). One of the main barriers keeping RNAi from being useful therapeutic agents is cytotoxicity. By overloading the cellular RNA machinery, siRNA or shRNA can also have non-specific effects by blocking the normal function of endogenous miRNAs and blocking non-target mRNAs through sequence complementarity. The following proper design is essential to improve the specificity and reduce the toxicity of siRNA/shRNA: (i) reduce homology to non-target mRNAs; (ii) steer clear of perfect dsRNA stretches of 11 bp; and (iii) reduce inclusion of the sense strand into RISC (Boden et al. 2004).

Before RNA interference (RNAi) can be used as a viable treatment for HIV infection and other human diseases, a better knowledge of the mechanisms causing toxicity is necessary. Nowadays, conditional expression schemes are another way to reduce the toxicity of RNA interference, and doxycycline or ecdysone-controlled reversible on/off switch systems are already accessible over pol III and pol II promoters (Zhang et al. 2007; Wiznerowicz et al. 2006).

Vaccines & antibodies & nanotechnology

HIV vaccine research has largely aimed to generate antibodies that block the virus from infecting host cells, often using protein subunit vaccines with recombinant viral proteins as immunogens (Haynes et al. 2017). Challenges in developing broadly neutralizing antibody (bnAb) vaccines include tolerance mechanisms that limit bnAb B cell precursor development, peripheral anergy, and the unique traits required for bnAbs to neutralize HIV. Additionally, due

to HIV's rapid mutation and integration into host genes, achieving sterilizing immunity requires sustained, high levels of antibodies targeting multiple bnAb Env epitopes at the time of infection (Haynes et al. 2019). It has been gradually demonstrated that polyvalent HIV vaccines may be created and used to target conserved regions on the viral envelope, despite the high rate of variability (Marusic et al. 2009). Since most HIV strains can be neutralized by broadly neutralizing antibodies (bNAbs), this is the focus of the majority of current efforts. One significant benefit of bNAbs is their broad cross-reactivity, which allows them to neutralize a variety of HIV strains (Del Moral-Sánchez et al. 2019; Gruell et al. 2018).

However, by improving drug delivery, triggering efficient immune responses against HIV-infected cells, and—most importantly—directly targeting HIV latent reservoirs, nanomedicine-based techniques can enhance HIV therapy. Once medicines are combined with nanomedicine, there may be a chance to cure HIV. The clinical use of nanomedicine-based treatments has been sluggish, despite the field's revolutionary potential to advance anti-HIV medicine. To accelerate clinical translation and advance anti-HIV nanomedicine, more research is required to discover and better describe the pharmacokinetics, effectiveness, and biodistribution of nanotherapeutics (Andre et al. 2023).

Conclusion

Advancements in modern biotechnology have radically transformed HIV prevention, diagnosis, and treatment, presenting promising new methods for directly targeting the virus and overcoming longstanding challenges. Among these innovations, genome editing technologies, particularly CRISPR-Cas9, stand out for their ability to potentially modify the HIV genome and address the issue of latent reservoirs. Likewise, RNA interference (RNAi) has proven effective in silencing HIV-related genes, offering a precise method to hinder viral replication.

Monoclonal antibody therapies have also garnered attention for their ability to neutralize a wide range of HIV strains, providing a valuable addition to traditional antiretroviral

therapies. These treatments, often used in combination with existing drugs, have shown improved outcomes in controlling the virus and reducing viral loads. Concurrently, vaccine development has made significant strides, particularly with mRNA-based platforms and nanoparticle delivery systems, which have the potential to elicit stronger and more lasting immune responses, making long-term prevention and even immunity a tangible possibility.

On the diagnostic front, technological progress has enhanced the sensitivity, speed, and accessibility of HIV detection. From advanced point-of-care devices to sophisticated molecular assays, these innovations allow for earlier detection and continuous monitoring, contributing to better patient management. Furthermore, the integration of artificial intelligence and machine learning in biotechnological research is accelerating the discovery of novel therapeutic targets and optimizing treatment protocols.

However, challenges remain that must be addressed to fully realize the potential of these advances. HIV's genetic variability, its ability to establish latent reservoirs, and the complex dynamics between the virus and the immune system continue to complicate efforts toward a definitive cure. In addition, issues such as the high cost of new treatments and unequal access to healthcare pose significant barriers to the global impact of these innovations. Overcoming these obstacles will require sustained investment in research, international collaboration, and policies aimed at ensuring equitable access to new therapies and technologies.

In conclusion, modern biotechnological advances offer groundbreaking opportunities to reshape the future of HIV management. From genome editing and monoclonal antibody therapies to next-generation diagnostics and vaccines, these innovations are redefining how we approach the virus. While the journey toward eradication is still complex, the combination of scientific progress and global cooperation provides a clear path toward a world where HIV is no longer a significant threat to public health.

Future perspective

Continuous advancements in vaccine research, RNA treatments, and gene editing have the potential to completely transform HIV treatment. CRISPR-Cas9 and other gene-editing methods have the ability to target and eradicate the virus at the genetic level, while RNA-based treatments offer a more accurate method of regulating viral reproduction. mRNA vaccines' success against COVID-19 has raised hopes for comparable approaches to HIV prophylaxis. Machine learning and artificial intelligence are also speeding up medication research and making more individualized treatment plans possible. Addressing global disparities and moving closer to making HIV preventive, controllable, or even curable need ensuring that these discoveries are widely accessible.

Conflict of interest

There isn't any conflict of interest with this study.

Author contributions

Acquisition and interpretation of data is done by Tiyaisha Saha., Tanisha Bhowick and Dipti Das. Conception, design and revising of the article are done by Rupesh Dutta Banik.

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