HIV: Current Research

Extended Abstract

HIV Diagnosis and Treatment through Advanced Technologies

Qurban Ali

Abstract

Human immunodeficiency virus (HIV) is the chief contributor to global burden of disease. In 2010, HIV was the fifth leading cause of disability-adjusted life years in people of all ages and leading cause for people aged 30–44 years. It is classified as a member of the family Retroviridae and genus Lentivirus based on the biological, morphological, and genetic properties. It infects different cells of the immune system, such as CD4+ T cells (T-helper cells), dendritic cells, and macrophages. HIV has two subtypes: HIV-1 and HIV-2. Among these strains, HIV-1 is the most virulent and pathogenic. Advanced diagnostic methods are exploring new ways of treatment and contributing in the reduction of HIV cases. The diagnostic techniques like PCR, rapid test, EIA, p24 antigen, and western blot have markedly upgraded the diagnosis of HIV. Antiretroviral therapy and vaccines are promising candidates in providing therapeutic and preventive regimes, respectively. Invention of CRISPR/Cas9 is a breakthrough in the field of HIV disease management.

Keywords: HIV, retoviridae, lentivirus, macrophages, antiretroviral therapy, CRISPR/Cas9

Human immunodeficiency virus (HIV) originates from a monkey infecting virus, simian immunodeficiency virus (SIV), and a number of theories have been described in this regard. Many of the epidemiological, phylogenetic, and genomic characteristics of HIV are similar to those of SIV, and this strongly supports the idea of cross species transmission . HIV is classified as a member of the family Retroviridae and genus Lentivirus based on the biological, morphological, and genetic properties . Initial cases of HIV were reported in 1981 to Centre for Disease Control, and the virus was first isolated from patients with severe immune deficiency, later termed as Acquired Immune Deficiency Syndrome (AIDS), in 1983 .Since then, virology of HIV and pathogenesis of infection are constantly being studied. Proviral status is obtained by integration of this dsDNA into host cell genome by integrase enzyme. For further enhanced activation, a polypeptide scaffold Suntag is used by dCas9 that recruits multiple antibody-fusion proteins.

Epidemiology

Human immunodeficiency virus is the chief contributor to global burden of disease. In 2010, HIV was the fifth leading cause of disability-adjusted life years in people of all ages, and leading cause for people aged 30–44 years. In 2005, AIDS-related deaths peaked to 2.3 million globally, but reduced to 1.6 million by 2012. Group M of HIV-1 is the major cause of worldwide HIV epidemic. There are nine known phylogenetic subtypes, sub-subtypes of Group M, clades (A–K) and an inter-subtype circulating recombinant forms (CRFs) among which inter-subtype genetic diversity is 25% for the *env* gene and 15% for the *gag* gene. Subtypes and sub-subtypes are a result of founder effects at various time periods in the past, whereas if two different subtypes co-infect a patient it gives rise to the inter-subtype recombinants. These recombinants are called CRFs if they have a significant epidemic spread. Subtype B of HIV-1 dominates in Australia, Americas, and Europe, whereas subtype C predominates in India and Africa (which accounted for 48% of all the HIV-1 cases in 2007). In 2012, approximately 35.3 million individuals were living with HIV, with the highest global burden of HIV (70.8%) in Sub-saharan Africa . However, increasing access to antiretroviral therapies has significantly improved the global epidemiology of HIV infection. There has not been a significant increase in the prevalence of HIV globally, with 31 million cases reported in 2002 to 35.3 million cases reported in 2012. This is largely because people on antiretroviral therapies are living longer than before, while the global incidence has reduced by approximately 1 million from 2002 to 2012. According to the survey report of UNAIDS (2015), globally about 36.7 million people suffered from HIV infection and among them approximately 2.1 million new HIV infections were reported.

Qurban Ali

Centre of Excellence in Molecular Biology, University of the Punjab, Lahore, Pakistan
E-mail: qurban.ali@cemb.edu.pk

Recently, researchers have found out that RNA-guided mutations *via* CRISPR system not only can inhibit HIV replication but, on the other hand, also provide resistance. Mutations can eradicate HIV infection but some makes the HIV more resistant on getting high rate of surveillance by new mutations so there developed a difficulty in therapeutic targeting *via* CRISPR. RNA sequence of escaped HIV at cas9 cleavage site is investigated, and analysis showed that it is not the viral RT, which is the cause of these mutations but it is one of the cellular repair mechanism, i.e., NHEJ which by producing indels has ability to impair DNA functionality. Cas9 become unable to identify the target sequence anymore. It does no harm to virus; instead enable it to replicate further.

Conclusion

Since the terrible outbreak of HIV, the world is still suffering from its deadly consequences. As HIV is derived from SIV, so many of the epidemiological, phylogenetic, and genomic characteristics of HIV are similar to those of SIV, and this strongly supports the idea of cross-species transmission. ART has significantly altered the HIV global epidemiology. Initially, antiviral drugs were administered as monotherapy, but later on, the concept of combination therapy was introduced that is known as HAART having the potential to reduce the mortality and morbidity related to HIV-1 infection. Although there is no absolute treatment for HIV, continuous effort of researchers for developing better therapeutic approaches has become fruitful with the advent of CRISPR/Cas