Original Article

Molecular Epidemiology of HIV Gene in Pakistan

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Abstract

Introduction: AIDS is caused by the HIV virus, sometimes known as HIV. HIV comes in two different forms, HIV-1 and HIV-2.

Methods: The great majority of HIV infections worldwide are caused by HIV-1 because it is more virulent, easier to spread, and more contagious. HIV is a retrovirus that mostly affects immune system cells in people. The Centers for Disease Control and Prevention (CDC) of the United States first identified AIDS in 1981.

Results: Each retrovirus has two single chains of RNA, which make up its genome. For replication, a host cell is required, and the RNA must first be converted into DNA, which is accomplished by the enzyme reverse transcriptase. this organism has ten major genes make up *pol, vpr,tat, gag, rev, nef, vif, vpu and evn*.

Conclusion: In structural genes, *pol* gene is one of the genes encode reverse transcriptase, integrate and protease involve in reverse transcription, integration and cutting of proteins.The purpose of this study is to identify structure of *pol* gene and to analyze the different demographic factors associated with HIV in population of Pakistan also to ascertain the HIV prevalence in the Pakistani population.

Keyword: HIV, AIDs**,** Epidemiology, Genetics, pool

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Introductions

A lentivirus (a subclass of retroviruses) called the human immunodeficiency virus (HIV) is what causes HIV infection and, over time, AIDS. The Centers for Disease Control and Prevention (CDC) of the United

States first identified AIDS in 1981. There are two main forms of HIV: HIV type 1 (HIV-1) and HIV type 2. (HIV-2). HIV-1 is connected to viruses found in western African chimpanzees and gorillas, but HIV-2 is related to viruses found in the critically endangered sooty mangabey. Subgroups of HIV-1 viruses were further differentiated.
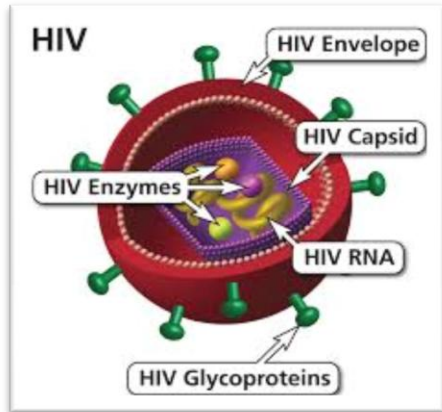

Fig 1: *structure of HIV*

HIV is spread mostly through sexual contact, prolonged exposure to bodily fluids or tissues containing the virus, and mother-to-child contact during pregnancy, childbirth, or breastfeeding (known as vertical transmission).

Unless these are contaminated with blood, there is no risk of contracting HIV via contact with faeces, nasal secretions, saliva, sputum, perspiration, tears, urine, or vomit.

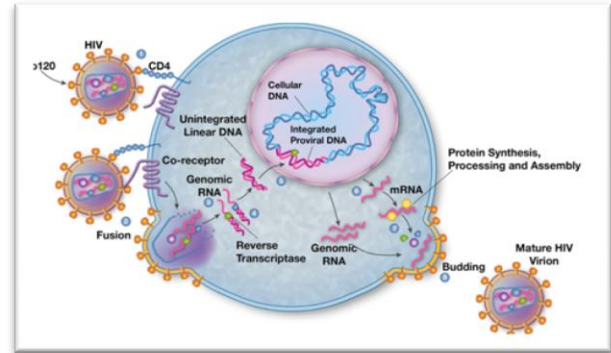**Fig 2:** *prevalence of HIV*

Fig 3: *life cycle of HIV*

Rapid weight loss, recurrent fevers or excessive sweating at night, acute exhaustion with no apparent cause, prolonged enlargement of the lymph glands in the armpits, groyne, or neck, protracted diarrhoea lasting more than a week, sores of the mouth, anus, or genitals, and pneumonia are other symptoms. Although it is possible to isolate HIV from blood or sperm, this process is not frequently available.

Antibody detection is often accomplished through the use of ELISA as a screening test and Western blot as a confirming test. Utilizing PCR-based assays, ascertain the "viral load" (i.e., the quantity of HIV RNA in the plasma).
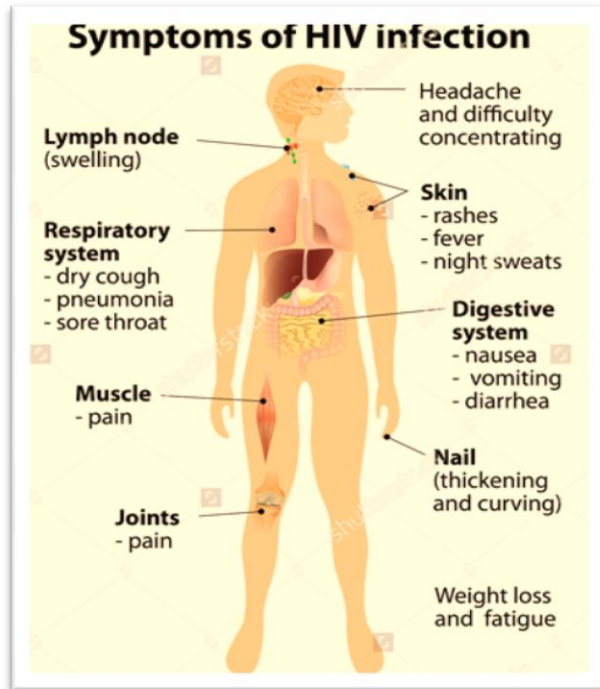
Fig 4: *symptoms of HIV infection*

Highly active antiretroviral therapy (HAART) consists of several drugs combined into various regimens is used for treatment. Treatment of the opportunistic infection depends on the organism. There is no vaccine.
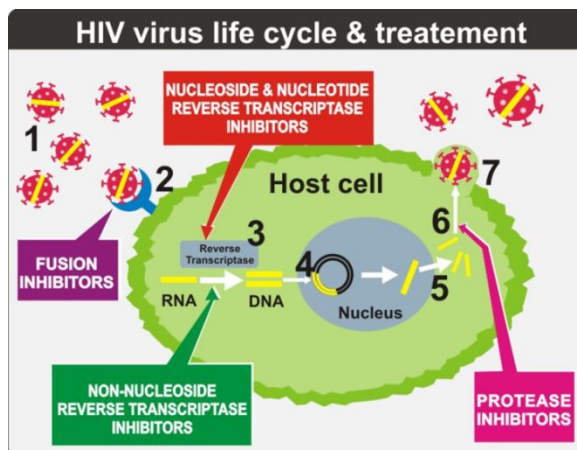

Fig 5: *HIV virus life cycle and treatment.*

Objectives

1. DNA extraction from blood sample

2. Primer designing for *pol* gene
3. Polymerase chain reaction will be carried on to amplify the desired gene
4. Bioinformatical analysis using software
5. Phylogenetic analysis of HIV *pol* gene

Methods

1. RNA extraction: RNA will be extract by kit method manually EDTA preserved blood. Gel electrophoresis will be done to visualize result.
2. **Primer design :** primer will be designed for the *pol* gene identification by using primer fox software
3. Real time PSR: RT-PCR will be carried on to amplify pol gene.
4. Sequencing : PCR products will be subjected to sequencing the gene to identify structure of gene .
5. Bioinformatics analysis: analysis will be done using statistics and bioinformatics software and excel sheet to determine phylogeny of HIV strain and studied parameter.

Results

1. To identify and characterizes HIV strains on the basis of *pol* gene.
2. To analyze the different demographic factor associated with HIV population in Pakistan.

3. To characterize HIV strains at molecular level amplication of *pol* gene.
4. To sequence amplified PCR products.
5. To analyze amplified PCR products rough various bioinformatics tools.
6. To analyze concerned domains of particular HIV strains and also to know about evolutionary history of HIV.
7. To determines the prevalence of HIV in Pakistani population**.**

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