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AWARENESS OF STRUCTURAL BIOLOGY OF HIV AMONG DENTAL STUDENTS

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ABSTRACT:
INTRODUCTION: The human immunodeficiency virus (HIV) is grouped to the genus Lentivirus within the family of Retroviridae, subfamily Orthoretrovirinae .On the basis of genetic characteristics and differences in the viral antigens, HIV is classified into the types 1 and 2 (HIV-1, HIV-2). The HIV genome consists of two identical single-stranded RNA molecules that are enclosed within the core of the virus particle. The genome of the HIV provirus also known as proviral DNA, is generated by the reverse transcription of the viral RNA genome into DNA, degradation of the RNA and integration of the double-stranded HIV DNA into the human genome.
AIM : To assess the knowledge of structural biology of HIV among dental students.
MATERIALS AND METHODS: A cross sectional questionnaire was designed and distributed to 100 dental students. Questionnaire includes email address,questions aboutstructure of HIV, genes and enzyme associated with HIV. Data was collected, statistically analysed and results were obtained.
RESULTS: Among the study population, majority (82%) aware that HIV belongs to genus Lentivirus whereas 18% of the study population told that HIV belongs to genus retrovirus. Among the study population, majority (80%) aware that HIV genome contains 3 structural genes whereas 18% of the study population told that HIV genome contains 2 structural genes and 1% of the study population told that HIV genome contains 1 structural gene.
CONCLUSION: The results observed in our study showed that awareness of structural biology of HIV among dental students were high. Dental students were also aware of enzymes, structural and non structural genes associated with HIV.

KEYWORDS: Human immunodeficiency virus, Reverse transcriptase, Lentivirus, Structural genes, Non structural genes.

1. INTRODUCTION:

The human immunodeficiency virus (HIV) is grouped to the genus Lentivirus within the family of Retroviridae, subfamily Orthoretrovirinae.On the basis of genetic characteristics and differences in the viral antigens, HIV is classified into the types 1 and 2 (HIV-1, HIV-2). The immunodeficiency viruses of non-human primates (simian immunodeficiency virus, SIV) are also grouped to the genus Lentivirus. Epidemiologic and phylogenetic analyses currently available imply that HIV was introduced into the human population around 1920 to 1940 (1).

The HIV genome consists of two identical single-stranded RNA molecules that are enclosed within the core of the virus particle. The genome of the HIV provirus also known as proviral DNA, is generated by the reverse transcription of the viral RNA genome into DNA, degradation of the RNA and integration of the double-stranded HIV DNA into the human genome. The DNA genome is flanked at both ends by LTR (long terminal repeat) sequences. The 5' LTR region codes for the promotor for transcription of the viral genes. In the direction 5' to 3' the reading frame of the gag gene follows, encoding the proteins of the outer core membrane (MA, p17), the capsid protein (CA, p24), the nucleocapsid (NC, p7) and a smaller, nucleic acid-stabilising protein.[31-36]The gag reading frame is followed by the pol reading frame coding for the enzymes protease (PR, p12), reverse transcriptase (RT, p51) and RNase H (p15) or RT plus RNase H (together p66) and integrase (IN, p32). Adjacent to the polgene, the env reading frame follows from which the two envelope glycoproteins gp120 (surface protein, SU) and gp41 (transmembrane protein, TM) are derived. In addition to the structural proteins, the HIV genome codes for several regulatory proteins: Tat (transactivator protein) and Rev (RNA splicing-regulator) are necessary for the initiation of HIV replication, while the other regulatory proteins Nef (negative regulating factor), Vif (viral infectivity factor), Vpr (virus protein r) and Vpu (virus protein unique) have an impact on viral replication, virus budding and pathogenesis (2,3). HIV-2 codes for Vpx (virus protein x) instead of Vpu, which is partially responsible for the reduced pathogenicity of HIV-2 (4). The genome structure of the immunodeficiency viruses of chimpanzees (SIVcpz) and gorillas (SIVgor) is identical to that of HIV-1 (5).

The initial steps of infection of a cell are characterised by complex protein-protein interactions. The surface glycoprotein gp120 of the mature HIV particle binds to the CD4 receptor on the host cell. After attachment to the CD4 molecule via the C4-domain of gp120, a conformational change in CD4 and gp120 occurs, opening up an additional site for gp120 to enable binding to the co-receptor (6,7).

Binding of gp120 to CD4 and to the co-receptor triggers an additional conformational change in gp120 and subsequently in gp41 (1,8). The N-terminus of gp41 is presented on the viral membrane, forms a channel and, due to its high hydrophobicity, inserts into the plasma membrane of the target cell. Fusion of cell membrane and viral envelope is then completed. Fusion of the viral and cellular membranes leads to translocation of the viral capsid into the cytoplasm. The capsid is taken up by an endosome, and a change in the pH value in the phagosome induces the release of the capsid contents into the cytoplasm (9). Activation of reverse transcriptase (RT) takes place in the cytoplasm. HIV RT transcribes the single-strand HIV RNA genome into DNA (complementary DNA or cDNA). In parallel to DNA synthesis, the RNA strand is degraded enzymatically by RNase H, followed by conversion of single-stranded cDNA into doublestranded DNA (proviral DNA) by the DNA-dependent DNA polymerase activity of RT (10). This proviral DNA is transported via nucleopores into the cell nucleus in the form of a complex consisting of the integrase (IN) and linear or circular proviral DNA. The integrase then inserts at random the proviral genome into the human host cell genome. Integration of the proviral DNA finalises the HIV infection of the cell and the establishment of a persistent infection. The proviral genome can be replicated together with and as part of the host cell genome during cell division (latent infection which seems to be rare). However, after activation of infected cells the LTR promotor of the proviral genome can serve as attachment site for cellular DNA-dependent RNA polymerases and a variety of transcription factors initiating the synthesis of viral mRNA and genomic RNA. The synthesis of full-length viral mRNA is regulated among others by Tat and maximally accelerated by Tat (p14) (11). The attachment of HIV to a CD4-positive cell requires around 30 min up to 2 h, the transcription of the viral RNA genome into the proviral DNA is completed after approximately 6 h, and the integration into the host genome takes an additional 6 h. After

integration, the first virus particles are detectable after approximately 12 h; i.e. approximately 24 h after infection the first progeny viruses are released from the infected cell.
If HIV replication is unrestricted a daily turnover of 108-109 viral particles is expected, i.e. newly produced by infected cells and destroyed by the immune system (12,13). Assuming a mutation rate of 1 in 104 nucleotides per genome during one replication cycle, a broad spectrum of various quasispecies can therefore develop in a patient in the course of time. Since epitopes for neutralising antibodies are also affected by mutation, these quasispecies are able to continually evade the immune system, infect new cells and therefore maintain HIV production (14,15)Not all nucleotide changes result in the exchange of an amino acid. However, mutations in essential regions of the structural proteins or influencing active centres of enzymes give rise to replication-incompetent HIV mutants. Infected T lymphocytes are eliminated with a half-life of 2-4 days from the blood of an HIV-infected person by cytotoxic HIV components, lysis of virus-producing cells or by cytotoxic T lymphocytes as part of the immune response Since HIV-infected T helper cells are also lysed and the production of such cells is inhibited simultaneously, a gradual decline of T helper cells is observed. HIV-specific proteins like Nef and Tat are responsible for insufficient maturation and replacement of T helper cells (15). Therefore, part of the newly produced T helper lymphocytes do not develop normal functions. After a long-lasting HIV infection the continuous loss of T helper lymphocytes results in immunodeficiency. HIV integrated into the host genome of long-lived cells like macrophages, astrocytes or memory T cells can persist in the latent stage for several years (half-life of certain target cells is 7 years). Activation of such cells results in the production of infectious HIV particles (16). Aim of the study is to assess the knowledge of structural biology of HIV among dental students.

2. MATERIALS AND METHODS:

The study was conducted during the academic year december 2020 among the dental students.

STUDY SAMPLE SIZE:

The descriptive cross sectional study was based among 100 dental students .

INCLUSION AND EXCLUSION CRITERIA:

Dental students who were studying 2rd, 3rd year, and final year. Dental students who are not willing to participate were excluded in this study.

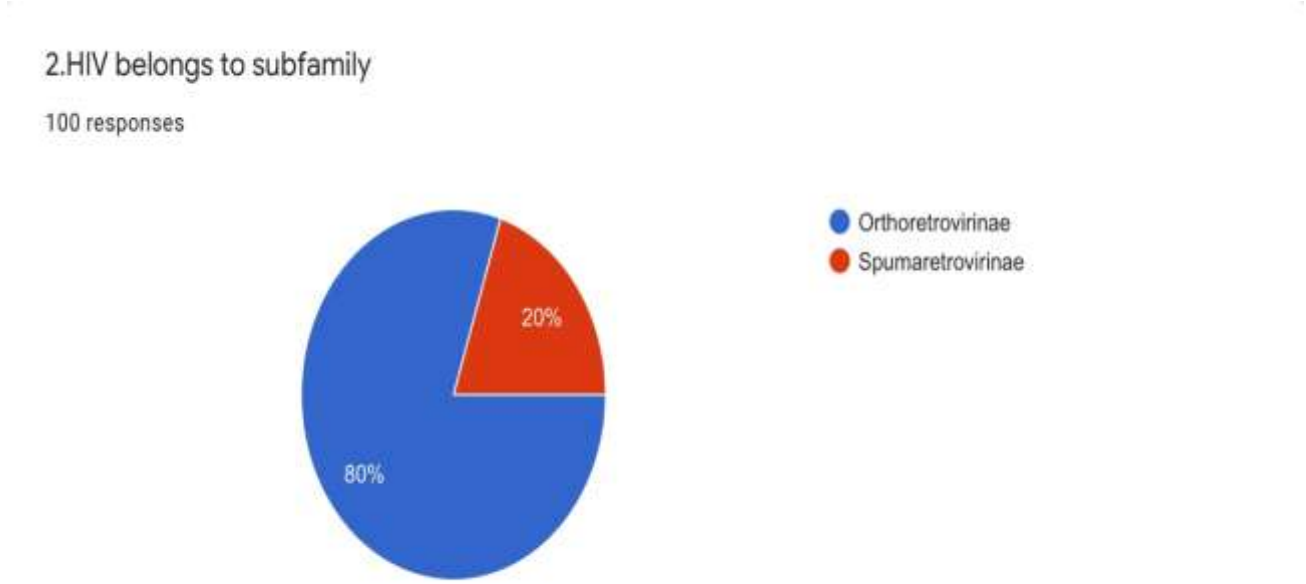
QUESTIONNAIRE:

The questionnaire was not targeted at a specific group but all dental students in general to assess their knowledge of structural biology of HIV. A validated questionnaire was distributed among the dental students in this study. This included questions about the knowledge of HIV structure ,enzymes associated with HIV, structural and non structural genes associated with HIV. The data extracted were tabulated, statistically analysed and results were obtained using SPSS software.

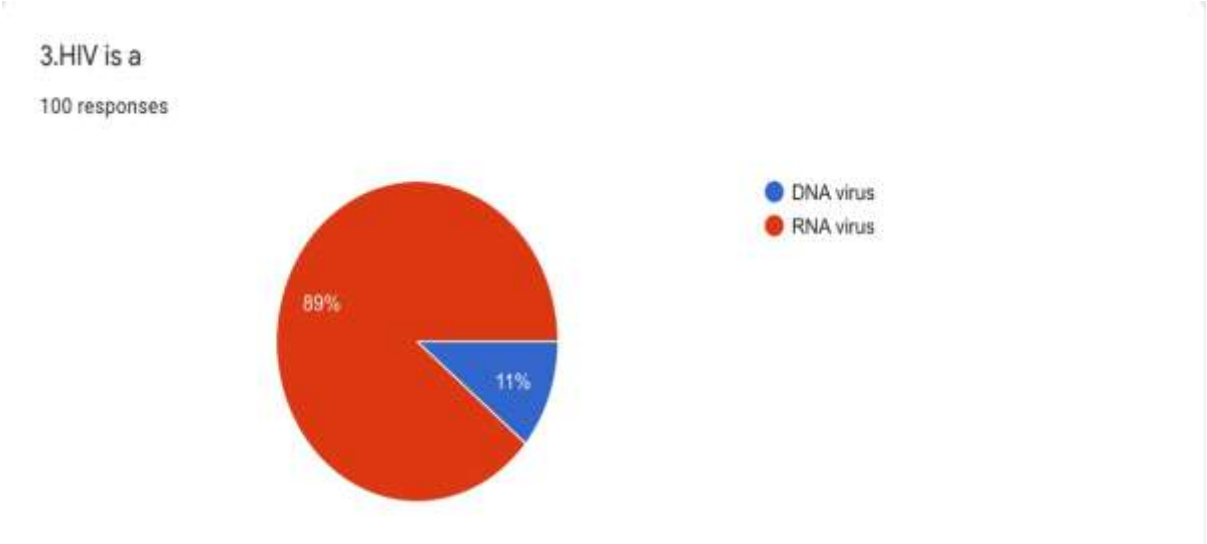
3. RESULTS:

Among the study population, majority (82%) aware that HIV belongs to genus Lentivirus whereas 18% of the study population told that HIV belongs to genus retrovirus.

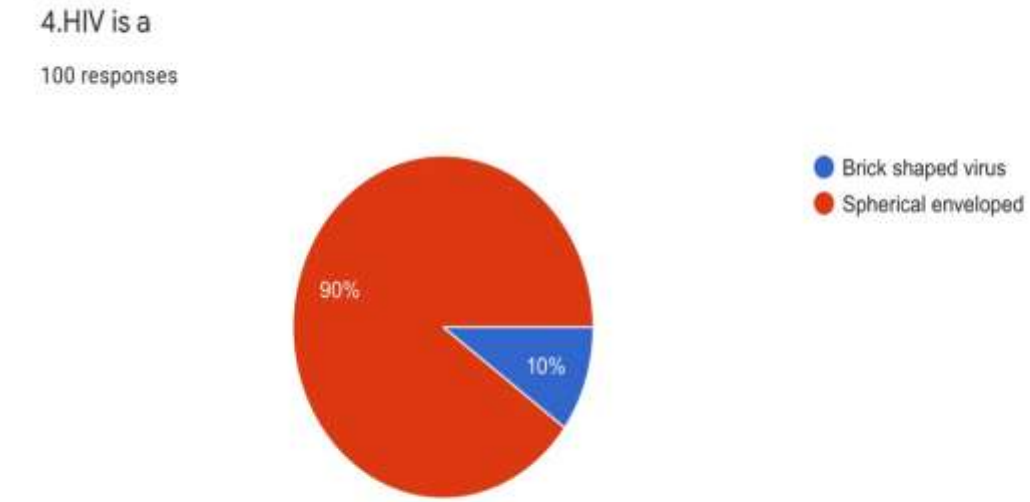
Among the study population, majority (80%) aware that HIV belongs to subfamily of Orthoretrovirinaewhereas 20% of the study population told that HIV belongs to subfamily of Spumaretrovirinae.



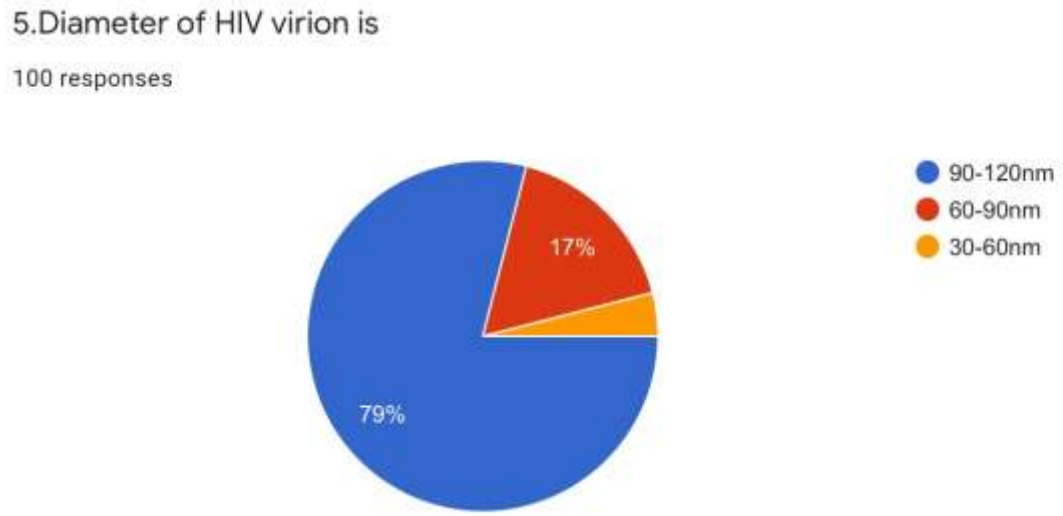
Among the study population, majority (89%) aware that HIV is a RNA virus whereas 11% of the study population told that HIV is a DNA virus.



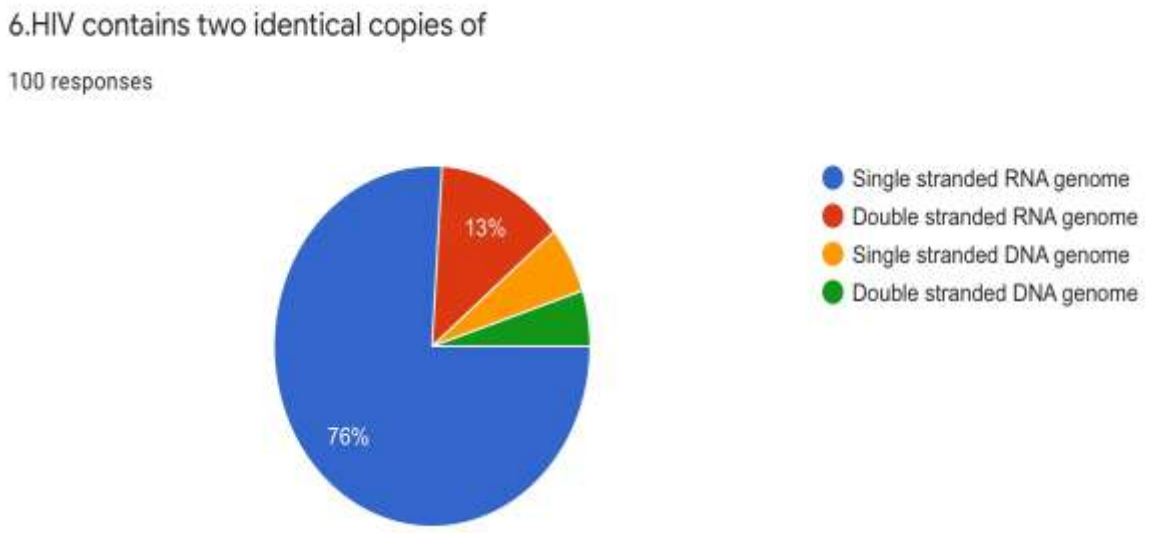
Among the study population, majority (90%) aware that HIV is a spherical enveloped virus whereas 10% of the study population told that HIV is a brick shaped virus.



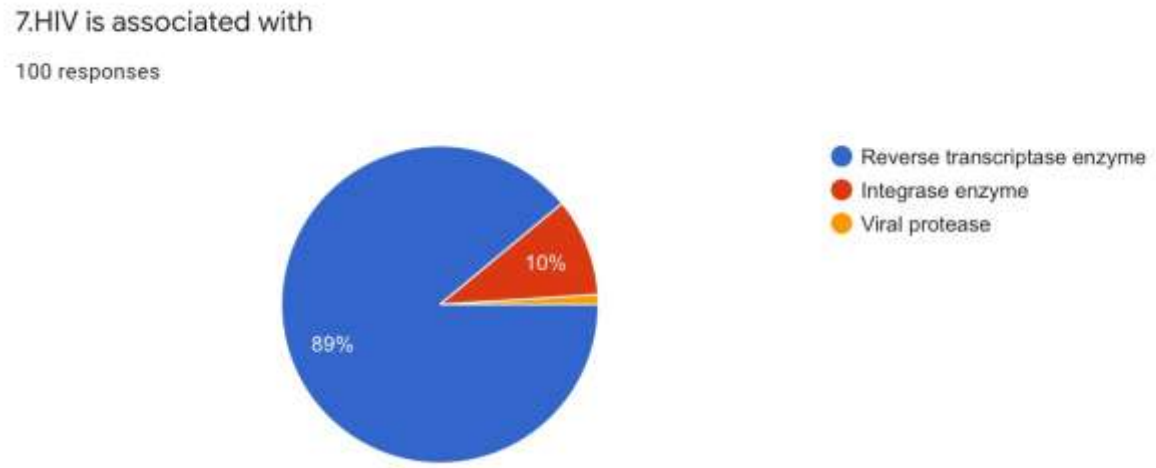
Among the study population, majority (79%) aware of diameter of HIVvirionis 90-120nm whereas 17% of the study population told that diameter of HIV virion is 60-90nm and 4% of the study population told that diameter of HIV virion is 30-60nm.



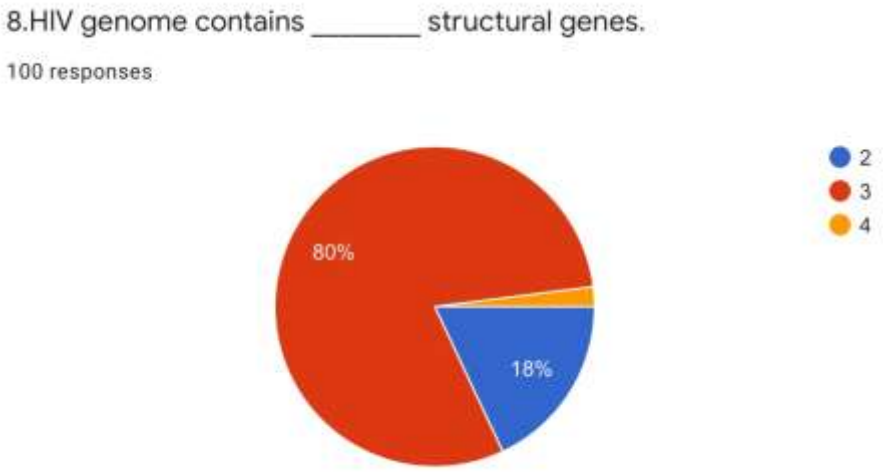
Among the study population, majority (76%) aware that HIV contains two identical copies of single stranded RNA genome whereas 13% of the study population told that HIV contains two identical copies of double stranded RNA genome, 6% of the study population told that HIV contains two identical copies of single stranded DNA genome and 5% of the study population told that HIV contains two identical copies of single stranded DNA genome



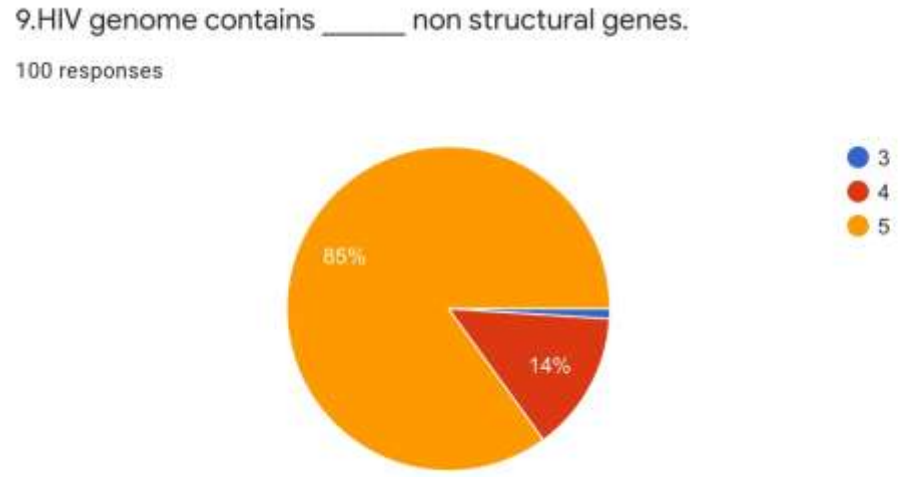
Among the study population, majority (89%) aware that HIV is associated with reverse transcriptase enzyme whereas 10% of the study population told that HIV is associated with integrase enzyme and 1% of the study population told that HIV is associated with viral protease enzyme.



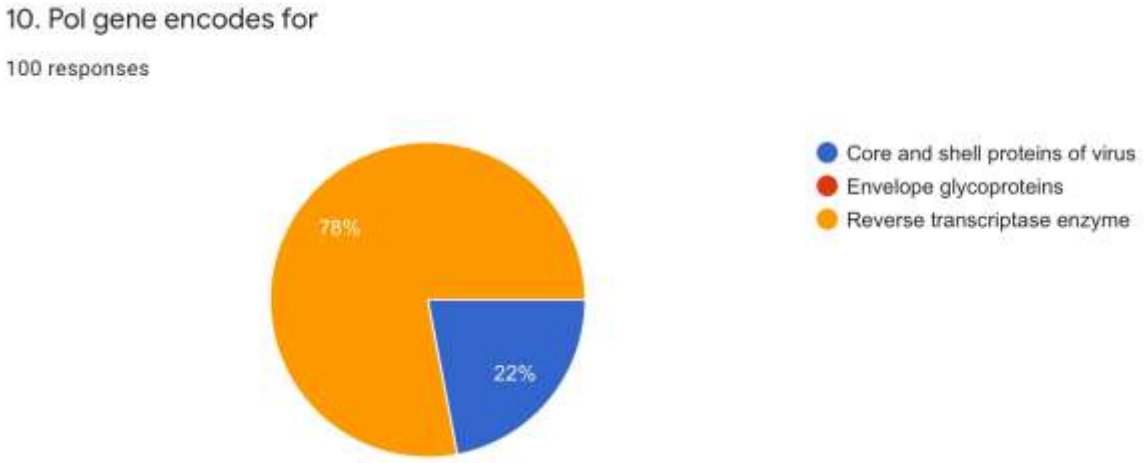
Among the study population, majority (80%) aware that HIV genome contains 3 structural genes whereas 18% of the study population told that HIV genome contains 2 structural genes and 1% of the study population told that HIV genome contains 1 structural gene.



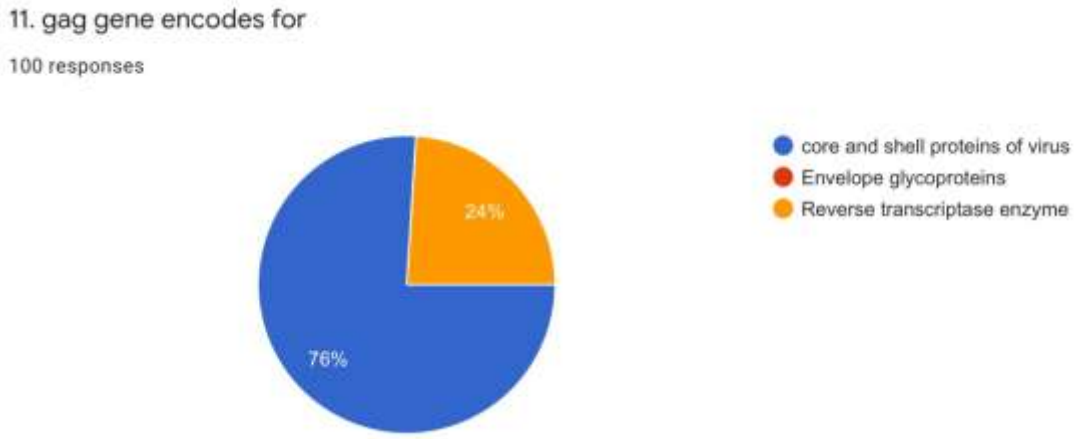
Among the study population, majority (85%) aware that HIV genome contains 5 non structural genes whereas 14% of the study population told that HIV genome contains 4 non structural genes and 1% of the study population told that HIV genome contains 1 non structural gene.



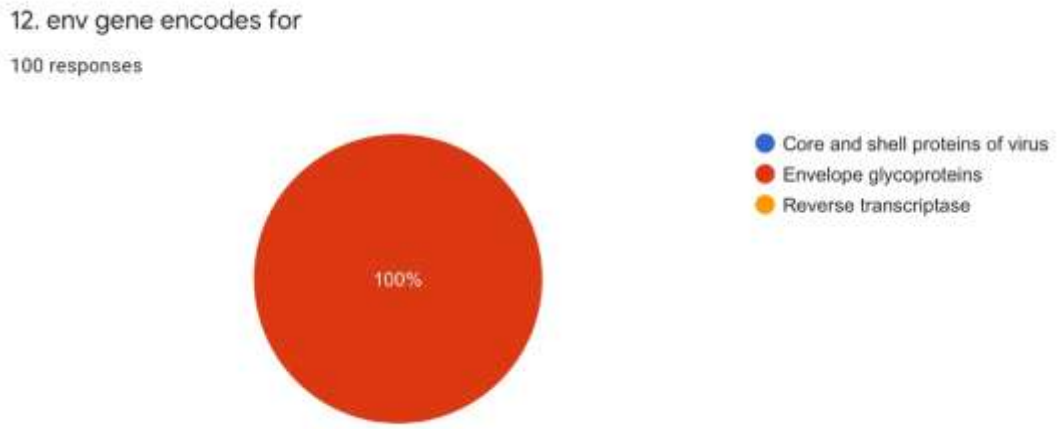
Among the study population, majority (78%) aware that Pol gene encodes for reverse transcriptase enzyme whereas 22% of the study population told that Pol gene encodes for core and shell proteins of virus.



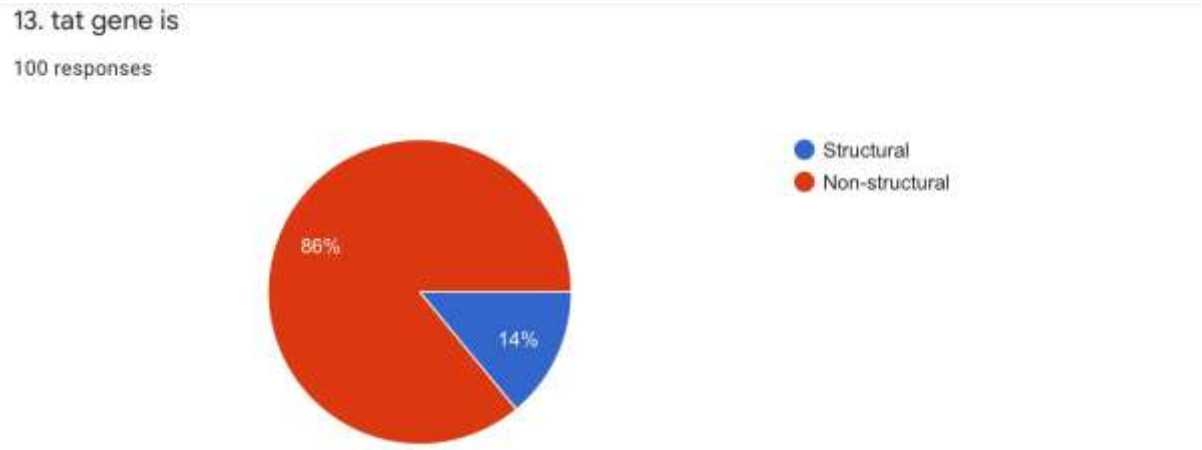
Among the study population, majority (76%) aware that gag gene encodes for core and shell proteins of virus whereas 24% of the study population told that gag gene encodes for reverse transcriptase enzyme.



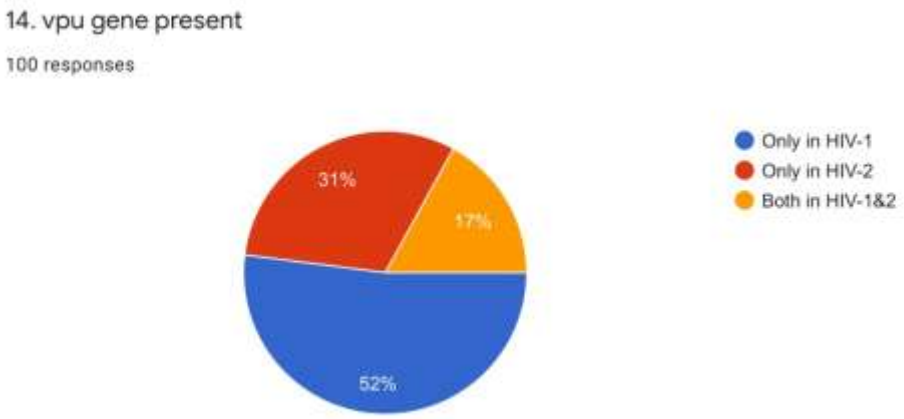
100% of the study population aware that env gene encodes for envelope glycoproteins.



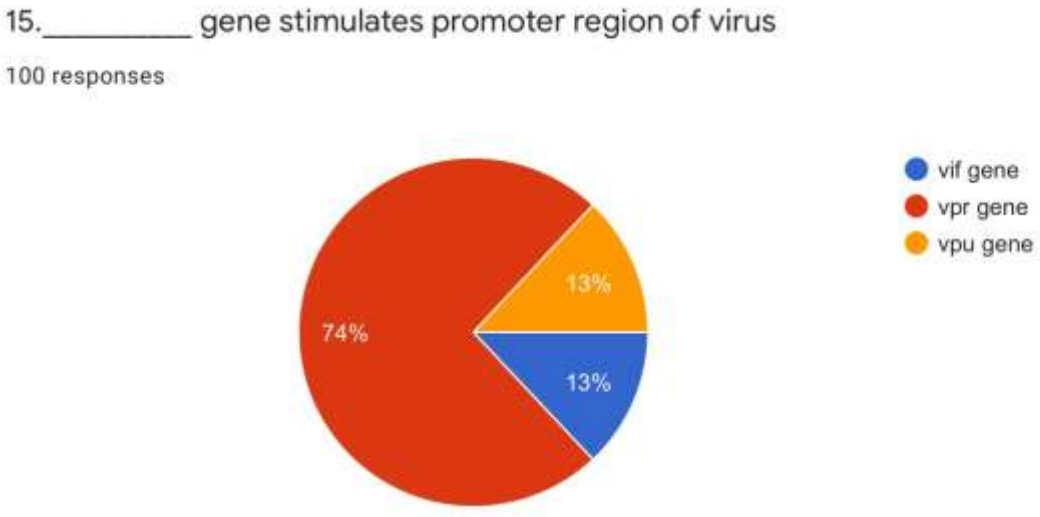
Among the study population, majority (86%) aware that tat gene is a non structural gene whereas 14% of the study population told that tat gene is a structural gene.



Among the study population, majority (52%) aware that vpugene present only in HIV-1 whereas 31% of the study population told that vpugene present only in HIV-2 and 17% of the study population told that vpu gene present both in HIV-1 and HIV-2.



Among the study population, majority (74%) aware that vprgene stimulates promotor region of virus whereas 13% of the study population told that vpu gene stimulates promotor region of virus and 13% of the study population told that vif gene stimulates promotor region of virus.



4. DISCUSSION:

HIV is a major contributor to the global burden of disease. In 2010, HIV was the leading cause of disability adjusted life years worldwide for people aged 30–44 years, and the fifth

leading cause for all ages (17). Global AIDS related deaths peaked at 2·3 million in 2005, and decreased to 1·6 million by 2012 (18). People with HIV have a 50% increased risk of myocardial infarctions than do people without HIV after adjustment for vascular risk factors (19). Liver disease is common, mainly because of coinfection with hepatitis B and C, which share similar routes of transmission with HIV (20).

The most important factor that increases the risk of sexual transmission of HIV-1 is the number of copies per mL of plasma HIV-1 RNA (viral load), with a 2·4 times increased risk of sexual transmission for every 1 log10 increase. Acute HIV infection, which causes very high plasma viral loads in the first few months, is an important driver of HIV epidemics. A reduction in plasma viral load of is estimated to reduce HIV-1 transmission by 0·7 log10 50%. Seminal and endocervical viral load independently predict risk of HIV-1 sexual transmission, after adjustment for plasma viral load (21,22). Other factors associated with increased risk of sexual transmission of HIV include sexually transmitted infections (notably genital ulcers of any cause, herpes simplex type-2 infection, and bacterialvaginosis), pregnancy, and receptive anal intercourse. Male circumcision is associated with a reduced risk of sexual transmission of HIV (23-25). Findings of some observational studies showed an increased risk of HIV-1 acquisition in women who used long-acting injectable progestogens for contraception, but not with combined oral contraceptives. A health priority in eastern and southern Africa, where the incidence of HIV-1 in young women is very high, is to find out whether long-acting injectable progestogens (the commonest form of contraception used in this region) increase HIV-1 transmission. Behavioural factors that increase HIV-1 sexual transmission include many sexual partners, and concurrent partnerships.Findings of a studyof African heterosexual serodiscordant couples showed that selfreported condom use reduced the per-coital act risk of HIV-1 transmission by 78%. Sex inequality is an important driver of the HIV epidemic, especially in subSaharan Africa where women account for 57% of people living with HIV.Injection and non-injection drug use, including alcohol, are associated with increased sexual risk behaviour, whereas injection drug use causes HIV transmission by shared needles. (26-30) Women who reported intimate partner violence had an increased incidence of HIV infection in a South African study. UNAIDS have identified stigma against HIV, and discrimination and punitive laws against high-risk groups (eg, men who have sex with men, people who inject drugs, and commercial sex workers) as barriers for people to undergo HIV testing, access care, and access prevention measures (31).

5. CONCLUSION:

Theresults observed in our study showed that awareness of structural biology of HIV among dental students were high. Dental students were also aware of enzymes, structural and non structural genes associated with HIV.

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