

HIV VACCINES: PRESENT SCENARIO AND FUTURE PROSPECTS

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Summary

AIDS, first described in early 1980s, has reached the far corners of the globe and is the main cause of death throughout the world. Potential adverse effects of the present anti-HIV drugs, multidrug regimens leading to drug resistance and conferring mutations in the virus leading to more virulent forms have provoked the urgency for vaccine development. However, the development of an HIV vaccine faces formidable scientific challenges related to the high genetic variability in the virus, the lack of immune correlates of protection, lack of animal models and logistical problems associated with the conduct of multiple clinical trials. Yet, live vectored recombinant vaccines, replication incompetent viral vectors, subunit vaccines and DNA vaccines have paved the way for the development of a variety of novel and specific vaccine approaches. Researchers are currently exploring the uncharted immunologic terrain which could also prove invaluable. Although they have turned the virus inside-out and carefully detailed how it destroys the immune system, it is yet to unravel which immune responses can fend off an infection indicating, AIDS vaccine research for more than a decade is "flying without a compass."

Keywords: (AIDS) Acquired Immunodeficiency syndrome, (CTLs) Cytotoxic T-lymphocytes, (HIV) Human Immunodeficiency Virus, Vaccines

INTRODUCTION

Although HIV transmission is in theory largely preventable, in practice, without the development of an effective vaccine, HIV will continue to infect millions throughout the world. According to recent United Nations AIDS estimates at least 39.5 million (34.1–47.1 million) people were living with HIV in 2006 which includes 37.2 (32.1–44.5 million) adults, 17.7 million (15.1–20.9 million) women and 2.3 million (1.7–3.5 million) children less than 15 years of age. Around 4.3 million (3.6–6.6 million) people were newly infected with HIV in 2006 and the death toll was 2.9 million (2.5–3.5 million)(1).

The current HIV therapy has many drawbacks (2, 3), such as:

- No ready access to antiretroviral treatment (ART).
- Potential adverse effects of the anti-HIV drugs.
- Extensive drug-drug interactions.
- High cost.
- Emergence of drug resistance.

An alternative objective of AIDS vaccine is to prevent disease rather than infection. Vaccine-induced protection against HIV disease could be achieved by:

- Complete protection from infection (sterile immunity)
- Clearance of virus and infected cells (abortive infection)
- Persistent infection without disease

Because HIV may induce AIDS even after a long asymptomatic period, the desired goal of most AIDS vaccine trials to date has been to induce sterile immunity. Sterile immunity may be difficult to achieve, however, as most existing viral vaccines prevent disease and do not prevent infection(4). An alternative goal for AIDS vaccine development might therefore be to induce immune responses that would contain HIV replication, resulting in a prolonged (perhaps indefinite) asymptomatic period, similar to long-term nonprogressors(5, 6).

CELLULAR AND MOLECULAR BIOLOGY OF HIV

The complete understanding of the cellular structure of HIV is significant for the vaccine design. HIV is a member of the Lentivirinae subfamily of Retroviruses. Retroviruses belong to the diverse family of enveloped RNA viruses. They are typically 100nm in diameter and contain 2 single strands of RNA, which permits recombination between the strands. The genome is 10kb in size and contains 3 major genes-*gags*; *pol* and *env*. HIV virion measures 80nm to 130 nm in diameter and has a unique 3 layered structure. It contains an inner conical structure and 72 external spikes formed by the 2 major viral envelope proteins gp120 and gp41. Also it contains gp160-precursor of envelope glycoproteins. These gp120 and gp41 are assembled into a trimeric complex(7).

The HIV lipid bilayer consists of a number of host proteins including the Class 1 and 2 MHC antigens, acquired during virion budding. The viral core contains core proteins, the p24 capsid proteins (phosphorylated), p17 matrix protein and the p7, p6 nucleocapsid proteins, each of which is proteolytically cleaved from a 55kDa Gag precursor by the HIV-1 protease. The capsid protein forms the chief component of the inner shell of the virion, where as the matrix protein is associated with inner surface of the lipid bilayer and probably stabilizes the external and internal components of the virion. The p7 nucleocapsid protein binds directly to the genomic RNA through a zinc finger

structural motif and together with p6 nucleocapsid forms the retroviral core. It also contains 2 copies of single stranded HIV1 genomic RNA that are associated with the various preformed viral enzymes including reverse transcriptase, integrase and protease(8). (fig-1)

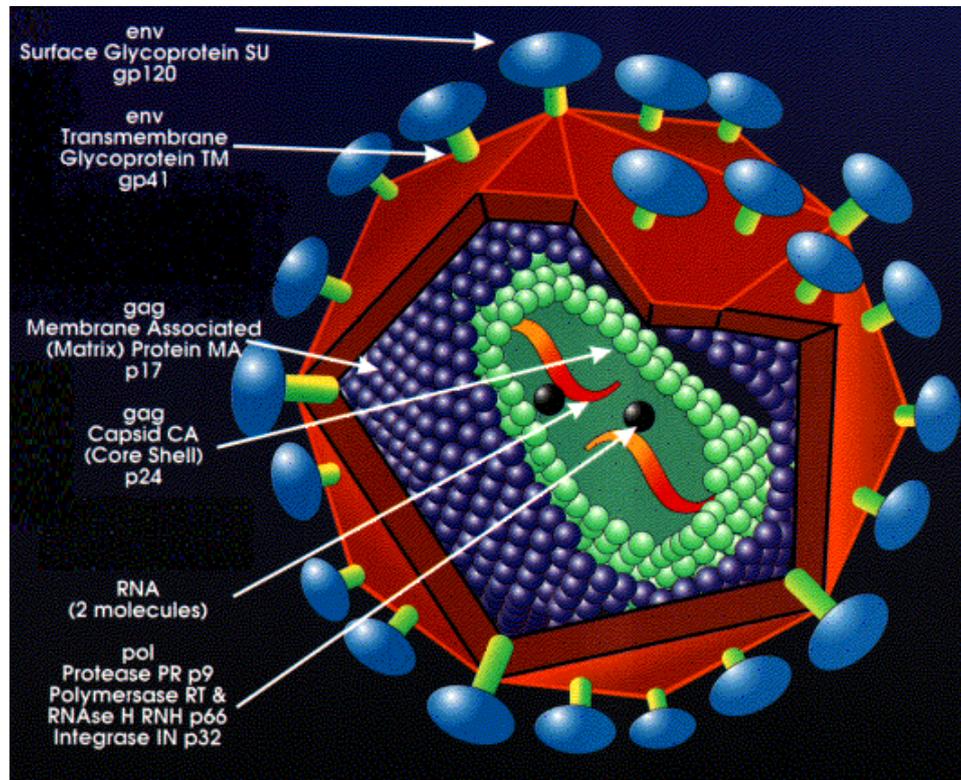


Figure 1: structure of HIV

PATHOGENESIS

It involves the attachment of viral protein gp120 to the host cell surface receptor CD4 leading to a conformational change in gp120 and the receptor followed by displacement of gp120. As a result of this process, proteolytic cleavage of V3 loop or its envelope counterpart occurs. Then it involves the interaction of the fusion domain of HIV (gp41) with a fusion receptor on the host cell surface leading to viral fusion with the host cell membrane. This is followed by entry of viral RNA associated with core and polymerase proteins into the cytoplasm. The double stranded DNA (cDNA) is made from a viral RNA by reverse transcription involving the reverse transcriptase enzyme. This proviral cDNA is then transported into the cell nucleus, where it integrates into the host cell chromosome DNA. Viral mRNA and genomic RNA are produced from the integrated proviral DNA. The extent of this production is dependent on the expression of HIV regulatory genes (*tat*, *rev*, *nef*, *vpr*). Viral proteins are produced from full length and spliced mRNA and viral genomic RNA is incorporated into the capsid forming at the cell membrane. *Gag* and *gag-pol* polyproteins are processed via protease at the cell surface or in budding virions. Finally, the viral capsid buds through the cell membrane incorporating both the processed viral envelope glycoprotein and some host cell proteins present on the host cell surface. This final stage may involve the function of the viral *vif* gene (8).

Table 1: GENES AND GENE PRODUCTS OF HIV-1 & 2 (6,7)

| GENE | PROTEINS | FUNCTIONS/PROPERTIES |
|------------------|--|--|
| Gag | p17 p24 p6 p7 | Matrix protein: interacts with gp41 Core protein Core protein; binds to <i>Vpr</i> Nucleocapsid: binds to RNA |
| Pol | Protease Reverse transcriptase Integrase | Proteolytic cleavage of <i>gag</i> and <i>pol</i> Polymerase and RNase H activity Integration into chromosome |
| Env | gp120 gp41 | Envelope: viral entry into cell Transmembrane protein: cell fusion |
| Vif | Virion infectivity protein | Efficient cell free transmission |
| Vpr | Viral protein R | Enhances viral replication in primary cells, Virion associated protein: g2/M phase arrest: nuclear localization |
| Tat | Transactivator of transcription | Major viral transactivator |
| Rev | Regulator of expression of virion protein | Enhances expression of unspliced and singly spliced RNA's |
| vpu # | Viral protein U | Enhances virion releases from cells: downs regulates CD4 |
| Nef | Negative regulator factory | Inhibits or enhances viral replication depending on strain and cell type. Downregulates CD4; MHC-I. |
| Vpx ## | Virion protein X | Packaged into virion |

HIV-1 only

HIV-2 only.

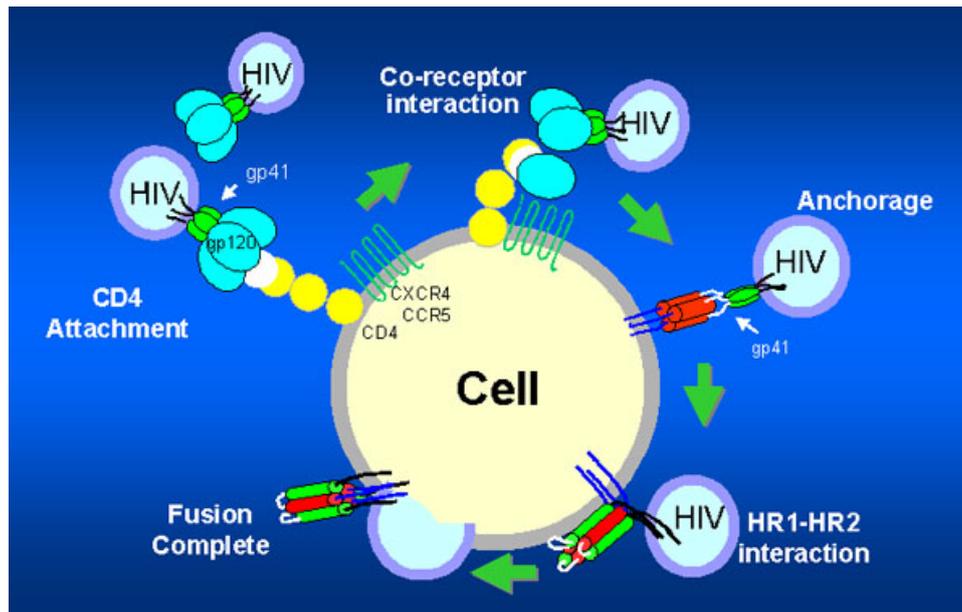


Figure 2: Interaction of HIV and CD4 molecule.

CHALLENGES AND OBSTACLES IN VACCINE DEVELOPMENT

Obstacles to the development of an effective AIDS vaccine include factors related to the biology of HIV-1 infection and practical realities of developing and testing an AIDS vaccine. The molecular and cellular entities of HIV allow it to escape from the host immune system and this presents a major challenge for the designing of an effective vaccine (9).

ANTIGENIC VARIATION

Intense genetic variations occur in the HIV gene sequences and thus in the viral antigens. There is no doubt that new antigenic variants of HIV constantly arise during the long course of AIDS because of the low fidelity of reverse transcription. The mutation rate of HIV-1 is high because reverse transcriptase lacks a proof reading domain thereby allowing a great deal of sequence variation in viral nucleic acids. Mutations occur during viral replication giving rise to virulent forms of the virus with increased cytopathic capacity and altered cell tropisms(10, 11). The V3 loop of the HIV1 envelope contains GP-GRA amino acid sequences that encode major antigens reflecting the variability. A competent vaccine is required to induce immune responses against neutralizing epitopes from diverse isolates. Among diverse HIV-1 isolates, there are five to six amino acids at the tip of the V3 loop, where comparatively fewer mutations are identifiable (conserved region). Such a conserved neutralizing epitope may allow vaccination against multiple strains(12).

INTEGRATION OF VIRAL DNA

The immune system is unable to detect cells infected with a retrovirus as the viral DNA remains integrated into host cell DNA, but not expressed. Integration of the viral DNA with the host cell DNA is catalyzed by the enzymes reverse transcriptase and integrase, which makes double stranded DNA copy of the viral RNA genome which integrates into the chromosomal DNA of the

host cells. In this pro-viral form, the viral genome remains in a “latent” state of expression in which the viral RNA and protein synthesis is limited (13-15).

INFECTION AND DESTRUCTION OF CRUCIAL CD4 CELLS

CD4 molecule present on the surface of the T-helper cells provides the high affinity receptor for HIV cell binding (16). But the binding is not successfully complete unless a co-receptor is present on the cell surface in addition to CD4. For T-cells it is CXCR4 (fusin) or CXCR5 and for macrophages the co-receptor is CCR5. These co-receptors are transmembrane receptors containing a N-terminus extra cellular domain, seven membrane spanning regions and a C-terminus intracellular signaling domain that interacts with G-proteins. Activated CD4⁺ lymphocytes, the key cells targeted by HIV-1, bear both CCR5 and CXCR4¹⁷. Binding of CD4 to HIV-1 envelope gp120 induces conformational rearrangement in the envelope complex facilitating recognition of the CCR5 chemokine co-receptors and consequent viral entry into the cell. Zhang *et al* defined the mechanism of virus docking and cell fusion by revealing that CD4 induced conformational changes in the equilibrium state of gp120 lead both to the movement of V1/V2 loops and to the conformational rearrangement in the gp120 core structure and that both results in the greater exposure of the co receptor binding epitope in gp120 (18).

CyclophilinA, a cellular protein, involved in the receptor binding process, emerges out from HIV envelope membrane and sticks to heparan molecules (CD147) on the cell surface thus, facilitating HIV-1 to attach to new target cells even before the interaction of gp120 and CD4 cells. It is involved in T cell activation and functions as a “molecular chaperone” protein that helps other proteins to fold into their correct conformation (19-20).

EVADING ATTACK FROM NEUTRALIZING ANTIBODIES

HIV has developed sophisticated mechanisms to dodge immune attack, shrouding its surface protein in sugars (gp120 is heavily glycosylated) to hide vulnerable sites from antibodies and producing proteins that thwart production of other immune warriors. Wyatt *et al* described the spatial organization of conserved neutralization epitopes on gp120, using epitope maps along with the X-ray crystal structure of a ternary complex that includes a gp120 core, CD4 and a neutralizing antibody. A large fraction of the predicted accessible surface of gp120 in the trimer is composed of variable heavily glycosylated core and loop structures that surround the receptor binding regions (21, 22).

ESCAPE FROM ANTIVIRAL CYTOKINES

The interchange of viral phenotype from M- tropic (CCR5 using) to T -tropic (CXCR4 using) during late disease indicates the escape from the inhibitory effects of CCR5 binding chemokines-RANTES, MIP-1 α and MIP-1 β (10).

NEUROTROPISM OF HIV

Infection of cells in immune privileged sites is another main mechanism underlying HIV evasion of host immunity. These immunoprivileged sites are relatively insulated from the systemic immune defense mechanisms where the CTLs have poor penetration and reduced ability to clear infected cells, such as the CNS and microglia in the brain³.

LACK OF ANIMAL MODEL

Chimpanzees are the only animals that are susceptible to HIV. Not only the supply is scarce but also chimpanzees develop viremia and antibodies, they do not develop immunodeficiency. The SIV macaque model of Simian AIDS does develop disease and helpful for vaccine design studies (10- 23).

THE PROCESS OF DEVELOPMENT OF VACCINES

- **FIRST GENERATION APPROACHES-** Enveloped glycoprotein antigens.

Initial approaches were based on enveloped glycoprotein gp120 due to their functional importance for virus attachment and entry and as primary targets for neutralizing antibodies. CHO- derived rgp120(r = recombinant) emerged as the most immunogenic of early subunit vaccines (24-25). The disadvantages of this approach was that the serum antibody titers had short half life (<6 months) and when boosted, the peak level reaches only after third or fourth injections. Monomeric gp120 elicits antibody and CD4+ T cell responses, which are very type specific failing to neutralize commonly transmitted primary R5 HIV-1 isolates (26).

- **SECOND GENERATION APPROACHES-** Recombinant pox virus vectors

Pox virus vectors were used to express *gag* which induced the production of pseudo virus from infected cells (27). Canary pox was the recombinant pox virus vector evaluated in the clinical trials in mid 1990s. Canary pox is grown and manufactured in chicken embryo fibroblasts (CEF) but is replication incompetent in mammalian cells. Hence, it is used to deliver its recombinant gene to the cytoplasm, providing the machinery necessary for gene expression but unable to propagate itself to cause primary disease in the host cell. (28-29). The construct included a series of products that expressed gp160 (vCP125) gp120, gp41(transmembrane), *gag*, proteases(vCP205), vCP205 plus selected epitopes from *nef* and *pol* (vCP300), vCP300 plus E3L and K3L genes from Vaccinia that inhibit dsRNA and interferon inducible protein kinase and that inhibited the apoptosis of the infected cell(vCP1452). The data from above studies revealed that canary pox vectors are well tolerated at doses above 10^7 pfu (plaque forming unit). The HIV specific antibody response after recombinant canary pox immunization alone is weak, but subsequent boosting with recombinant envelope subunit protein induces HIV specific antibody titers of the same or higher magnitudes (32).

- **THIRD GENERATION APPROACHES-** More potent gene delivery vehicles along with DNA vaccination.

These studies utilized either recombinant modified Vaccinia Ankara (rMVA) or replication incompetent recombinant adenovirus (rAd) alone or in combination with DNA immunization. The combination of DNA priming followed by MVA or rAd boosting is a potent vaccine regimen for inducing high levels of HIV specific CD8+ CTL responses (30-31). The “prime boost” approach involves the administration of the same antigen in two different vectors given consecutively. Exposure to the antigen in the first vector “primes” the immune response; re-exposure to the same antigen in the second vector “boosts” the response. This approach can provide HIV proteins in non HIV- viral vectors to induce a cytotoxic cellular immune response; thus avoiding attenuation of boost effect from sequential use of the same viral vector. It is also used to augment the response to potentially convenient vaccines such as DNA plasmid products which themselves are not satisfactorily immunogenic. This approach stimulates various immune responses resulting in an

effectual combination of cellular and antibody responses elicited by a single vaccine³³. The rAd vectors are produced by inserting the recombinant genes of interest in the E1 gene cassette of the adenovirus genome and by producing the rAd particles in a cell line that constitutively expressed complementary E1 genes (32).

Table 2. Ongoing Trials: Phase II

| Protocol Number | Status as of February 2007 | Class | Producer | Product | Adjuvant |
|------------------------------------|----------------------------|--|----------|------------------|----------|
| HVTN 502/Merck 023 (Step) (n=3000) | Enrolling at clade B sites | Nonreplicating adenoviral vectors (clade B Gag-Pol-Nef) | Merck | MRKAd5 trivalent | |
| HVTN 204 (n=480) | Enrolling | DNA plasmids (clade B Gag, Pol, Nef; clade A,B,C Env) | NIH VRC | VRC-HIVDNA-016 | |
| HVTN 503 (n=3000) Prime | Enrolling | Nonreplicating adenoviral vectors (clade B Gag-Pol-Nef) | Merck | MRKAd5 trivalent | |
| HVTN 503 (n=3000) Boost | Enrolling | Nonreplicating adenoviral vectors (clade B Gag-Pol; clade A,B,C Env) | NIH VRC | VRC-ADV-014 | |

Table 3. Ongoing Trials: Phase I

| Protocol Number | Status as of February 2007 | Class | Producer | Product | Adjuvant |
|-----------------------------------|----------------------------|---|---------------------|------------------------------------|----------|
| HVTN 042/ANRS VAC19 (n=174) prime | Closed to accrual | Canarypox vector (clade B Env, Gag, Pro, RT, Nef) | Sanofi Pasteur | ALVAC vCP1452 | |
| HVTN 042/ANRS VAC19 (n=174) boost | Closed to accrual | Lipopeptides (poly-epitopic: clade B Gag, Pol, New) | Sanofi Pasteur/ANRS | LIPO-5 | |
| HVTN 049 (n= 96) prime | Closed to accrual | DNA plasmids (clade B Gag, Env) | Chiron | Gag and Env DNA/PLG microparticles | PLG |

| | | | | | |
|-------------------------------------|----------------------|---|--------|--|--|
| HVTN 049 (n=96) boost | Closed to accrual | Protein subunit (clade B Env) | Chiron | Oligomeric, V2-deleted HIV gp140 SF-162 | |
| HVTN 050/Merck 018 (n=435) | Closed to accrual | Nonreplicating adenoviral vector (clade B Gag) | Merck | MRKAd5 HIV-1 Gag | |
| HVTN 063 (n=156) prime | Enrolling | DNA plasmids (clade B Gag) | Wyeth | GENEVAX gag-2962 | DNA plasmid cytokine (IL-15) + bupivacaine |
| HVTN 063 (n=156) boost | Enrolling | Peptides (polyepitopic: clade B Env, Gag, Nef) | Wyeth | Wyeth multiepitope CTL peptide vaccine | RC529-SE, GM-CSF |

Table 4. Planned Trials: Phase I

| Protocol Number | Anticipated Start Date | Class | Producer | Product | Adjuvant |
|---------------------|---------------------------|--|-----------------------|------------------------|----------|
| HVTN 066 (n=132) | 2008 | VEE vectors (clade C Env, Gag-Nef-Pol) | AlphaVax | AVX-201 | |
| HVTN 067 (n=108) | Q2 2007 | DNA plasmid (polyepitopic: Gag, Pol, Vpr, Nef, Rev, Env) | Pharmexa- Epimmune | EP HIV- 1233 | |
| HVTN 071 (n=60) | Q2 2007 | Nonreplicating adenoviral vectors (clade type 5 B Gag, Pol, Nef) | Merck | MRKAd5 | |
| HVTN 072 (n=204) | Q3 2007 | DNA plasmids (clade A Env) | NIH VRC | VRC- HIVDNA- 044 | |

Table 5. Completed Trials

| Protocol Number | Start Date | Class | Producer | Product | Adjuvant |
|--------------------|------------|--|-----------------|-----------------------|----------|
| HVTN 041 (n=84) | 2003 | Protein (clade B Nef-Tat fusion protein + clade B Env subunit) | GlaxoSmithKline | NefTat + gp120W61D | AS02A |
| HVTN 040 (n=48) | 2005 | VEE vector (clade C Gag) | AlphaVax | AVX-101 | |

| | | | | | |
|--------------------|------|--|-----------------------|---|--|
| HVTN 048 (n=42) | 2005 | DNA plasmid (poly- epitopic: Gag, Pol, Vpr, Nef, Rev, and Env) | Pharmexa- Epimmune | EP HIV- 1090 | |
| HVTN 056 (n=96) | 2006 | Peptides (poly- epitopic: clade B Env, Gag, Nef) | Wyeth | Wyeth multiepitope CTL peptide vaccine | RC-529-SE, GM-CSF |
| HVTN 059 (n=96) | 2006 | VEE vector (clade C Gag) | AlphaVax | AVX-101 | DNA plasmid cytokine (IL2-Ig) |
| HVTN 044 (n=70) | 2006 | DNA plasmids (clade B Gag- Pol-Nef; clade A,B,C Env) | NIH VRC | VRC- HIVDNA- 009 | |

FUTURE CONCEPTS IN THE PIPELINE

• DNA VACCINE STRATEGY

In addition to the use of DNA for priming individuals before boosting with recombinant virus vectors, DNA plasmids encoding HIV derived genes are used as primer for subsequent envelope subunit protein administration and are given along with plasmids encoding the IL-2-Ig fusion proteins as adjuvant. The antigen is presented by both MHC class I and class II molecules, stimulating various immune responses. They induce cytotoxic T-cell responses which are of relatively low magnitude at least in absence of adjuvants. In monkey studies boosting with viral vectors expressing the same SIV antigens encoded in a DNA priming sequence showed an increased magnitude of CD8 responses (33-34).

SYNTHETIC PEPTIDES

Peptides are also used as immunogens because they are safe, prepared in large quantities, relatively inexpensive, free of contaminating host materials, induction of specific immune response and multiple epitopes with required immunogenic properties formulated solely. The disadvantage of this approach is the narrow size of the antigenic sites and low immunogenicity of peptides as that of complex antigens (32). The various approaches utilized to produce peptide immunogens as candidate AIDS vaccines are:

- Peptides based on the V3 loop sequence from one or multiple strains and covalently linked to an oligolysine backbone formulated with alum, which was not immunogenic in humans (35).
- To synthesize a hybrid linear peptide consisting of helper T-cell, B-cell, CTL epitopes formulated in incomplete Freund's adjuvant and was found immunogenic but caused sterile abscess in some subjects, hence the trial was stopped immediately (36).
- Peptides based on the highly conserved caveolin-I binding domains of HIV-1 gp41 in vaccine candidates. But the antibodies against the caveolin-1 binding domain are rare in

many HIV infected individuals, due to the presence of the hyper variable immunodominant epitopes (37).

VECTOR VACCINE STRATEGY

1. LIVE RECOMBINANT VIRUS VECTORS

Adenovirus vectors are used mostly because of the feasibility of oral delivery with gut replication, induction of systemic and mucosal immunity after a single oral dose and can be used safely for the prevention of respiratory diseases. Other viral vectors which are used are polio, influenza, rhinovirus and hepatitis B chimeras (38).

The advantages of using viral vectors lies in the fact that immunogens can be presented in the course of natural infection, antigens processed and presented in the form of MHC class-I molecules leading to CTL responses, multiple antigens may be simultaneously expressed, administration routes are simple and production and delivery inexpensive. The major limitations of these viruses are the amount of foreign genome that can be accommodated and the virulence properties of the parent vector (32).

2. LIVE RECOMBINANT BACTERIAL VECTORS

Attenuated *Salmonella* has been used as a vaccine vehicle for delivering recombinant HIV antigens or recombinant plasmid DNA. *Listeria monocytogenes* is another potential vector. They possess the similar advantages as that of a live virus vector but the post translational processing of the viral protein differs from that of mammalian processes and the induction of MHC class I restricted CTL responses are less efficient (39).

3. REPLICATION INCOMPETENT VIRUS BASED VECTORS.

The advantages of these vectors lie in their unique abilities to target specialized antigen presenting cells. A vaccine expressing gag from HIV-1 clade C isolate in *Venezuelan equine encephalitis* (VEE) virus is prepared and sent for clinical testing (40). Adeno-associated virus and replication defective *Herpes simplex* virus are also the favored approaches (41).

4. REPLICATION DEFECTIVE FUNGI VECTORS

Heat killed recombinant *Saccharomyces cerevisiae* represents a novel vaccine strategy for the delivery of the HIV vaccine antigens. Whole recombinant *Saccharomyces cerevisiae* yeast expresses HIV-1 antigens and potently induces antigen-specific, CTL responses, in vaccinated animals. Interactions between yeast and Dendritic cells(DC) led to DC maturation, IL-12 production and the efficient priming of MHC class I- and class II-restricted, antigen-specific T-cell responses. Yeast exerted a strong adjuvant effect, augmenting DC presentation of exogenous whole-protein antigen to MHC class I- and class II-restricted T cells (42).

NEW SUBUNIT PROTEIN VACCINE STRATEGY

The product from Chiron Corporation derived from primary HIV isolate SF162 is based on V2 deleted gp140 envelope construct and ready for clinical trials. There are also other groups pursuing methods to present a "receptor-triggered" envelope conformation to the immune system. Recently, a construct containing CD4-gp120-*env* single chain fusion protein has shown to elicit neutralizing

antibody response to some extent in mice and Rhesus macaques (43). Another vaccine approach involved the use of tat protein as an immunogen. Glaxo-Smithkline has developed a nef-tat fusion protein in combination with a monomeric rgp120 protein, evaluated in clinical trials (44).

MONOCLONAL ANTIBODY APPROACH

Antibodies that bind to epitopes overlapping the CD4-binding site (CD4bs) on gp120 can prevent HIV entry by competing with cell-associated CD4; their ability to outcompete CD4 is a major determinant of their neutralizing potency and is proportional to their avidity. Because CD4bs is highly conserved, it is reasonable to hypothesize that antibodies closely mimicking CD4 could exhibit relatively broad cross-reactivity and a high probability of preventing the emergence of resistant viruses. This approach was taken up by structurally imitating the CD4 molecule by a cross reactive HIV-1 neutralizing antibody with complementarity determining regions (CDRs) i.e.CDR-H2 and H3 possessing unique motifs. Prabhakaran *et al* carried out a study on the crystal structure of Fab m18 at 2.03Å resolution, revealing the unique conformation of heavy chain CDR2 and 3 (H2&H3). It shows striking similarity to the Ig CDR2 like C'C'' region of the CD4 first domain D1, involved with the binding of CD4 to gp120. Docking simulations suggested significant similarity between the m18 epitopes and the CD4 binding site (CD4bs) on gp120. Thus, vaccine immunogens can be based on the m18 epitope structure (45).

CONCLUSION

Despite limited progress toward the goal of developing a safe and effective AIDS vaccine, several encouraging developments have taken place over the past several years. Although there is still considerable debate about the mechanisms of protective immunity, there is now an emerging consensus that a successful AIDS vaccine should be able to induce both CTL and antibody responses able to neutralize primary viral isolates. The National Institutes of Health have recently embarked on an expanded effort to accelerate AIDS vaccine development, which has emphasized development of novel vaccine approaches. Despite these encouraging advances, considerable challenges remain, and substantial progression must still be made to develop a safe and effective AIDS vaccine.

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