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Neutralizing and other antiviral antibodies in HIV-1 infection and vaccination

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Abstract

Purpose of review—New findings continue to support the notion that broadly crossreactive neutralizing antibody induction is a worthwhile and achievable goal for HIV-1 vaccines. Immunogens are needed that can overcome the genetic variability and complex immune evasion tactics of the virus. Other antibodies might bridge innate and acquired immunity for possible beneficial vaccine effects. This review summarizes progress made over the past year that has enhanced our understanding of humoral immunity as it relates to HIV-1 vaccine development.

Recent findings—Although a clear path to designing an effective neutralizing antibody-based HIV-1 vaccine remains elusive, there is new information on how antibodies neutralize HIV-1, the epitopes involved, and clues to the possible nature of protective immunogens that keep this goal alive. Moreover, there is a greater understanding of HIV-1 diversity and its possible limits under immune pressure. Other antibodies might possess antiviral activity by mechanisms involving Fc receptor engagement or complement activation that would be of value for HIV-1 vaccines.

Summary—Recent developments strengthen the rationale for antibody-based HIV-1 vaccine immunogens and provide a stronger foundation for vaccine discovery.

Keywords

adjuvants; AIDS; antibodies; complement; Fc receptors; vaccines

Introduction

Neutralizing antibodies (NAbs) remain a major focus for HIV-1 vaccine development. In addition to a strong association with the success of many approved vaccines [1], NAbs are the only known immune response that has proved capable of completely blocking AIDS virus infection in animal models [2]. New evidence suggests that NAbs might also protect against HIV-1 superinfection in humans [3^{*}], and there is increasing evidence that maternal NAbs can protect against perinatal HIV-1 transmission [4^{**},5^{**}]. In principle, vaccine-elicited NAbs of sufficient quantity, breadth and duration could confer long-term sterilizing immunity in a large segment of the human population. In cases in which complete protection is not achieved, NAbs might assist in blunting peak viremia and lowering the viral setpoint [6^{*}], thereby making it less likely that an infected individual will develop disease and

transmit virus, especially if vaccine-elicited antiviral T-cell responses are also present [7]. What has dampened the prospects for an effective NAb-based vaccine is the extraordinary degree of genetic diversity and structural complexity exhibited by the HIV-1 envelope glycoproteins (Env) [8,9]. The results of recent studies are helping to shape the rationale for novel HIV-1 vaccine designs.

Neutralizing antibodies in HIV-1 infection

Previous studies in HIV-1-infected patients who were treated with highly active antiretroviral therapy suggested that a threshold level of viremia is needed to drive NAb production [10,11]. In support of this, low levels of NAbs were seen in a distinct subset of long-term non-progressors ('elite suppressors') who maintained viral loads of less than 50 copies/ml without antiretroviral therapy [12]. In another recent study [13], the magnitude of neutralization against heterologous viruses was predicted by the level of viremia in chronically infected individuals. Overall, the NAb response in HIV-1-infected individuals exhibits wide variation in kinetics, magnitude and breadth, but one pattern that is uniform is the substantial delay in NAb production relative to peak viremia after primary infection [14–16]. In general, the earliest NAb response is detected after 3–12 months of infection, and is highly specific for the corresponding early virus variant for up to 2 years of infection. Soon after these NAbs are generated, the virus mutates to evade them, and new serum antibodies slowly emerge that neutralize the escape variant [17–19].

Recent evidence suggests that there are constraints on both the number of escape cycles and the specificity of escape in HIV-1-infected individuals [13,20]. Although the virus ultimately wins the battle in most individuals, there is hope that previous vaccination will tip the balance in favor of the host. In this regard, viral evolution through multiple rounds of escape could be a driving force that explains the gradual broadening of serum neutralizing activity over time. Serum from approximately 10% of chronically infected individuals thus contains moderate titers of NAbs against a wide spectrum of viral variants across multiple genetic subtypes [15,21,22]. Of greater interest, serum from approximately 2% of chronically infected individuals contains high titers of broadly crossreactive NAbs (D.C. Montefiori, unpublished). Assuming that NAbs will have greater value either before infection or during acute infection, the neutralizing activity of serum from some HIV-1-positive individuals is evidence that effective NAb induction should be possible by vaccination with the right immunogen. The nature and specificity of the NAb response in these rare HIV-1-infected individuals are thus of considerable interest for vaccine development [23]. In addition, viruses from these individuals are of potential interest as novel vaccine immunogens [24].

The reasons why most HIV-1-infected individuals do not mount a more vigorous NAb response are poorly understood. In some cases, highly conserved and well exposed neutralization epitopes might be autoantigenic and subject to B cell tolerance [25]. In other cases, chronic B-cell activation by gp120 [26] and, perhaps more importantly, by microbial translocation from the gastrointestinal tract [27], could be contributing factors. It is also possible that sufficient numbers of cross-neutralizing epitopes on Env, particularly across HIV-1 genetic subtypes, either do not exist or perhaps we lack suitable antibody reagents to identify them. Such differences have previously been highlighted using monoclonal antibodies (MAbs), some of which fail to neutralize non-B subtypes because the epitopes are not present [28,29].

Other potential antiviral antibodies

Despite a delay in NAb production after primary HIV-1 infection, Env-specific binding antibodies are detected very early, and often coincide with the decline in peak plasma

viremia to setpoint levels. These antibodies have the potential to bind exposed epitopes on non-functional Env proteins on the virus surface [30*], where they could mediate biological activities related to Fc receptor (FcR) engagement or complement activation that might either curb or exacerbate disease [31]. HIV-1-positive serum and human MAbs with weak or no detectable neutralizing activity in a conventional peripheral blood mono-nuclear cell (PBMC)-based assay were recently found to possess potent antiviral activity when assayed in immature dendritic cells and macrophages [32*,33**]. This activity was Fc γ receptor-dependent and did not require natural killer cells. The authors proposed that such 'non-neutralizing inhibitory antibodies' might lead to endocytosis and the degradation of opsonized HIV-1 particles as a possible means of protecting against mucosal transmission. In another recent study [34*], the preactivation of monocyte-derived macrophages through the ligation of either Fc γ RI, Fc γ RIIa or Fc γ RIII by an unrelated immune complex led to the inhibition of HIV-1, HIV-2, SIVmac and SIVagm infection at a late stage in the virus replication cycle. The mechanism of virus inhibition in that case could not be identified, but it appeared to be unrelated to cytokine production.

Other antibodies might mediate antibody-dependent cellular cytotoxicity (ADCC) as an immune mechanism that results in the clearance of infected cells. Both acquired and innate immunity contribute to ADCC: acquired immunity provides cytophilic antibodies, whereas innate immunity provides the effector cell populations represented by Fc γ R-bearing granulocytes, natural killer cells, monocytes, macrophages and subsets of $\gamma\delta$ T cells. The engagement of Fc γ R on effector cells brings about the release of perforins and granzymes that destroy infected cells [35]. The humoral immune response in HIV-1 infection includes the early production of antibodies that can mediate ADCC [36,37], when the appearance of ADCC-mediating antibodies precedes the NAb response [38].

ADCC has received little attention for HIV-1 in the past, but this is changing as scientists seek to identify a clear correlate of immunity in non-human primate models of candidate AIDS vaccines. Of potential importance, broadly crossreactive ADCC responses can be elicited by current HIV-1 Env immunogens [39*]. Moreover, there was a correlation between ADCC and the partial control of acute viremia in a recent SIVmac vaccine study in which no NAb against the challenge virus were detected [40]. The authors took this latter observation one step further by purifying high titer ADCC-mediating IgG from the immunized animals, and found that passive infusion of this material into neonatal macaques was not sufficient to protect against oral SIV exposure [41]. This disappointing outcome might be explained by an immature neonatal immune system or by other differences in the design of the two studies. Notably, the passive transfer of non-neutralizing antibodies has provided protection in a similar neonatal model (see below) [42].

The antibody-mediated activation of monocytes, macrophages and natural killer cells through Fc γ R not only leads to the killing of infected cells, but can also lead to the release of cytokines and chemokines that can affect virus replication. Forthal and colleagues [43*] recently described how human and rhesus PBMCs depleted of CD8 and CD14 cells inhibit SIVmac251 in the presence of non-neutralizing antibodies. This inhibition involved both cytolytic and non-cytolytic mechanisms and was termed antibody-dependent cell-mediated virus inhibition (ADCVI). The study also showed that a non-neutralizing SIV-antibody-positive serum that protected neonatal macaques after oral SIVmac251 challenge contained potent ADCVI activity, suggesting that the activity is relevant *in vivo*. Potent ADCVI activity was also present in a separate non-protective passive IgG study [41].

Interactions between HIV-1 and complement also received attention during the past year. Two studies were published suggesting that HIV-1 is sensitive to complement-mediated lysis and destruction in the presence of antibody. In one study [44], Env-specific antibodies

that were detected before autologous NABs during peak viral load in primary HIV-1 infection caused viral lysis and inactivation through the classical complement pathway. Complement-mediated inactivation in that case was seen with both autologous and heterologous viruses that were made and assayed in non-lymphoid cells. Notably, no effect was observed when PBMC-grown virus was used. In a second study [45*], non-neutralizing antibodies caused complement-mediated lysis and the inactivation of autologous PBMC-grown virus that correlated with lower plasma viral loads during acute infection.

The results of both studies need to be weighed against strong evidence that HIV-1 evades complement lysis by acquiring complement regulatory proteins as it buds from the host cell membrane [31]. These proteins, which include CD46, CD55 and CD59, are differentially expressed on various cell types and act by blocking activation of the terminal complement pathway that is needed for formation of the membrane attack complex. At the very least, both studies mentioned above indicated that HIV-1-specific complement-activating antibodies are produced very early in infection. The role these antibodies play is uncertain and could involve either virus opsonization or viral lysis by complement [31]. As suggested recently [46**], any role for complement-opsonized HIV-1 is likely to involve interactions with CR2 (CD21)-expressing cells (e.g. B cells, follicular dendritic cells) more so than interactions with CR1 (CD35) on erythrocytes as proposed earlier [47].

Neutralization requirements and mechanisms

Recent progress has been made in understanding the mechanisms of, and requirements for, antibody-mediated HIV-1 neutralization. Crooks *et al.* [48] described a creative set of assays designed to determine the specific stage in virus entry that is targeted by a particular NAB. It was confirmed that all three major stages are potential targets: (1) gp120 binding to its CD4 cell receptor; (2) subsequent binding of gp120 to either its CCR5 or CXCR4 co-receptor; and (3) gp41-mediated membrane fusion. Moreover, relevant NABs in HIV-1-infected individuals targeted early steps in receptor binding. These assays will be useful in dissecting vaccine-elicited NAB responses and for gaining a better understanding of effective NAB induction. In another recent study [49*], neutralization potency appeared to be influenced by the levels of CCR5 but not CD4 cell expression. Therefore, unusually high levels of CCR5 on genetically engineered cell lines might explain, at least partly, several rare occasions in which a new generation of assays failed to detect neutralization that is readily detected in PBMC assays [50].

Three studies published in 2006 advanced our understanding of the requirements for neutralization. In one study [51*], the introduction of an unrelated epitope into the gp120 V4 region of multiple viral variants was used to show that HIV-1 is not intrinsically resistant to neutralization and that neutralization potency is directly related to the affinity of antibody binding. In a second study [52*], pseudoviruses containing phenotypically mixed Env trimers were used to confirm that antibodies must bind functional trimers in order to neutralize, where binding to a single monomer in each functional trimer on the virus is effective. In a third study [53*], the potency of NABs against the receptor-binding domain of gp120 was related to the number of different conformational states of monomeric and trimeric gp120 the antibody could bind.

Env structure and neutralization avoidance

It has long been recognized that HIV-1 rapidly evolves to escape autologous NABs, explaining why the response fails to contain the virus. Insights into how escape occurs first emerged when variable loop deletions and the removal of certain N-linked glycans on gp120 revealed complex structure-based epitope-masking mechanisms. Additional insights were provided by crystal structures of liganded HIV-1 gp120 core molecules and later by crystal

structures of an unliganded SIV gp120 core molecule, showing how one of the most critical regions for neutralization, the CD4 cell binding site, resides in a recessed pocket that is predicted to be poorly accessible to many antibodies. HIV-1 also imposes entropic barriers to antibodies in the context of a conformationally flexible Env. Excellent reviews on how HIV-1 uses these structural features and entropic barriers to evade NABs have been published [8,9].

Last year saw the first descriptions of the three-dimensional structure of Env trimer spikes, as visualized on the surface of HIV-1 and SIV by cryoelectron microscopy tomography. Those studies are important because they permit unmodified Env trimers to be examined in their prefusion state as the natural targets for NABs. One group [54**] reported a deduced structural model of trimeric gp120 that fit well with the crystal structure of an unliganded SIV core gp120 molecule in a profile that resembled a tri-lobed head with an arched apical peak. The most striking finding in that study was that each gp41 monomer in a trimer spike had a 'leg' and a 'foot' that protruded away from the gp120 head in a tripod fashion and anchored distally in the membrane. Using similar methods, a second group [55**] described a 'mushroom' shaped spike with a compact gp41 'stem' in which no separation of gp41 monomers was observed. These opposing models of trimeric gp41 are difficult to explain [56*] and will be important to resolve. For example, a clear model of native gp41 structure might help to explain why some neutralizing antibodies can bind gp41 after virus attachment [48], whereas neutralization epitopes on gp120 are poorly accessible at the virus-cell interface [57].

Genetic and antigenic properties of early transmitted viruses

Viruses transmitted either heterosexually or through homosexual contact, and those transmitted from mother to child via breast-feeding, are primary targets for vaccine-elicited antibody responses. It is possible that the bottleneck that occurs at transmission, when no NABs are present, selects viruses that show differences in receptor affinities, Env structure, and replication fitness that impact certain neutralization epitopes. Recent studies have thus suggested that early transmitted viruses (ETVs) of subtypes A and C possess unique genetic and antigenic properties, including shorter variable loops and fewer predicted *N*-linked glycans, which might provide less cloaking of neutralization-sensitive targets [58*,59*,60]. Another recent study suggested that these differences might be greater between newly transmitted subtype B and C viruses than between early and late viruses within each subtype [61**]. Although it is not entirely clear that ETVs exhibit greater overall sensitivity to neutralization compared with late viruses, the observation that some ETVs from sexually acquired subtype C infections are more sensitive to neutralization by autologous transmitter plasma compared with the major viral variant in the transmitter [62] suggests that neutralization-escape comes at a cost to transmission fitness. This is not seen in perinatally infected infants, probably because transmission in that case occurs in the presence of maternal NABs [4**,5**]. It might be that genetic subtype as well as the route of infection play a role in determining the variants that are transmitted. Whether the higher levels of NABs seen in HIV-1 subtype C-infected patients are caused by an inherent sensitivity of transmitted subtype C viruses or a greater immunogenicity of subtype C Env remains to be determined, as does the impact this will have on vaccine design [58*].

Subtype-specific virus panels for measuring antibody neutralization

Over the past few years a number of virus panels have been compiled in an attempt to standardize the measurement of antibody-mediated neutralization, particularly in vaccine trials. The use of molecularly cloned Env-pseudotyped viruses in luciferase reporter gene assays has facilitated the reproducibility and overall accuracy of measuring antibody-

mediated neutralization, and has provided higher throughput and lower cost. Moreover, in most cases this assay detects the same antibody specificities as the PBMC assay but with slightly greater sensitivity. The use of this assay in a three-tiered approach is now the recommended format for assessing vaccine-elicited NAb responses, with a focus on primary viruses from multiple subtypes that comprise tier 2 and tier 3 reference strains [63]. A subtype B and African subtype C panel of reference strains from acute and early sexually acquired infections have recently been developed and are available through the National Institutes of Health Reference and Reagent Repository [61,64]. Subtype C is the major global subtype, and therefore additional panels from India, China and possibly other African countries where subtype C dominates are urgently needed, as are panels of subtypes A, D, CRF01_AE and CRF02_AG. Collectively, this covers 90% of all HIV-1 strains worldwide. Viruses chosen for such panels need to be collected within 3 months of infection, transmitted sexually and not be unusually sensitive or resistant to neutralization. A rigorous and regular programme of proficiency testing will ensure adequate competency in laboratories around the world. It is possible that initial panels of reference strains will need to be modified as new information is gained on how to improve their correlative value.

Novel immunogen design and delivery

The failure of soluble monomeric gp120 immunogens to elicit NAbs against most primary HIV-1 isolates and to show efficacy in humans highlights the need for more creative immunogens [65]. In this regard, lead approaches focus on oligomeric Env immunogens that may more effectively present epitopes as they exist on native viral Env. One solution is to introduce a C-terminal trimeric GCN-4 transcription factor motif to form stable gp140 Env trimers. Recent studies have confirmed that these gp140 trimeric proteins elicit higher titers of NAbs than the corresponding monomeric gp120 [66]; however, further design modifications will be required to generate more broadly reactive NAbs. Env trimer construction often requires the elimination of the gp120–gp41 cleavage site to prevent subunit dissociation. A potential problem with this approach is that the uncleaved Env proteins are antigenically distinct from native cleaved Env. To circumvent this problem, Beddows and colleagues [67] constructed a gp140 Env with an intact cleavage site and stabilized the protein by introducing intermolecular disulfide bonds (SOS gp140) between gp120 and gp41. Both clade A and B SOS gp140s are being studied for immunogenicity.

Improving the breadth of the NAb response may also be possible by the inclusion of polyvalent Envs. In preclinical studies using DNA priming and oligomeric protein boosting, a combined clade B and C Env immunogen generated high titers of antibodies to both vaccine strains of virus [68]. Similarly, Wang and colleagues [69] used the DNA/protein platform to immunize rabbits with Envs from clades A, B, C, D, E, F and G. In both studies, NAbs against some non-clade B viruses were elicited but the total breadth of the NAb response remained limited. An alternative approach is to construct immunogens based on centralized (ancestral or consensus) Env sequences to minimize the genetic distance between vaccine strains. Such immunogens might elicit NAbs to conserved antibody determinants on Env. Initial centralized Env constructs based on group M and subtype C HIV-1 have been found to elicit both T-cell and antibody responses in small animals; further studies are ongoing [70]. Liao *et al.* [71] compared a group M consensus Env immunogen to wild-type Envs from clades A, B and C, and found the former to elicit NAb responses at least as good as any individual wild-type Env.

Although much of the existing effort towards improving NAb responses is based on novel immunogen design, there has been some progress in improving NAb responses by using prime-boost delivery platforms and through the use of adjuvants. Several recent studies have confirmed that either plasmid DNA or recombinant adenovirus immunization effectively

primes for soluble protein boosting and results in high titers of NAbs [68,69,72]. In addition, the co-delivery of granulocyte macrophage colony-stimulating factor DNA with Env DNA in monkeys led to a more rapid and higher avidity antibody response than Env DNA without adjuvant [73]. For soluble trimeric protein, use of the GSK series of adjuvants (AS01B, AS02A and AS03; Glaxo-SmithKline Biologicals, Rixensart, Belgium) generated higher titer NAb responses than a commercially available Ribi adjuvant [66].

Neutralization epitope mapping

Improved Env designs could be guided by assays that not only measure virus neutralization but, more specifically, what epitopes those NAbs target. Several groups of investigators have begun to analyze vaccine sera to understand better the antibody specificities generated. Three papers published last year reported that vaccine-elicited autologous virus neutralization was mediated by NAbs against the V1 region of gp120 [66,74,75]. Interestingly, all three groups identified the same hypervariable region at the tip of the V1 loop. Whether or not some common and partly conserved motifs exist in V1 that could serve as a useful vaccine antigen remains to be determined.

Antibodies against the V3 region of gp120 are also readily generated by many Env immunogens. Anti-V3 antibodies have inherent limitations because the V3 region of most HIV-1 strains is not accessible. Nonetheless, a minority of HIV-1 isolates, probably 10–15%, are sensitive to V3 MAbs. Efforts to optimize the NAb response against V3 include protein scaffolds that present the known V3 MAb 447–52D epitope [76] and specific design modifications to stabilize and increase the immunogenicity of V3 [74,75]. A potentially interesting observation is that anti-V3 antibodies derived from non-clade B-infected patients, or non-clade B immunization, might be more crossreactive than anti-V3 antibodies from clade B HIV-1-infected subjects [74,77].

As new assays to map neutralization epitopes become more refined, they may be applied to sera from HIV-1-infected patients, particularly those who possess broadly NAbs. Such studies might provide insight about how neutralization breadth can be achieved. For example, it is not known whether broadly neutralizing sera target conserved Env regions or contain polyclonal antibodies that target several variable neutralization epitopes simultaneously. One study of 92 HIV-1-positive plasma samples found little or no reactivity to the membrane proximal external region of HIV-1 gp41 engrafted into SIV [78*], whereas another study found that cloned viral Envs from two patients with broadly neutralizing sera developed mAb 2F5 and 4E10 escape mutations, suggesting that NAbs to the membrane proximal external region may play a role in driving virus evolution [24]. Decker *et al.* [79] used non-conventional strains of HIV-2 to show that sera from HIV-1-infected individuals contain high titers of antibodies against highly conserved neutralization epitopes in the co-receptor binding domain of gp120. Unfortunately, these epitopes are poorly exposed on most strains of the virus [57,61**]. Further studies of broadly neutralizing sera will be required to understand how neutralization breadth is achieved in natural HIV-1 infection.

Conclusion

Two decades of intensive research have failed to yield an effective antibody-based HIV-1 vaccine. Despite the obstacles towards effective Env vaccine design, new evidence has emerged to support the notion that NAbs and possibly other types of antiviral antibodies are indeed worth pursuing. The field continues to make progress in understanding viral Env structure and to engage in a combination of empirical and rational approaches to immunogen design. The interface of these approaches may yet yield an effective vaccine. Future prospects would benefit from progress in a number of key areas: (1) detailed studies of

ETVs from the major genetic subtypes derived from multiple routes of infection, including breast-milk transmissions; (2) the crystal structure of native unliganded trimeric Env as well as gp120 structures from non-B subtypes; (3) broadly neutralizing MAbs with novel specificities, including specificities that are both immunogenic and antigenic; (4) additional assays to scrutinize the epitope specificities of NABs generated by infection and vaccination; (5) better adjuvants; (6) closer inspection of non-neutralizing antibodies; and (7) a greater understanding of the ontogeny of the B-cell response to HIV-1 Env, including host genetic factors.

Abbreviations

ADCC	antibody-dependent cellular cytotoxicity
ADCVI	antibody-dependent cell-mediated virus inhibition
ETV	early transmitted virus
MAb	monoclonal antibody
NAb	neutralizing antibody
PBMC	peripheral blood mononuclear cell

References and recommended reading

Papers of particular interest, published within the annual period of review, have been highlighted as:

- of special interest
- of outstanding interest

Additional references related to this topic can also be found in the Current World Literature section in this issue (pp. 241–242).

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